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Sir:

Transmitted herewith for filing is the patent application of:

Inventors: Markus Pompejus *et al.*

For: *"Corynebacterium Glutamicum Genes Encoding Proteins Involved in Homeostasis and Adaptation"*

Enclosed are:

- ☒ 69 pages of specification, 5 pages of claims and 1 page of abstract;
- ☒ 7 pages of Table 1;
- ☒ 16 pages of Table 2;
- ☒ 6 pages of Table 3;
- ☒ 18 pages of Table 4;
- ☒ 164 pages of Appendix A;
- ☒ 53 pages of Appendix B;
- ☒ 676 pages of Sequence Listing;
- ☒ Zip Disk Containing Sequence Listing;
- ☒ Transmittal Letter for Zip Disk Containing Sequence Listing;
- ☒ An *unexecuted* Declaration, Petition and Power of Attorney;
- ☒ A pre-paid acknowledgment postcard.

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☐ A check in the amount of $_____ to cover the recording of assignment documents is also enclosed.

☒ Address all future communications (May only be completed by applicant, or attorney or agent of record) to **Elizabeth A. Hanley, Esq. at Customer Number: 000959** whose address is:

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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION

Related Applications

This application claims priority to prior filed U.S. Provisional Patent Application Serial No. 60/141031, filed June 25, 1999, U.S. Provisional Patent Application Serial No. 60/143694, filed July 14, 2000, and U.S. Provisional Patent Application Serial No. 60/151778, filed August 31, 1999. This application also claims priority to German Application No. 19931418.7, filed July 8, 1999, German Application No. 19932124.8, filed July 9, 1999, German Application No. 19932126.4, filed July 9, 1999, German Application No. 19932127.2, filed July 9, 1999, German Application No. 19932133.7, filed July 9, 1999, German Application No. 19932207.4, filed July 9, 1999, German Application No. 19932208.2, filed July 9, 1999, German Application No. 19932225.2, filed July 9, 1999, German Application No. 19932229.5, filed July 9, 1999, German Application No. 19932914.1, filed July 9, 1999, German Application No. 19933006.9, filed July 9, 1999, German Application No. 19940765.7, filed August 27, 1999, German Application No. 19940768.1, filed August 27, 1999, German Application No. 19940831.9, filed August 27, 1999, German Application No. 19940832.7, filed August 27, 1999, German Application No. 19941385.1, filed August 31, 1999, German Application No. 19941396.7, filed August 31, 1999, and German Application No. 19942087.4, filed September 3, 1999. The entire contents of all of the aforementioned applications are hereby expressly incorporated herein by this reference.

Background of the Invention

Certain products and by-products of naturally-occurring metabolic processes in cells have utility in a wide array of industries, including the food, feed, cosmetics, and pharmaceutical industries. These molecules, collectively termed 'fine chemicals', include organic acids, both proteinogenic and non-proteinogenic amino acids, nucleotides and nucleosides, lipids and fatty acids, diols, carbohydrates, aromatic compounds, vitamins and cofactors, and enzymes. Their production is most conveniently performed through the large-scale culture of bacteria developed to produce and secrete large quantities of one or more desired molecules. One particularly useful organism for this purpose is *Corynebacterium glutamicum*, a gram positive, nonpathogenic bacterium. Through strain selection, a number of mutant strains have been developed which produce an array of desirable compounds. However, selection of strains improved for the production of a particular molecule is a time-consuming and difficult process.

Summary of the Invention

The invention provides novel bacterial nucleic acid molecules which have a variety of uses. These uses include the identification of microorganisms which can be used to produce fine chemicals, the modulation of fine chemical production in *C. glutamicum* or related bacteria, the typing or identification of *C. glutamicum* or related bacteria, as reference points for mapping the *C. glutamicum* genome, and as markers for transformation. These novel nucleic acid molecules encode proteins, referred to herein as homeostasis and adaptation (HA) proteins.

C. glutamicum is a gram positive, aerobic bacterium which is commonly used in industry for the large-scale production of a variety of fine chemicals, and also for the degradation of hydrocarbons (such as in petroleum spills) and for the oxidation of terpenoids. The HA nucleic acid molecules of the invention, therefore, can be used to identify microorganisms which can be used to produce fine chemicals, *e.g.*, by fermentation processes. Modulation of the expression of the HA nucleic acids of the invention, or modification of the sequence of the HA nucleic acid molecules of the invention, can be used to modulate the production of one or more fine chemicals from a microorganism (*e.g.*, to improve the yield or production of one or more fine chemicals from a Corynebacterium or Brevibacterium species).

The HA nucleic acids of the invention may also be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof, or to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to species pathogenic in humans, such as *Corynebacterium diphtheriae* (the causative agent of diphtheria); the detection of such organisms is of significant clinical relevance.

The HA nucleic acid molecules of the invention may also serve as reference points for mapping of the *C. glutamicum* genome, or of genomes of related organisms. Similarly, these molecules, or variants or portions thereof, may serve as markers for genetically engineered Corynebacterium or Brevibacterium species.

The HA proteins encoded by the novel nucleic acid molecules of the invention are capable of, for example, performing a function involved in the maintenance of homeostasis in *C. glutamicum*, or in the ability of this microorganism to adapt to

different environmental conditions. Given the availability of cloning vectors for use in *Corynebacterium glutamicum*, such as those disclosed in Sinskey *et al.*, U.S. Patent No. 4,649,119, and techniques for genetic manipulation of *C. glutamicum* and the related *Brevibacterium* species (*e.g.*, *lactofermentum*) (Yoshihama et al, *J. Bacteriol.* 162: 591-597 (1985); Katsumata *et al.*, *J. Bacteriol.* 159: 306-311 (1984); and Santamaria *et al.*, *J. Gen. Microbiol.* 130: 2237-2246 (1984)), the nucleic acid molecules of the invention may be utilized in the genetic engineering of this organism to make it a better or more efficient producer of one or more fine chemicals. This improved production or efficiency of production of a fine chemical may be due to a direct effect of manipulation of a gene of the invention, or it may be due to an indirect effect of such manipulation.

There are a number of mechanisms by which the alteration of an HA protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by engineering enzymes which modify or degrade aromatic or aliphatic compounds such that these enzymes are increased or decreased in activity or number, it may be possible to modulate the production of one or more fine chemicals which are the modification or degradation products of these compounds. Similarly, enzymes involved in the metabolism of inorganic compounds provide key molecules (*e.g.* phosphorous, sulfur, and nitrogen molecules) for the biosynthesis of such fine chemicals as amino acids, vitamins, and nucleic acids. By altering the activity or number of these enzymes in *C. glutamicum*, it may be possible to increase the conversion of these inorganic compounds (or to use alternate inorganic compounds) to thus permit improved rates of incorporation of inorganic atoms into these fine chemicals. Genetic engineering of *C. glutamicum* enzymes involved in general cellular processes may also directly improve fine chemical production, since many of these enzymes directly modify fine chemicals (*e.g.*, amino acids) or the enzymes which are involved in fine chemical synthesis or secretion. Modulation of the activity or number of cellular proteases may also have a direct effect on fine chemical production, since many proteases may degrade fine chemicals or enzymes involved in fine chemical production or breakdown.

Further, the aforementioned enzymes which participate in aromatic/aliphatic compound modification or degradation, general biocatalysis, inorganic compound metabolism or proteolysis are each themselves fine chemicals, desirable for their activity in various *in vitro* industrial applications. By altering the number of copies of the gene for one or more of these enzymes in *C. glutamicum* it may be possible to increase the number of these proteins produced by the cell, thereby increasing the potential yield or efficiency of production of these proteins from large-scale *C. glutamicum* or related bacterial cultures.

The alteration of an HA protein of the invention may also indirectly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by modulating the activity and/or number of those proteins involved in the construction or rearrangement of the cell wall, it may be possible to modify the structure of the cell wall itself such that the cell is able to better withstand the mechanical and other stresses present during large-scale fermentative culture. Also, large-scale growth of *C. glutamicum* requires significant cell wall production. Modulation of the activity or number of cell wall biosynthetic or degradative enzymes may allow more rapid rates of cell wall biosynthesis, which in turn may permit increased growth rates of this microorganism in culture and thereby increase the number of cells producing the desired fine chemical.

By modifying the HA enzymes of the invention, one may also indirectly impact the yield, production, or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, many of the general enzymes in *C. glutamicum* may have a significant impact on global cellular processes (*e.g.*, regulatory processes) which in turn have a significant effect on fine chemical metabolism. Similarly, proteases, enzymes which modify or degrade possibly toxic aromatic or aliphatic compounds, and enzymes which promote the metabolism of inorganic compounds all serve to increase the viability of *C. glutamicum*. The proteases aid in the selective removal of misfolded or misregulated proteins, such as those that might occur under the relatively stressful environmental conditions encountered during large-scale fermentor culture. By altering these proteins, it may be possible to further enhance this activity and to improve the viability of *C. glutamicum* in culture. The aromatic/aliphatic modification or degradation proteins not only serve to detoxify these waste compounds (which may be encountered as impurities in culture medium or as waste products from cells themselves), but also to permit the cells to utilize alternate carbon sources if the optimal carbon source is limiting in the culture. By increasing their number and/or activity, the survival of *C. glutamicum* cells in culture may be enhanced. The inorganic metabolism proteins of the invention supply the cell with inorganic molecules required for all protein and nucleotide (among others) synthesis, and thus are critical for the overall viability of the cell. An increase in the number of viable cells producing one or more desired fine chemicals in large-scale culture should result in a concomitant increase in the yield, production, and/or efficiency of production of the fine chemical in the culture.

The invention provides novel nucleic acid molecules which encode proteins, referred to herein as HA proteins, which are capable of, for example, performing a function involved in the maintenance of homeostasis in *C. glutamicum*, or of

participating in the ability of this microorganism to adapt to different environmental conditions. Nucleic acid molecules encoding an HA protein are referred to herein as HA nucleic acid molecules. In a preferred embodiment, an HA protein participates in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or possesses a *C. glutamicum* enzymatic or proteolytic activity. Examples of such proteins include those encoded by the genes set forth in Table 1.

Accordingly, one aspect of the invention pertains to isolated nucleic acid molecules (*e.g.*, cDNAs, DNAs, or RNAs) comprising a nucleotide sequence encoding an HA protein or biologically active portions thereof, as well as nucleic acid fragments suitable as primers or hybridization probes for the detection or amplification of HA-encoding nucleic acids (*e.g.*, DNA or mRNA). In particularly preferred embodiments, the isolated nucleic acid molecule comprises one of the nucleotide sequences set forth in Appendix A or the coding region or a complement thereof of one of these nucleotide sequences. In other particularly preferred embodiments, the isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes to or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80% or 90%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence set forth in Appendix A, or a portion thereof. In other preferred embodiments, the isolated nucleic acid molecule encodes one of the amino acid sequences set forth in Appendix B. The preferred HA proteins of the present invention also preferably possess at least one of the HA activities described herein.

In another embodiment, the isolated nucleic acid molecule encodes a protein or portion thereof wherein the protein or portion thereof includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B, *e.g.*, sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains an HA activity. Preferably, the protein or portion thereof encoded by the nucleic acid molecule maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. In one embodiment, the protein encoded by the nucleic acid molecule is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90% and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an amino acid sequence of Appendix B (*e.g.*, an entire amino acid sequence selected from those sequences set forth in Appendix B). In another preferred embodiment, the protein is a full length *C. glutamicum* protein which is substantially homologous to an entire

amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

In another preferred embodiment, the isolated nucleic acid molecule is derived from *C. glutamicum* and encodes a protein (*e.g.*, an HA fusion protein) which includes a biologically active domain which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1, and which also includes heterologous nucleic acid sequences encoding a heterologous polypeptide or regulatory regions.

In another embodiment, the isolated nucleic acid molecule is at least 15 nucleotides in length and hybridizes under stringent conditions to a nucleic acid molecule comprising a nucleotide sequence of Appendix A. Preferably, the isolated nucleic acid molecule corresponds to a naturally-occurring nucleic acid molecule. More preferably, the isolated nucleic acid encodes a naturally-occurring *C. glutamicum* HA protein, or a biologically active portion thereof.

Another aspect of the invention pertains to vectors, *e.g.*, recombinant expression vectors, containing the nucleic acid molecules of the invention, and host cells into which such vectors have been introduced. In one embodiment, such a host cell is used to produce an HA protein by culturing the host cell in a suitable medium. The HA protein can be then isolated from the medium or the host cell.

Yet another aspect of the invention pertains to a genetically altered microorganism in which an HA gene has been introduced or altered. In one embodiment, the genome of the microorganism has been altered by introduction of a nucleic acid molecule of the invention encoding wild-type or mutated HA sequence as a transgene. In another embodiment, an endogenous HA gene within the genome of the microorganism has been altered, *e.g.*, functionally disrupted, by homologous recombination with an altered HA gene. In another embodiment, an endogenous or introduced HA gene in a microorganism has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional HA protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an HA gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the HA gene is modulated. In a preferred embodiment, the microorganism belongs to the genus *Corynebacterium* or *Brevibacterium*, with *Corynebacterium glutamicum* being particularly preferred. In a preferred embodiment, the microorganism is also utilized for

the production of a desired compound, such as an amino acid, with lysine being particularly preferred.

In another aspect, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject.

Still another aspect of the invention pertains to an isolated HA protein or a portion, *e.g.*, a biologically active portion, thereof. In a preferred embodiment, the isolated HA protein or portion thereof can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different environmental conditions. In another preferred embodiment, the isolated HA protein or portion thereof is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions.

The invention also provides an isolated preparation of an HA protein. In preferred embodiments, the HA protein comprises an amino acid sequence of Appendix B. In another preferred embodiment, the invention pertains to an isolated full length protein which is substantially homologous to an entire amino acid sequence of Appendix B (encoded by an open reading frame set forth in Appendix A). In yet another embodiment, the protein is at least about 50%, preferably at least about 60%, and more preferably at least about 70%, 80%, or 90%, and most preferably at least about 95%, 96%, 97%, 98%, or 99% or more homologous to an entire amino acid sequence of Appendix B. In other embodiments, the isolated HA protein comprises an amino acid sequence which is at least about 50% or more homologous to one of the amino acid sequences of Appendix B and is able to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions, or has one or more of the activities set forth in Table 1.

Alternatively, the isolated HA protein can comprise an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, or is at least about 50%, preferably at least about 60%, more preferably at least about 70%, 80%, or 90%, and even more preferably at least about 95%, 96%, 97%, 98,%, or 99% or more homologous, to a nucleotide sequence of Appendix B. It is also preferred that the preferred forms of HA proteins also have one or more of the HA bioactivities described herein.

The HA polypeptide, or a biologically active portion thereof, can be operatively linked to a non-HA polypeptide to form a fusion protein. In preferred embodiments, this fusion protein has an activity which differs from that of the HA protein alone. In other preferred embodiments, this fusion protein participates in the maintenance of homeostasis in *C. glutamicum*, or performs a function involved in the adaptation of this microorganism to different environmental conditions. In particularly preferred embodiments, integration of this fusion protein into a host cell modulates production of a desired compound from the cell.

In another aspect, the invention provides methods for screening molecules which modulate the activity of an HA protein, either by interacting with the protein itself or a substrate or binding partner of the HA protein, or by modulating the transcription or translation of an HA nucleic acid molecule of the invention.

Another aspect of the invention pertains to a method for producing a fine chemical. This method involves the culturing of a cell containing a vector directing the expression of an HA nucleic acid molecule of the invention, such that a fine chemical is produced. In a preferred embodiment, this method further includes the step of obtaining a cell containing such a vector, in which a cell is transfected with a vector directing the expression of an HA nucleic acid. In another preferred embodiment, this method further includes the step of recovering the fine chemical from the culture. In a particularly preferred embodiment, the cell is from the genus *Corynebacterium* or *Brevibacterium*, or is selected from those strains set forth in Table 3.

Another aspect of the invention pertains to methods for modulating production of a molecule from a microorganism. Such methods include contacting the cell with an agent which modulates HA protein activity or HA nucleic acid expression such that a cell associated activity is altered relative to this same activity in the absence of the agent. In a preferred embodiment, the cell is modulated for one or more *C. glutamicum* processes involved in cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activities. The agent which modulates HA protein activity can be an agent which stimulates HA protein activity or HA nucleic acid expression. Examples of agents which stimulate HA protein activity or HA nucleic acid expression include small molecules, active HA proteins, and nucleic acids encoding HA proteins that have been introduced into the cell. Examples of agents which inhibit HA activity or expression include small molecules and antisense HA nucleic acid molecules.

Another aspect of the invention pertains to methods for modulating yields of a desired compound from a cell, involving the introduction of a wild-type or mutant HA gene into a cell, either maintained on a separate plasmid or integrated into the genome of

the host cell. If integrated into the genome, such integration can be random, or it can take place by homologous recombination such that the native gene is replaced by the introduced copy, causing the production of the desired compound from the cell to be modulated. In a preferred embodiment, said yields are increased. In another preferred embodiment, said chemical is a fine chemical. In a particularly preferred embodiment, said fine chemical is an amino acid. In especially preferred embodiments, said amino acid is L-lysine.

Detailed Description of the Invention

The present invention provides HA nucleic acid and protein molecules which are involved in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity. The molecules of the invention may be utilized in the modulation of production of fine chemicals from microorganisms, such as *C. glutamicum*, either directly (*e.g.*, where overexpression or optimization of activity of a protein involved in the production of a fine chemical (*e.g.*, an enzyme) has a direct impact on the yield, production, and/or efficiency of production of a fine chemical from the modified *C. glutamicum*), or an indirect impact which nonetheless results in an increase of yield, production, and/or efficiency of production of the desired compound (*e.g.*, where modulation of the activity or number of copies of a *C. glutamicum* aromatic or aliphatic modification or degradation protein results in an increase in the viability of *C. glutamicum* cells, which in turn permits increased production in a large-scale culture setting). Aspects of the invention are further explicated below.

I. Fine Chemicals

The term 'fine chemical' is art-recognized and includes molecules produced by an organism which have applications in various industries, such as, but not limited to, the pharmaceutical, agriculture, and cosmetics industries. Such compounds include organic acids, such as tartaric acid, itaconic acid, and diaminopimelic acid, both proteinogenic and non-proteinogenic amino acids, purine and pyrimidine bases, nucleosides, and nucleotides (as described *e.g.* in Kuninaka, A. (1996) Nucleotides and related compounds, p. 561-612, in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, and references contained therein), lipids, both saturated and unsaturated fatty acids (*e.g.*, arachidonic acid), diols (*e.g.*, propane diol, and butane diol), carbohydrates (*e.g.*, hyaluronic acid and trehalose), aromatic compounds (*e.g.*, aromatic amines, vanillin, and indigo), vitamins and cofactors (as described in Ullmann's Encyclopedia of

Industrial Chemistry, vol. A27, "Vitamins", p. 443-613 (1996) VCH: Weinheim and references therein; and Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press, (1995)), enzymes, polyketides (Cane *et al.* (1998) *Science* 282: 63-68), and all other chemicals described in Gutcho (1983) Chemicals by Fermentation, Noyes Data Corporation, ISBN: 0818805086 and references therein. The metabolism and uses of certain of these fine chemicals are further explicated below.

A. *Amino Acid Metabolism and Uses*

Amino acids comprise the basic structural units of all proteins, and as such are essential for normal cellular functioning in all organisms. The term "amino acid" is art-recognized. The proteinogenic amino acids, of which there are 20 species, serve as structural units for proteins, in which they are linked by peptide bonds, while the nonproteinogenic amino acids (hundreds of which are known) are not normally found in proteins (see Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97 VCH: Weinheim (1985)). Amino acids may be in the D- or L- optical configuration, though L-amino acids are generally the only type found in naturally-occurring proteins. Biosynthetic and degradative pathways of each of the 20 proteinogenic amino acids have been well characterized in both prokaryotic and eukaryotic cells (see, for example, Stryer, L. Biochemistry, 3rd edition, pages 578-590 (1988)). The 'essential' amino acids (histidine, isoleucine, leucine, lysine, methionine, phenylalanine, threonine, tryptophan, and valine), so named because they are generally a nutritional requirement due to the complexity of their biosyntheses, are readily converted by simple biosynthetic pathways to the remaining 11 'nonessential' amino acids (alanine, arginine, asparagine, aspartate, cysteine, glutamate, glutamine, glycine, proline, serine, and tyrosine). Higher animals do retain the ability to synthesize some of these amino acids, but the essential amino acids must be supplied from the diet in order for normal protein synthesis to occur.

Aside from their function in protein biosynthesis, these amino acids are interesting chemicals in their own right, and many have been found to have various applications in the food, feed, chemical, cosmetics, agriculture, and pharmaceutical industries. Lysine is an important amino acid in the nutrition not only of humans, but also of monogastric animals such as poultry and swine. Glutamate is most commonly used as a flavor additive (mono-sodium glutamate, MSG) and is widely used throughout the food industry, as are aspartate, phenylalanine, glycine, and cysteine. Glycine, L-methionine and tryptophan are all utilized in the pharmaceutical industry. Glutamine,

valine, leucine, isoleucine, histidine, arginine, proline, serine and alanine are of use in both the pharmaceutical and cosmetics industries. Threonine, tryptophan, and D/ L-methionine are common feed additives. (Leuchtenberger, W. (1996) Amino aids – technical production and use, p. 466-502 in Rehm *et al.* (eds.) Biotechnology vol. 6, chapter 14a, VCH: Weinheim). Additionally, these amino acids have been found to be useful as precursors for the synthesis of synthetic amino acids and proteins, such as N-acetylcysteine, S-carboxymethyl-L-cysteine, (S)-5-hydroxytryptophan, and others described in Ulmann's Encyclopedia of Industrial Chemistry, vol. A2, p. 57-97, VCH: Weinheim, 1985.

The biosynthesis of these natural amino acids in organisms capable of producing them, such as bacteria, has been well characterized (for review of bacterial amino acid biosynthesis and regulation thereof, see Umbarger, H.E.(1978) *Ann. Rev. Biochem.* 47: 533-606). Glutamate is synthesized by the reductive amination of α-ketoglutarate, an intermediate in the citric acid cycle. Glutamine, proline, and arginine are each subsequently produced from glutamate. The biosynthesis of serine is a three-step process beginning with 3-phosphoglycerate (an intermediate in glycolysis), and resulting in this amino acid after oxidation, transamination, and hydrolysis steps. Both cysteine and glycine are produced from serine; the former by the condensation of homocysteine with serine, and the latter by the transferal of the side-chain β-carbon atom to tetrahydrofolate, in a reaction catalyzed by serine transhydroxymethylase. Phenylalanine, and tyrosine are synthesized from the glycolytic and pentose phosphate pathway precursors erythrose 4-phosphate and phosphoenolpyruvate in a 9-step biosynthetic pathway that differ only at the final two steps after synthesis of prephenate. Tryptophan is also produced from these two initial molecules, but its synthesis is an 11-step pathway. Tyrosine may also be synthesized from phenylalanine, in a reaction catalyzed by phenylalanine hydroxylase. Alanine, valine, and leucine are all biosynthetic products of pyruvate, the final product of glycolysis. Aspartate is formed from oxaloacetate, an intermediate of the citric acid cycle. Asparagine, methionine, threonine, and lysine are each produced by the conversion of aspartate. Isoleucine is formed from threonine. A complex 9-step pathway results in the production of histidine from 5-phosphoribosyl-1-pyrophosphate, an activated sugar.

Amino acids in excess of the protein synthesis needs of the cell cannot be stored, and are instead degraded to provide intermediates for the major metabolic pathways of the cell (for review see Stryer, L. Biochemistry 3rd ed. Ch. 21 "Amino Acid Degradation and the Urea Cycle" p. 495-516 (1988)). Although the cell is able to convert unwanted amino acids into useful metabolic intermediates, amino acid production is costly in terms of energy, precursor molecules, and the enzymes necessary to synthesize them.

Thus it is not surprising that amino acid biosynthesis is regulated by feedback inhibition, in which the presence of a particular amino acid serves to slow or entirely stop its own production (for overview of feedback mechanisms in amino acid biosynthetic pathways, see Stryer, L. Biochemistry, 3rd ed. Ch. 24: "Biosynthesis of Amino Acids and Heme" p. 575-600 (1988)). Thus, the output of any particular amino acid is limited by the amount of that amino acid present in the cell.

B. Vitamin, Cofactor, and Nutraceutical Metabolism and Uses

Vitamins, cofactors, and nutraceuticals comprise another group of molecules which the higher animals have lost the ability to synthesize and so must ingest, although they are readily synthesized by other organisms such as bacteria. These molecules are either bioactive substances themselves, or are precursors of biologically active substances which may serve as electron carriers or intermediates in a variety of metabolic pathways. Aside from their nutritive value, these compounds also have significant industrial value as coloring agents, antioxidants, and catalysts or other processing aids. (For an overview of the structure, activity, and industrial applications of these compounds, see, for example, Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996.) The term "vitamin" is art-recognized, and includes nutrients which are required by an organism for normal functioning, but which that organism cannot synthesize by itself. The group of vitamins may encompass cofactors and nutraceutical compounds. The language "cofactor" includes nonproteinaceous compounds required for a normal enzymatic activity to occur. Such compounds may be organic or inorganic; the cofactor molecules of the invention are preferably organic. The term "nutraceutical" includes dietary supplements having health benefits in plants and animals, particularly humans. Examples of such molecules are vitamins, antioxidants, and also certain lipids (*e.g.*, polyunsaturated fatty acids).

The biosynthesis of these molecules in organisms capable of producing them, such as bacteria, has been largely characterized (Ullman's Encyclopedia of Industrial Chemistry, "Vitamins" vol. A27, p. 443-613, VCH: Weinheim, 1996; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley & Sons; Ong, A.S., Niki, E. & Packer, L. (1995) "Nutrition, Lipids, Health, and Disease" Proceedings of the UNESCO/Confederation of Scientific and Technological Associations in Malaysia, and the Society for Free Radical Research – Asia, held Sept. 1-3, 1994 at Penang, Malaysia, AOCS Press: Champaign, IL X, 374 S).

Thiamin (vitamin B_1) is produced by the chemical coupling of pyrimidine and thiazole moieties. Riboflavin (vitamin B_2) is synthesized from guanosine-5'-triphosphate

(GTP) and ribose-5'-phosphate. Riboflavin, in turn, is utilized for the synthesis of flavin mononucleotide (FMN) and flavin adenine dinucleotide (FAD). The family of compounds collectively termed 'vitamin B_6' (*e.g.*, pyridoxine, pyridoxamine, pyridoxa-5'-phosphate, and the commercially used pyridoxin hydrochloride) are all derivatives of the common structural unit, 5-hydroxy-6-methylpyridine. Pantothenate (pantothenic acid, (R)-(+)-N-(2,4-dihydroxy-3,3-dimethyl-1-oxobutyl)-β-alanine) can be produced either by chemical synthesis or by fermentation. The final steps in pantothenate biosynthesis consist of the ATP-driven condensation of β-alanine and pantoic acid. The enzymes responsible for the biosynthesis steps for the conversion to pantoic acid, to β-alanine and for the condensation to panthotenic acid are known. The metabolically active form of pantothenate is Coenzyme A, for which the biosynthesis proceeds in 5 enzymatic steps. Pantothenate, pyridoxal-5'-phosphate, cysteine and ATP are the precursors of Coenzyme A. These enzymes not only catalyze the formation of panthothante, but also the production of (R)-pantoic acid, (R)-pantolacton, (R)-panthenol (provitamin B_5), pantetheine (and its derivatives) and coenzyme A.

Biotin biosynthesis from the precursor molecule pimeloyl-CoA in microorganisms has been studied in detail and several of the genes involved have been identified. Many of the corresponding proteins have been found to also be involved in Fe-cluster synthesis and are members of the nifS class of proteins. Lipoic acid is derived from octanoic acid, and serves as a coenzyme in energy metabolism, where it becomes part of the pyruvate dehydrogenase complex and the α-ketoglutarate dehydrogenase complex. The folates are a group of substances which are all derivatives of folic acid, which is turn is derived from L-glutamic acid, p-amino-benzoic acid and 6-methylpterin. The biosynthesis of folic acid and its derivatives, starting from the metabolism intermediates guanosine-5'-triphosphate (GTP), L-glutamic acid and p-amino-benzoic acid has been studied in detail in certain microorganisms.

Corrinoids (such as the cobalamines and particularly vitamin B_{12}) and porphyrines belong to a group of chemicals characterized by a tetrapyrole ring system. The biosynthesis of vitamin B_{12} is sufficiently complex that it has not yet been completely characterized, but many of the enzymes and substrates involved are now known. Nicotinic acid (nicotinate), and nicotinamide are pyridine derivatives which are also termed 'niacin'. Niacin is the precursor of the important coenzymes NAD (nicotinamide adenine dinucleotide) and NADP (nicotinamide adenine dinucleotide phosphate) and their reduced forms.

The large-scale production of these compounds has largely relied on cell-free chemical syntheses, though some of these chemicals have also been produced by large-scale culture of microorganisms, such as riboflavin, Vitamin B_6, pantothenate, and

biotin. Only Vitamin B_{12} is produced solely by fermentation, due to the complexity of its synthesis. *In vitro* methodologies require significant inputs of materials and time, often at great cost.

C. Purine, Pyrimidine, Nucleoside and Nucleotide Metabolism and Uses

Purine and pyrimidine metabolism genes and their corresponding proteins are important targets for the therapy of tumor diseases and viral infections. The language "purine" or "pyrimidine" includes the nitrogenous bases which are constituents of nucleic acids, co-enzymes, and nucleotides. The term "nucleotide" includes the basic structural units of nucleic acid molecules, which are comprised of a nitrogenous base, a pentose sugar (in the case of RNA, the sugar is ribose; in the case of DNA, the sugar is D-deoxyribose), and phosphoric acid. The language "nucleoside" includes molecules which serve as precursors to nucleotides, but which are lacking the phosphoric acid moiety that nucleotides possess. By inhibiting the biosynthesis of these molecules, or their mobilization to form nucleic acid molecules, it is possible to inhibit RNA and DNA synthesis; by inhibiting this activity in a fashion targeted to cancerous cells, the ability of tumor cells to divide and replicate may be inhibited. Additionally, there are nucleotides which do not form nucleic acid molecules, but rather serve as energy stores (*i.e.*, AMP) or as coenzymes (*i.e.*, FAD and NAD).

Several publications have described the use of these chemicals for these medical indications, by influencing purine and/or pyrimidine metabolism (*e.g.* Christopherson, R.I. and Lyons, S.D. (1990) "Potent inhibitors of *de novo* pyrimidine and purine biosynthesis as chemotherapeutic agents." *Med. Res. Reviews* 10: 505-548). Studies of enzymes involved in purine and pyrimidine metabolism have been focused on the development of new drugs which can be used, for example, as immunosuppressants or anti-proliferants (Smith, J.L., (1995) "Enzymes in nucleotide synthesis." *Curr. Opin. Struct. Biol.* 5: 752-757; (1995) *Biochem Soc. Transact.* 23: 877-902). However, purine and pyrimidine bases, nucleosides and nucleotides have other utilities: as intermediates in the biosynthesis of several fine chemicals (*e.g.*, thiamine, S-adenosyl-methionine, folates, or riboflavin), as energy carriers for the cell (*e.g.*, ATP or GTP), and for chemicals themselves, commonly used as flavor enhancers (*e.g.*, IMP or GMP) or for several medicinal applications (see, for example, Kuninaka, A. (1996) Nucleotides and Related Compounds in Biotechnology vol. 6, Rehm *et al.*, eds. VCH: Weinheim, p. 561-612). Also, enzymes involved in purine, pyrimidine, nucleoside, or nucleotide metabolism are increasingly serving as targets against which chemicals for crop protection, including fungicides, herbicides and insecticides, are developed.

The metabolism of these compounds in bacteria has been characterized (for reviews see, for example, Zalkin, H. and Dixon, J.E. (1992) "*de novo* purine nucleotide biosynthesis", in: Progress in Nucleic Acid Research and Molecular Biology, vol. 42, Academic Press:, p. 259-287; and Michal, G. (1999) "Nucleotides and Nucleosides", Chapter 8 in: Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York). Purine metabolism has been the subject of intensive research, and is essential to the normal functioning of the cell. Impaired purine metabolism in higher animals can cause severe disease, such as gout. Purine nucleotides are synthesized from ribose-5-phosphate, in a series of steps through the intermediate compound inosine-5'-phosphate (IMP), resulting in the production of guanosine-5'-monophosphate (GMP) or adenosine-5'-monophosphate (AMP), from which the triphosphate forms utilized as nucleotides are readily formed. These compounds are also utilized as energy stores, so their degradation provides energy for many different biochemical processes in the cell. Pyrimidine biosynthesis proceeds by the formation of uridine-5'-monophosphate (UMP) from ribose-5-phosphate. UMP, in turn, is converted to cytidine-5'-triphosphate (CTP). The deoxy- forms of all of these nucleotides are produced in a one step reduction reaction from the diphosphate ribose form of the nucleotide to the diphosphate deoxyribose form of the nucleotide. Upon phosphorylation, these molecules are able to participate in DNA synthesis.

D. Trehalose Metabolism and Uses

Trehalose consists of two glucose molecules, bound in α, α-1,1 linkage. It is commonly used in the food industry as a sweetener, an additive for dried or frozen foods, and in beverages. However, it also has applications in the pharmaceutical, cosmetics and biotechnology industries (see, for example, Nishimoto *et al.*, (1998) U.S. Patent No. 5,759,610; Singer, M.A. and Lindquist, S. (1998) *Trends Biotech.* 16: 460-467; Paiva, C.L.A. and Panek, A.D. (1996) *Biotech. Ann. Rev.* 2: 293-314; and Shiosaka, M. (1997) J. Japan 172: 97-102). Trehalose is produced by enzymes from many microorganisms and is naturally released into the surrounding medium, from which it can be collected using methods known in the art.

II. Maintenance of Homeostasis in *C. glutamicum* and Environmental Adaptation

The metabolic and other biochemical processes by which cells function are sensitive to environmental conditions such as temperature, pressure, solute concentration, and availability of oxygen. When one or more such environmental condition is perturbed or altered in a fashion that is incompatible with the normal functioning of these cellular processes, the cell must act to maintain an intracellular

environment which will permit them to occur despite the hostile extracellular environment. Gram positive bacterial cells, such as *C. glutamicum* cells, have a number of mechanisms by which internal homeostasis may be maintained despite unfavorable extracellular conditions. These include a cell wall, proteins which are able to degrade possibly toxic aromatic and aliphatic compounds, mechanisms of proteolysis whereby misfolded or misregulated proteins may be rapidly destroyed, and catalysts which permit intracellular reactions to occur which would not normally take place under the conditions optimal for bacterial growth.

Aside from merely surviving in a hostile environment, bacterial cells (*e.g. C. glutamicum* cells) are also frequently able to adapt such that they are able to take advantage of such conditions. For example, cells in an environment lacking desired carbon sources may be able to adapt to growth on a less-suitable carbon source. Also, cells may be able to utilize less desirable inorganic compounds when the commonly utilized ones are unavailable. *C. glutamicum* cells possess a number of genes which permit them to adapt to utilize inorganic and organic molecules which they would normally not encounter under optimal growth conditions as nutrients and precursors for metabolism. Aspects of cellular processes involved in homeostasis and adaptation are further explicated below.

A. Modification and Degradation of Aromatic and Aliphatic Compounds

Bacterial cells are routinely exposed to a variety of aromatic and aliphatic compounds in nature. Aromatic compounds are organic molecules having a cyclic ring structure, while aliphatic compounds are organic molecules having open chain structures rather than ring structures. Such compounds may arise as by-products of industrial processes (*e.g.*, benzene or toluene), but may also be produced by certain microorganisms (*e.g.*, alcohols). Many of these compounds are toxic to cells, particularly the aromatic compounds, which are highly reactive due to the high-energy ring structure. Thus, certain bacteria have developed mechanisms by which they are able to modify or degrade these compounds such that they are no longer hazardous to the cell. Cells may possess enzymes that are able to, for example, hydroxylate, isomerize, or methylate aromatic or aliphatic compounds such that they are either rendered less toxic, or such that the modified form is able to be processed by standard cellular waste and degradation pathways. Also, cells may possess enzymes which are able to specifically degrade one or more such potentially hazardous substance, thereby protecting the cell. Principles and examples of these types of modification and degradation processes in bacteria are described in several publications, *e.g.*, Sahm, H. (1999) "Procaryotes in Industrial Production" in Lengeler, J.W. *et al.*, eds.

Biology of the Procaryotes, Thieme Verlag: Stuttgart; and Schlegel, H.G. (1992) Allgemeine Mikrobiologie, Thieme: Stuttgart).

Aside from simply inactivating hazardous aromatic or aliphatic compounds, many bacteria have evolved to be able to utilize these compounds as carbon sources for continued metabolism when the preferred carbon sources of the cell are not available. For example, Pseudomonas strains able to utilize toluene, benzene, and 1,10-dichlorodecane as carbon sources are known (Chang, B.V. *et al.* (1997) *Chemosphere* 35(12): 2807-2815; Wischnak, C. *et al.* (1998) *Appl. Environ. Microbiol.* 64(9): 3507-3511; Churchill, S.A. *et al.* (1999) *Appl. Environ. Microbiol.* 65(2): 549-552). There are similar examples from many other bacterial species which are known in the art.

The ability of certain bacteria to modify or degrade aromatic and aliphatic compounds has begun to be exploited. Petroleum is a complex mixture of chemicals which includes aliphatic molecules and aromatic compounds. By applying bacteria having the ability to degrade or modify these toxic compounds to an oil spill, for example, it is possible to eliminate much of the environmental damage with high efficiency and low cost (see, for example, Smith, M.R. (1990) "The biodegradation of aromatic hydrocarbons by bacteria" *Biodegradation* 1(2-3): 191-206; and Suyama, T. *et al.* (1998) "Bacterial isolates degrading aliphatic polycarbonates," *FEMS Microbiol. Lett.* 161(2): 255-261).

B. Metabolism of Inorganic Compounds

Cells (*e.g.*, bacterial cells) contain large quantities of different molecules, such as water, inorganic ions, and organic substances (*e.g.*, proteins, sugars, and other macromolecules). The bulk of the mass of a typical cell consists of only 4 types of atoms: carbon, oxygen, hydrogen, and nitrogen. Although they represent a smaller percentage of the content of a cell, inorganic substances are equally as important to the proper functioning of the cell. Such molecules include phosphorous, sulfur, calcium, magnesium, iron, zinc, manganese, copper, molybdenum, tungsten, and cobalt. Many of these compounds are critical for the construction of important molecules, such as nucleotides (phosphorous) and amino acids (nitrogen and sulfur). Others of these inorganic ions serve as cofactors for enzymic reactions or contribute to osmotic pressure. All such molecules must be taken up by the bacterium from the surrounding environment.

For each of these inorganic compounds it is desirable for the bacterium to take up the form which can be most readily used by the standard metabolic machinery of the cell. However, the bacterium may encounter environments in which these preferred forms are not readily available. In order to survive under these circumstances, it is important for bacteria to have additional biochemical mechanisms which are able to convert less metabolically active but readily available forms of these inorganic compounds to ones which may be used

in cellular metabolism. Bacteria frequently possess a number of genes encoding enzymes for this purpose, which are not expressed unless the desired inorganic species are not available. Thus, these genes for the metabolism of various inorganic compounds serve as another tool which bacteria may use to adapt to suboptimal environmental conditions.

After carbon, the most important element in the cell is nitrogen. A typical bacterial cell contains between 12-15% nitrogen. It is a constituent of amino acids and nucleotides, as well as many other important molecules in the cell. Further, nitrogen may serve as a substitute for oxygen as a terminal electron acceptor in energy metabolism. Good sources of nitrogen include many organic and inorganic compounds, such ammonia gas or ammonia salts (*e.g.*, NH_4Cl, $(NH_4)_2SO_4$, or NH_4OH), nitrates, urea, amino acids, or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract, etc. Ammonia nitrogen is fixed by the action of particular enzymes: glutamate dehydrogenase, glutamine synthase, and glutamine-2-oxoglutarate aminotransferase. The transfer of amino-nitrogen from one organic molecule to another is accomplished by the aminotransferases, a class of enzymes which transfer one amino group from an alpha-amino acid to an alpha-keto acid. Nitrate may be reduced via nitrate reductase, nitrite reductase, and further redox enzymes until it is converted to molecular nitrogen or ammonia, which may be readily utilized by the cell in standard metabolic pathways.

Phosphorous is typically found intracellularly in both organic and inorganic forms, and may be taken up by the cell in either of these forms as well, though most microorganisms preferentially take up inorganic phosphate. The conversion of organic phosphate to a form which the cell can utilize requires the action of phosphatases (*e.g.*, phytases, which hydrolyze phyate-yielding phosphate and inositol derivatives). Phosphate is a key element in the synthesis of nucleic acids, and also has a significant role in cellular energy metabolism (*e.g.*, in the synthesis of ATP, ADP, and AMP).

Sulfur is a requirement for the synthesis of amino acids (*e.g.*, methionine and cysteine), vitamins (*e.g.*, thiamine, biotin, and lipoic acid) and iron sulfur proteins. Bacteria obtain sulfur primarily from inorganic sulfate, though thiosulfate, sulfite, and sulfide are also commonly utilized. Under conditions where these compounds may not be readily available, many bacteria express genes which enable them to utilize sulfonate compounds such as 2-aminosulfonate (taurine) (Kertesz, M.A. (1993) "Proteins induced by sulfate limitation in *Escherichia coli*, *Pseudomonas putida*, or *Staphylococcus aureus*." *J. Bacteriol.* 175: 1187-1190).

Other inorganic atoms, *e.g.*, metal or calcium ions, are also critical for the viability of cells. Iron, for example, plays a key role in redox reactions and is a cofactor of iron-sulfur proteins, heme proteins, and cytochromes. The uptake of iron into bacterial cells may be accomplished by the action of siderophores, chelating agents

which bind extracellular iron ions and translocate them to the interior of the cell. For reference on the metabolism of iron and other inorganic compounds, see: Lengeler *et al.* (1999) Biology of Prokaryotes, Thieme Verlag: Stuttgart; Neidhardt, F.C. *et al.*, eds. *Escherichia coli* and *Salmonella*. ASM Press: Washington, D.C.; Sonenshein, A.L. *et al.*, eds. (199?) *Bacillus subtilis* and Other Gram-Positive Bacteria, ASM Press: Washington, D.C.; Voet, D. and Voet, J.G. (1992) Biochemie, VCH: Weinheim; Brock, T.D. and Madigan, M.T. (1991) Biology of Microorgansisms, 6th ed. Prentice Hall: Englewood Cliffs, p. 267-269; Rhodes, P.M. and Stanbury, P.F. Applied Microbial Physiology – A Practical Approach, Oxford Univ. Press: Oxford.

C. Enzymes and Proteolysis

The intracellular conditions for which bacteria such as *C. glutamicum* are optimized are frequently not conditions under which many biochemical reactions would normally take place. In order to make such reactions proceed under physiological conditions, cells utilize enzymes. Enzymes are proteinaceous biological catalysts, spatially orienting reacting molecules or providing a specialized environment such that the energy barrier to a biochemical reaction is lowered. Different enzymes catalyze different reactions, and each enzyme may be the subject of transcriptional, translational, or posttranslational regulation such that the reaction will only take place under appropriate conditions and at specified times. Enzymes may contribute to the degradation (*e.g.*, the proteases), synthesis (*e.g.*, the synthases), or modification (*e.g.*, transferases or isomerases) of compounds, all of which enable the production of necessary compounds within the cell. This, in turn, contributes to the maintenance of cellular homeostasis.

However, the fact that enzymes are optimized for activity under the physiological conditions at which the bacterium is most viable means that when environmental conditions are perturbed, there is a significant possibility that enzyme activity will also be perturbed. For example, changes in temperature may result in aberrantly folded proteins, and the same is true for changes of pH – protein folding is largely dependent on electrostatic and hydrophobic interactions of amino acids within the polypeptide chain, so any alteration to the charges on individual amino acids (as might be brought about by a change in cellular pH) may have a profound effect on the ability of the protein to correctly fold. Changes in temperature effectively change the amount of kinetic energy that the polypeptide molecule possesses, which affects the ability of the polypeptide to settle into a correctly folded, energetically stable configuration. Misfolded proteins may be harmful to the cell for two reasons. First, the aberrantly folded protein may have a similarly aberrant activity, or no activity

whatsoever. Second, misfolded proteins may lack the conformational regions necessary for proper regulation by other cellular systems and thus may continue to be active but in an uncontrolled fashion.

The cell has a mechanism by which misfolded enzymes and regulatory proteins may be rapidly destroyed before any damage occurs to the cell: proteolysis. Proteins such as those of the la/lon family and those of the Clp family specifically recognize and degrade misfolded proteins (see, *e.g.*, Sherman, M.Y., Goldberg, A.L. (1999) *EXS* 77: 57-78 and references therein and Porankiewicz J. (1999) *Molec. Microbiol.* 32(3): 449-58, and references therein; Neidhardt, F.C., *et al.* (1996) *E. coli* and *Salmonella*, ASM Press: Washington, D.C. and references therein; and Pritchard, G.G., and Coolbear, T. (1993) *FEMS Microbiol.* Rev. 12(1-3): 179-206 and references therein). These enzymes bind to misfolded or unfolded proteins and degrade them in an ATP-dependent manner. Proteolysis thus serves as an important mechanism employed by the cell to prevent damage to normal cellular functions upon environmental changes, and it further permits cells to survive under conditions and in environments which would otherwise be toxic due to misregulated and/or aberrant enzyme or regulatory activity.

Proteolysis also has important functions in the cell under optimal environmental conditions. Within normal metabolic processes, proteases aid in the hydrolysis of peptide bonds, in the catabolism of complex molecules to provide necessary degradation products, and in protein modification. Secreted proteases play an important role in the catabolism of external nutrients even prior to the entry of these compounds into the cell. Further, proteolytic activity itself may serve regulatory functions; sporulation in *B. subtilis* and cell cycle progression in *Caulobacter* spp. are known to be regulated by key proteolytic events in each of these species (Gottesman, S. (1999) *Curr. Opin. Microbiol.* 2(2): 142-147). Thus, proteolytic processes are key for cellular survival under both suboptimal and optimal environmental conditions, and contribute to the overall maintenance of homeostasis in cells.

D. Cell Wall Production and Rearrangements

While the biochemical machinery of the cell may be able to readily adapt to different and possibly unfavorable environments, cells still require a general mechanism by which they may be protected from the environment. For many bacteria, the cell wall affords such protection, and also plays roles in adhesion, cell growth and division, and transport of desired solutes and waste materials.

In order to function, cells require intracellular concentrations of metabolites and other molecules that are substantially higher than those of the surrounding media. Since these metabolites are largely prevented from leaving the cell due to the presence of the

hydrophobic membrane, the tendency of the system is for water molecules to enter the cell from the external medium such that the interior concentrations of solutes match the exterior concentrations. Water molecules are readily able to cross the cellular membrane, and this membrane is not able to withstand the resulting swelling and pressure, which may lead to osmotic lysis of the cell. The rigidity of the cell wall greatly improves the ability of the cell to tolerate these pressures, and offers a further barrier to the unwanted diffusion of these metabolites and desired solutes from the cell. Similarly, the cell wall also serves to prevent unwanted material from entering the cell.

The cell wall also participates in a number of other cellular processes, such as adhesion and cell growth and division. Due to the fact that the cell wall completely surrounds the cell, any interaction of the cell with its surroundings must be mediated by the cell wall. Thus, the cell wall must participate in any adherence of the cell to other cells and to desired surfaces. Further, the cell cannot grow or divide without concomitant changes in the cell wall. Since the protection that the wall affords requires its presence during growth, morphogenesis and multiplication, one of the key steps in cell division is cell wall synthesis within the cell such that a new cell divides from the old. Thus, frequently cell wall biosynthesis is regulated in tandem with cell growth and cell division (see, *e.g.*, Sonenshein, A.L. et al, eds. (1993) *Bacillus subtilis* and Other Gram-Positive Bacteria, ASM: Washington, D.C.).

The structure of the cell wall varies between gram-positive and gram-negative bacteria. However, in both types, the fundamental structural unit of the wall remains similar: an overlapping lattice of two polysaccharides, N-acetyl glucosamine (NAG) and N-acetyl muramic acid (NAM) which are cross-linked by amino acids (most commonly L-alanine, D-glutamate, diaminopimelic acid, and D-alanine), termed 'peptidoglycan'. The processes involved in the synthesis of the cell wall are known (see, *e.g.*, Michal, G., ed. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, Wiley: New York).

In gram-negative bacteria, the inner cellular membrane is coated by a single-layered peptidoglycan (approximately 10 nm thick), termed the murein-sacculus. This peptidoglycan structure is very rigid, and its structure determines the shape of the organism. The outer surface of the murein-sacculus is covered with an outer membrane, containing porins and other membrane proteins, phospholipids, and lipopolysaccharides. To maintain a tight association with the outer membrane, the gram-negative cell wall also has interspersed lipid molecules which serve to anchor it to the surrounding membrane.

In gram-positive bacteria, such as *Corynebacterium glutamicum*, the cytoplasmic membrane is covered by a multi-layered peptidoglycan, which ranges from 20-80 nm in thickness (see, *e.g.*, Lengeler *et al.* (1999) Biology of Prokaryotes Thieme Verlag: Stuttgart,

p. 913-918, p. 875-899, and p. 88-109 and references therein). The gram-positive cell wall also contains teichoic acid, a polymer of glycerol or ribitol linked through phosphate groups. Teichoic acid is also able to associate with amino acids, and forms covalent bonds with muramic acid. Also present in the cell wall may be lipoteichoic acids and teichuronic acids. If present, cellular surface structures such as flagella or capsules will be anchored in this layer as well.

III. Elements and Methods of the Invention

The present invention is based, at least in part, on the discovery of novel molecules, referred to herein as HA nucleic acid and protein molecules, which participate in the maintenance of homeostasis in *C. glutamicum*, or which perform a function involved in the adaptation of this microorganism to different environmental conditions. In one embodiment, the HA molecules participate in *C. glutamicum* cell wall biosynthesis or rearrangements, in the metabolism of inorganic compounds, in the modification or degradation of aromatic or aliphatic compounds, or have an enzymatic or proteolytic activity. In a preferred embodiment, the activity of the HA molecules of the present invention with regard to *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activity has an impact on the production of a desired fine chemical by this organism. In a particularly preferred embodiment, the HA molecules of the invention are modulated in activity, such that the *C. glutamicum* cellular processes in which the HA molecules participate (*e.g.*, *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or enzymatic or proteolytic activity) are also altered in activity, resulting either directly or indirectly in a modulation of the yield, production, and/or efficiency of production of a desired fine chemical by *C. glutamicum*.

The language, "HA protein" or "HA polypeptide" includes proteins which participate in a number of cellular processes related to *C. glutamicum* homeostasis or the ability of *C. glutamicum* cells to adapt to unfavorable environmental conditions. For example, an HA protein may be involved in *C. glutamicum* cell wall biosynthesis or rearrangements, in the metabolism of inorganic compounds in *C. glutamicum*, in the modification or degradation of aromatic or aliphatic compounds in *C. glutamicum*, or have a *C. glutamicum* enzymatic or proteolytic activity. Examples of HA proteins include those encoded by the HA genes set forth in Table 1 and Appendix A. The terms "HA gene" or "HA nucleic acid sequence" include nucleic acid sequences encoding an HA protein, which consist of a coding region and also corresponding untranslated 5' and

3' sequence regions. Examples of HA genes include those set forth in Table 1. The terms "production" or "productivity" are art-recognized and include the concentration of the fermentation product (for example, the desired fine chemical) formed within a given time and a given fermentation volume (*e.g.*, kg product per hour per liter). The term "efficiency of production" includes the time required for a particular level of production to be achieved (for example, how long it takes for the cell to attain a particular rate of output of a fine chemical). The term "yield" or "product/carbon yield" is art-recognized and includes the efficiency of the conversion of the carbon source into the product (*i.e.*, fine chemical). This is generally written as, for example, kg product per kg carbon source. By increasing the yield or production of the compound, the quantity of recovered molecules, or of useful recovered molecules of that compound in a given amount of culture over a given amount of time is increased. The terms "biosynthesis" or a "biosynthetic pathway" are art-recognized and include the synthesis of a compound, preferably an organic compound, by a cell from intermediate compounds in what may be a multistep and highly regulated process. The terms "degradation" or a "degradation pathway" are art-recognized and include the breakdown of a compound, preferably an organic compound, by a cell to degradation products (generally speaking, smaller or less complex molecules) in what may be a multistep and highly regulated process. The language "metabolism" is art-recognized and includes the totality of the biochemical reactions that take place in an organism. The metabolism of a particular compound, then, (*e.g.*, the metabolism of an amino acid such as glycine) comprises the overall biosynthetic, modification, and degradation pathways in the cell related to this compound. The term "homeostasis" is art-recognized and includes all of the mechanisms utilized by a cell to maintain a constant intracellular environment despite the prevailing extracellular environmental conditions. A non-limiting example of such processes is the utilization of a cell wall to prevent osmotic lysis due to high intracellular solute concentrations. The term "adaptation" or "adaptation to an environmental condition" is art-recognized and includes mechanisms utilized by the cell to render the cell able to survive under nonpreferred environmental conditions (generally speaking, those environmental conditions in which one or more favored nutrients are absent, or in which an environmental condition such as temperature, pH, osmolarity, oxygen percentage and the like fall outside of the optimal survival range of the cell). Many cells, including *C. glutamicum* cells, possess genes encoding proteins which are expressed under such environmental conditions and which permit continued growth in such suboptimal conditions.

In another embodiment, the HA molecules of the invention are capable of modulating the production of a desired molecule, such as a fine chemical, in a

microorganism such as *C. glutamicum*. There are a number of mechanisms by which the alteration of an HA protein of the invention may directly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by engineering enzymes which modify or degrade aromatic or aliphatic compounds such that these enzymes are increased or decreased in activity or number, it may be possible to modulate the production of one or more fine chemicals which are the modification or degradation products of these compounds. Similarly, enzymes involved in the metabolism of inorganic compounds provide key molecules (*e.g.* phosphorous, sulfur, and nitrogen molecules) for the biosynthesis of such fine chemicals as amino acids, vitamins, and nucleic acids. By altering the activity or number of these enzymes in *C. glutamicum*, it may be possible to increase the conversion of these inorganic compounds (or to use alternate inorganic compounds) to thus permit improved rates of incorporation of inorganic atoms into these fine chemicals. Genetic engineering of *C. glutamicum* enzymes involved in general cellular processes may also directly improve fine chemical production, since many of these enzymes directly modify fine chemicals (*e.g.*, amino acids) or the enzymes which are involved in fine chemical synthesis or secretion. Modulation of the activity or number of cellular proteases may also have a direct effect on fine chemical production, since many proteases may degrade fine chemicals or enzymes involved in fine chemical production or breakdown.

Further, the aforementioned enzymes which participate in aromatic/aliphatic compound modification or degradation, general biocatalysis, inorganic compound metabolism or proteolysis are each themselves fine chemicals, desirable for their activity in various *in vitro* industrial applications. By altering the number of copies of the gene for one or more of these enzymes in *C. glutamicum* it may be possible to increase the number of these proteins produced by the cell, thereby increasing the potential yield or efficiency of production of these proteins from large-scale *C. glutamicum* or related bacterial cultures.

The alteration of an HA protein of the invention may also indirectly affect the yield, production, and/or efficiency of production of a fine chemical from a *C. glutamicum* strain incorporating such an altered protein. For example, by modulating the activity and/or number of those proteins involved in the construction or rearrangement of the cell wall, it may be possible to modify the structure of the cell wall itself such that the cell is able to better withstand the mechanical and other stresses present during large-scale fermentative culture. Also, large-scale growth of *C. glutamicum* requires significant cell wall production. Modulation of the activity or number of cell wall biosynthetic or degradative enzymes may allow more rapid rates of

cell wall biosynthesis, which in turn may permit increased growth rates of this microorganism in culture and thereby increase the number of cells producing the desired fine chemical.

By modifying the HA enzymes of the invention, one may also indirectly impact the yield, production, or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, many of the general enzymes in *C. glutamicum* may have a significant impact on global cellular processes (*e.g.*, regulatory processes) which in turn have a significant effect on fine chemical metabolism. Similarly, proteases, enzymes which modify or degrade possibly toxic aromatic or aliphatic compounds, and enzymes which promote the metabolism of inorganic compounds all serve to increase the viability of *C. glutamicum*. The proteases aid in the selective removal of misfolded or misregulated proteins, such as those that might occur under the relatively stressful environmental conditions encountered during large-scale fermentor culture. By altering these proteins, it may be possible to further enhance this activity and to improve the viability of *C. glutamicum* in culture. The aromatic/aliphatic modification or degradation proteins not only serve to detoxify these waste compounds (which may be encountered as impurities in culture medium or as waste products from cells themselves), but also to permit the cells to utilize alternate carbon sources if the optimal carbon source is limiting in the culture. By increasing their number and/or activity, the survival of *C. glutamicum* cells in culture may be enhanced. The inorganic metabolism proteins of the invention supply the cell with inorganic molecules required for all protein and nucleotide (among others) synthesis, and thus are critical for the overall viability of the cell. An increase in the number of viable cells producing one or more desired fine chemicals in large-scale culture should result in a concomitant increase in the yield, production, and/or efficiency of production of the fine chemical in the culture.

The isolated nucleic acid sequences of the invention are contained within the genome of a *Corynebacterium glutamicum* strain available through the American Type Culture Collection, given designation ATCC 13032. The nucleotide sequence of the isolated *C. glutamicum* HA DNAs and the predicted amino acid sequences of the *C. glutamicum* HA proteins are shown in Appendices A and B, respectively. Computational analyses were performed which classified and/or identified these nucleotide sequences as sequences which encode proteins that participate in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity.

The present invention also pertains to proteins which have an amino acid sequence which is substantially homologous to an amino acid sequence of Appendix B.

As used herein, a protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence is least about 50% homologous to the selected amino acid sequence, *e.g.*, the entire selected amino acid sequence. A protein which has an amino acid sequence which is substantially homologous to a selected amino acid sequence can also be least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, or 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to the selected amino acid sequence.

The HA protein or a biologically active portion or fragment thereof of the invention can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different environmental conditions, or have one or more of the activities set forth in Table 1.

Various aspects of the invention are described in further detail in the following subsections.

A. Isolated Nucleic Acid Molecules

One aspect of the invention pertains to isolated nucleic acid molecules that encode HA polypeptides or biologically active portions thereof, as well as nucleic acid fragments sufficient for use as hybridization probes or primers for the identification or amplification of HA-encoding nucleic acid (*e.g.*, HA DNA). As used herein, the term "nucleic acid molecule" is intended to include DNA molecules (*e.g.*, cDNA or genomic DNA) and RNA molecules (*e.g.*, mRNA) and analogs of the DNA or RNA generated using nucleotide analogs. This term also encompasses untranslated sequence located at both the 3' and 5' ends of the coding region of the gene: at least about 100 nucleotides of sequence upstream from the 5' end of the coding region and at least about 20 nucleotides of sequence downstream from the 3'end of the coding region of the gene. The nucleic acid molecule can be single-stranded or double-stranded, but preferably is double-stranded DNA. An "isolated" nucleic acid molecule is one which is separated from other nucleic acid molecules which are present in the natural source of the nucleic acid. Preferably, an "isolated" nucleic acid is free of sequences which naturally flank the nucleic acid (*i.e.*, sequences located at the 5' and 3' ends of the nucleic acid) in the genomic DNA of the organism from which the nucleic acid is derived. For example, in various embodiments, the isolated HA nucleic acid molecule can contain less than about 5 kb, 4kb, 3kb, 2kb, 1 kb, 0.5 kb or 0.1 kb of nucleotide sequences which naturally flank the nucleic acid molecule in genomic DNA of the cell from which the nucleic acid is derived (e.g, a *C. glutamicum* cell). Moreover, an "isolated" nucleic acid molecule, such as a DNA molecule, can be substantially free of other cellular material, or culture

medium when produced by recombinant techniques, or chemical precursors or other chemicals when chemically synthesized.

A nucleic acid molecule of the present invention, *e.g.*, a nucleic acid molecule having a nucleotide sequence of Appendix A, or a portion thereof, can be isolated using standard molecular biology techniques and the sequence information provided herein. For example, a *C. glutamicum* HA DNA can be isolated from a *C. glutamicum* library using all or portion of one of the sequences of Appendix A as a hybridization probe and standard hybridization techniques (*e.g.*, as described in Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989). Moreover, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this sequence (*e.g.*, a nucleic acid molecule encompassing all or a portion of one of the sequences of Appendix A can be isolated by the polymerase chain reaction using oligonucleotide primers designed based upon this same sequence of Appendix A). For example, mRNA can be isolated from normal endothelial cells (*e.g.*, by the guanidinium-thiocyanate extraction procedure of Chirgwin *et al.* (1979) *Biochemistry* 18: 5294-5299) and DNA can be prepared using reverse transcriptase (*e.g.*, Moloney MLV reverse transcriptase, available from Gibco/BRL, Bethesda, MD; or AMV reverse transcriptase, available from Seikagaku America, Inc., St. Petersburg, FL). Synthetic oligonucleotide primers for polymerase chain reaction amplification can be designed based upon one of the nucleotide sequences shown in Appendix A. A nucleic acid of the invention can be amplified using cDNA or, alternatively, genomic DNA, as a template and appropriate oligonucleotide primers according to standard PCR amplification techniques. The nucleic acid so amplified can be cloned into an appropriate vector and characterized by DNA sequence analysis. Furthermore, oligonucleotides corresponding to an HA nucleotide sequence can be prepared by standard synthetic techniques, *e.g.*, using an automated DNA synthesizer.

In a preferred embodiment, an isolated nucleic acid molecule of the invention comprises one of the nucleotide sequences shown in Appendix A. The sequences of Appendix A correspond to the *Corynebacterium glutamicum* HA DNAs of the invention. This DNA comprises sequences encoding HA proteins (*i.e.*, the "coding region", indicated in each sequence in Appendix A), as well as 5' untranslated sequences and 3' untranslated sequences, also indicated in Appendix A. Alternatively, the nucleic acid molecule can comprise only the coding region of any of the sequences in Appendix A.

For the purposes of this application, it will be understood that each of the sequences set forth in Appendix A has an identifying RXA, RXN, RXS, or RXC number having the designation "RXA", "RXN", "RXS", or "RXC" followed by 5 digits (*i.e.*, RXA02702, RXN02707, RXS02560, and RXC00110). Each of these sequences comprises up to three parts: a 5' upstream region, a coding region, and a downstream region. Each of these three regions is identified by the same RXA, RXN, RXS, or RXC designation to eliminate confusion. The recitation "one of the sequences in Appendix A", then, refers to any of the sequences in Appendix A, which may be distinguished by their differing RXA, RXN, RXS, or RXC designations. The coding region of each of these sequences is translated into a corresponding amino acid sequence, which is set forth in Appendix B. The sequences of Appendix B are identified by the same RXA, RXN, RXS, or RXC designations as Appendix A, such that they can be readily correlated. For example, the amino acid sequences in Appendix B designated RXA02702, RXN02707, RXS02560, and RXC00110 are translations of the coding regions of the nucleotide sequence of nucleic acid molecules RXA02702, RXN02707, RXS02560, and RXC00110, respectively, in Appendix A. Each of the RXA, RXN, RXS, and RXC nucleotide and amino acid sequences of the invention has also been assigned a SEQ ID NO, as indicated in Table 1.

Several of the genes of the invention are "F-designated genes". An F-designated gene includes those genes set forth in Table 1 which have an 'F' in front of the RXA, RXN, RXS, or RXC designation. For example, SEQ ID NO:1, designated, as indicated on Table 1, as "F RXA02702", is an F-designated gene, as are SEQ ID NOs: 9, 11, and 13 (designated on Table 1 as "F RXA02707", "F RXA02708", and "F RXA02709", respectively).

In one embodiment, the nucleic acid molecules of the present invention are not intended to include those compiled in Table 2. In the case of the dapD gene, a sequence for this gene was published in Wehrmann, A., *et al.* (1998) *J. Bacteriol.* 180(12): 3159-3165. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

In another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleic acid molecule which is a complement of one of the nucleotide sequences shown in Appendix A, or a portion thereof. A nucleic acid molecule which is complementary to one of the nucleotide sequences shown in Appendix A is one which is sufficiently complementary to one of the nucleotide

sequences shown in Appendix A such that it can hybridize to one of the nucleotide sequences shown in Appendix A, thereby forming a stable duplex.

In still another preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to a nucleotide sequence shown in Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited ranges, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In an additional preferred embodiment, an isolated nucleic acid molecule of the invention comprises a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to one of the nucleotide sequences shown in Appendix A, or a portion thereof.

Moreover, the nucleic acid molecule of the invention can comprise only a portion of the coding region of one of the sequences in Appendix A, for example a fragment which can be used as a probe or primer or a fragment encoding a biologically active portion of an HA protein. The nucleotide sequences determined from the cloning of the HA genes from *C. glutamicum* allows for the generation of probes and primers designed for use in identifying and/or cloning HA homologues in other cell types and organisms, as well as HA homologues from other *Corynebacteria* or related species. The probe/primer typically comprises substantially purified oligonucleotide. The oligonucleotide typically comprises a region of nucleotide sequence that hybridizes under stringent conditions to at least about 12, preferably about 25, more preferably about 40, 50 or 75 consecutive nucleotides of a sense strand of one of the sequences set forth in Appendix A, an anti-sense sequence of one of the sequences set forth in Appendix A, or naturally occurring mutants thereof. Primers based on a nucleotide sequence of Appendix A can be used in PCR reactions to clone HA homologues. Probes based on the HA nucleotide sequences can be used to detect transcripts or genomic sequences encoding the same or homologous proteins. In preferred embodiments, the probe further comprises a label group attached thereto, *e.g.* the label group can be a radioisotope, a fluorescent compound, an enzyme, or an enzyme co-factor. Such probes can be used as a part of a diagnostic test kit for identifying cells which misexpress an HA protein, such as by measuring a level of an HA-encoding

nucleic acid in a sample of cells, *e.g.*, detecting HA mRNA levels or determining whether a genomic HA gene has been mutated or deleted.

In one embodiment, the nucleic acid molecule of the invention encodes a protein or portion thereof which includes an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. As used herein, the language "sufficiently homologous" refers to proteins or portions thereof which have amino acid sequences which include a minimum number of identical or equivalent (*e.g.*, an amino acid residue which has a similar side chain as an amino acid residue in one of the sequences of Appendix B) amino acid residues to an amino acid sequence of Appendix B such that the protein or portion thereof is able to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. Proteins involved in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or that have a *C. glutamicum* enzymatic or proteolytic activity, as described herein, may play a role in the production and secretion of one or more fine chemicals. Examples of such activities are also described herein. Thus, "the function of an HA protein" contributes either directly or indirectly to the yield, production, and/or efficiency of production of one or more fine chemicals. Examples of HA protein activities are set forth in Table 1.

In another embodiment, the protein is at least about 50-60%, preferably at least about 60-70%, and more preferably at least about 70-80%, 80-90%, 90-95%, and most preferably at least about 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B.

Portions of proteins encoded by the HA nucleic acid molecules of the invention are preferably biologically active portions of one of the HA proteins. As used herein, the term "biologically active portion of an HA protein" is intended to include a portion, *e.g.*, a domain/motif, of an HA protein that can participate in the maintenance of homeostasis in *C. glutamicum*, or that can perform a function involved in the adaptation of this microorganism to different environmental conditions, or has an activity as set forth in Table 1. To determine whether an HA protein or a biologically active portion thereof can participate in *C. glutamicum* cell wall biosynthesis or rearrangements, metabolism of inorganic compounds, modification or degradation of aromatic or aliphatic compounds, or has a *C. glutamicum* enzymatic or proteolytic activity, an assay

of enzymatic activity may be performed. Such assay methods are well known to those of ordinary skill in the art, as detailed in Example 8 of the Exemplification.

Additional nucleic acid fragments encoding biologically active portions of an HA protein can be prepared by isolating a portion of one of the sequences in Appendix B, expressing the encoded portion of the HA protein or peptide (*e.g.*, by recombinant expression *in vitro*) and assessing the activity of the encoded portion of the HA protein or peptide.

The invention further encompasses nucleic acid molecules that differ from one of the nucleotide sequences shown in Appendix A (and portions thereof) due to degeneracy of the genetic code and thus encode the same HA protein as that encoded by the nucleotide sequences shown in Appendix A. In another embodiment, an isolated nucleic acid molecule of the invention has a nucleotide sequence encoding a protein having an amino acid sequence shown in Appendix B. In a still further embodiment, the nucleic acid molecule of the invention encodes a full length *C. glutamicum* protein which is substantially homologous to an amino acid sequence of Appendix B (encoded by an open reading frame shown in Appendix A).

It will be understood by one of ordinary skill in the art that in one embodiment the sequences of the invention are not meant to include the sequences of the prior art, such as those Genbank sequences set forth in Tables 2 or 4 which were available prior to the present invention. In one embodiment, the invention includes nucleotide and amino acid sequences having a percent identity to a nucleotide or amino acid sequence of the invention which is greater than that of a sequence of the prior art (*e.g.*, a Genbank sequence (or the protein encoded by such a sequence) set forth in Tables 2 or 4). For example, the invention includes a nucleotide sequence which is greater than and/or at least 36% identical to the nucleotide sequence designated RXA00009 (SEQ ID NO:85), a nucleotide sequence which is greater than and/or at least 40% identical to the nucleotide sequence designated RXA00277 (SEQ ID NO:91), and a nucleotide sequence which is greater than and/or at least 43% identical to the nucleotide sequence designated RXA00499 (SEQ ID NO:173). One of ordinary skill in the art would be able to calculate the lower threshold of percent identity for any given sequence of the invention by examining the GAP-calculated percent identity scores set forth in Table 4 for each of the three top hits for the given sequence, and by subtracting the highest GAP-calculated percent identity from 100 percent. One of ordinary skill in the art will also appreciate that nucleic acid and amino acid sequences having percent identities greater than the lower threshold so calculated (*e.g.*, at least 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%,

76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more identical) are also encompassed by the invention.

In addition to the *C. glutamicum* HA nucleotide sequences shown in Appendix A, it will be appreciated by those of ordinary skill in the art that DNA sequence polymorphisms that lead to changes in the amino acid sequences of HA proteins may exist within a population (*e.g.*, the *C. glutamicum* population). Such genetic polymorphism in the HA gene may exist among individuals within a population due to natural variation. As used herein, the terms "gene" and "recombinant gene" refer to nucleic acid molecules comprising an open reading frame encoding an HA protein, preferably a *C. glutamicum* HA protein. Such natural variations can typically result in 1-5% variance in the nucleotide sequence of the HA gene. Any and all such nucleotide variations and resulting amino acid polymorphisms in HA that are the result of natural variation and that do not alter the functional activity of HA proteins are intended to be within the scope of the invention.

Nucleic acid molecules corresponding to natural variants and non-*C. glutamicum* homologues of the *C. glutamicum* HA DNA of the invention can be isolated based on their homology to the *C. glutamicum* HA nucleic acid disclosed herein using the *C. glutamicum* DNA, or a portion thereof, as a hybridization probe according to standard hybridization techniques under stringent hybridization conditions. Accordingly, in another embodiment, an isolated nucleic acid molecule of the invention is at least 15 nucleotides in length and hybridizes under stringent conditions to the nucleic acid molecule comprising a nucleotide sequence of Appendix A. In other embodiments, the nucleic acid is at least 30, 50, 100, 250 or more nucleotides in length. As used herein, the term "hybridizes under stringent conditions" is intended to describe conditions for hybridization and washing under which nucleotide sequences at least 60% homologous to each other typically remain hybridized to each other. Preferably, the conditions are such that sequences at least about 65%, more preferably at least about 70%, and even more preferably at least about 75% or more homologous to each other typically remain hybridized to each other. Such stringent conditions are known to those of ordinary skill in the art and can be found in *Current Protocols in Molecular Biology*, John Wiley & Sons, N.Y. (1989), 6.3.1-6.3.6. A preferred, non-limiting example of stringent hybridization conditions are hybridization in 6X sodium chloride/sodium citrate (SSC) at about 45°C, followed by one or more washes in 0.2 X SSC, 0.1% SDS at 50-65°C. Preferably, an isolated nucleic acid molecule of the invention that hybridizes under stringent conditions to a sequence of Appendix A corresponds to a naturally-occurring nucleic acid molecule. As used herein, a "naturally-occurring" nucleic acid molecule

refers to an RNA or DNA molecule having a nucleotide sequence that occurs in nature (*e.g.*, encodes a natural protein). In one embodiment, the nucleic acid encodes a natural *C. glutamicum* HA protein.

In addition to naturally-occurring variants of the HA sequence that may exist in the population, one of ordinary skill in the art will further appreciate that changes can be introduced by mutation into a nucleotide sequence of Appendix A, thereby leading to changes in the amino acid sequence of the encoded HA protein, without altering the functional ability of the HA protein. For example, nucleotide substitutions leading to amino acid substitutions at "non-essential" amino acid residues can be made in a sequence of Appendix A. A "non-essential" amino acid residue is a residue that can be altered from the wild-type sequence of one of the HA proteins (Appendix B) without altering the activity of said HA protein, whereas an "essential" amino acid residue is required for HA protein activity. Other amino acid residues, however, (*e.g.*, those that are not conserved or only semi-conserved in the domain having HA activity) may not be essential for activity and thus are likely to be amenable to alteration without altering HA activity.

Accordingly, another aspect of the invention pertains to nucleic acid molecules encoding HA proteins that contain changes in amino acid residues that are not essential for HA activity. Such HA proteins differ in amino acid sequence from a sequence contained in Appendix B yet retain at least one of the HA activities described herein. In one embodiment, the isolated nucleic acid molecule comprises a nucleotide sequence encoding a protein, wherein the protein comprises an amino acid sequence at least about 50% homologous to an amino acid sequence of Appendix B and is capable of participating in the maintenance of homeostasis in *C. glutamicum*, or of performing a function involved in the adaptation of this microorganism to different environmental conditions, or has one or more of the activities set forth in Table 1. Preferably, the protein encoded by the nucleic acid molecule is at least about 50-60% homologous to one of the sequences in Appendix B, more preferably at least about 60-70% homologous to one of the sequences in Appendix B, even more preferably at least about 70-80%, 80-90%, 90-95% homologous to one of the sequences in Appendix B, and most preferably at least about 96%, 97%, 98%, or 99% homologous to one of the sequences in Appendix B.

To determine the percent homology of two amino acid sequences (*e.g.*, one of the sequences of Appendix B and a mutant form thereof) or of two nucleic acids, the sequences are aligned for optimal comparison purposes (*e.g.*, gaps can be introduced in the sequence of one protein or nucleic acid for optimal alignment with the other protein or nucleic acid). The amino acid residues or nucleotides at corresponding amino acid

positions or nucleotide positions are then compared. When a position in one sequence (*e.g.*, one of the sequences of Appendix B) is occupied by the same amino acid residue or nucleotide as the corresponding position in the other sequence (*e.g.*, a mutant form of the sequence selected from Appendix B), then the molecules are homologous at that position (*i.e.*, as used herein amino acid or nucleic acid "homology" is equivalent to amino acid or nucleic acid "identity"). The percent homology between the two sequences is a function of the number of identical positions shared by the sequences (*i.e.*, % homology = # of identical positions/total # of positions x 100).

An isolated nucleic acid molecule encoding an HA protein homologous to a protein sequence of Appendix B can be created by introducing one or more nucleotide substitutions, additions or deletions into a nucleotide sequence of Appendix A such that one or more amino acid substitutions, additions or deletions are introduced into the encoded protein. Mutations can be introduced into one of the sequences of Appendix A by standard techniques, such as site-directed mutagenesis and PCR-mediated mutagenesis. Preferably, conservative amino acid substitutions are made at one or more predicted non-essential amino acid residues. A "conservative amino acid substitution" is one in which the amino acid residue is replaced with an amino acid residue having a similar side chain. Families of amino acid residues having similar side chains have been defined in the art. These families include amino acids with basic side chains (*e.g.*, lysine, arginine, histidine), acidic side chains (*e.g.*, aspartic acid, glutamic acid), uncharged polar side chains (*e.g.*, glycine, asparagine, glutamine, serine, threonine, tyrosine, cysteine), nonpolar side chains (*e.g.*, alanine, valine, leucine, isoleucine, proline, phenylalanine, methionine, tryptophan), beta-branched side chains (*e.g.*, threonine, valine, isoleucine) and aromatic side chains (*e.g.*, tyrosine, phenylalanine, tryptophan, histidine). Thus, a predicted nonessential amino acid residue in an HA protein is preferably replaced with another amino acid residue from the same side chain family. Alternatively, in another embodiment, mutations can be introduced randomly along all or part of an HA coding sequence, such as by saturation mutagenesis, and the resultant mutants can be screened for an HA activity described herein to identify mutants that retain HA activity. Following mutagenesis of one of the sequences of Appendix A, the encoded protein can be expressed recombinantly and the activity of the protein can be determined using, for example, assays described herein (see Example 8 of the Exemplification).

In addition to the nucleic acid molecules encoding HA proteins described above, another aspect of the invention pertains to isolated nucleic acid molecules which are antisense thereto. An "antisense" nucleic acid comprises a nucleotide sequence which is complementary to a "sense" nucleic acid encoding a protein, *e.g.*, complementary to the

coding strand of a double-stranded DNA molecule or complementary to an mRNA sequence. Accordingly, an antisense nucleic acid can hydrogen bond to a sense nucleic acid. The antisense nucleic acid can be complementary to an entire HA coding strand, or to only a portion thereof. In one embodiment, an antisense nucleic acid molecule is antisense to a "coding region" of the coding strand of a nucleotide sequence encoding an HA protein. The term "coding region" refers to the region of the nucleotide sequence comprising codons which are translated into amino acid residues (*e.g.*, the entire coding region of SEQ ID NO. 1 (RXA02702) comprises nucleotides 1 to1458). In another embodiment, the antisense nucleic acid molecule is antisense to a "noncoding region" of the coding strand of a nucleotide sequence encoding HA. The term "noncoding region" refers to 5' and 3' sequences which flank the coding region that are not translated into amino acids (*i.e.*, also referred to as 5' and 3' untranslated regions).

Given the coding strand sequences encoding HA disclosed herein (*e.g.*, the sequences set forth in Appendix A), antisense nucleic acids of the invention can be designed according to the rules of Watson and Crick base pairing. The antisense nucleic acid molecule can be complementary to the entire coding region of HA mRNA, but more preferably is an oligonucleotide which is antisense to only a portion of the coding or noncoding region of HA mRNA. For example, the antisense oligonucleotide can be complementary to the region surrounding the translation start site of HA mRNA. An antisense oligonucleotide can be, for example, about 5, 10, 15, 20, 25, 30, 35, 40, 45 or 50 nucleotides in length. An antisense nucleic acid of the invention can be constructed using chemical synthesis and enzymatic ligation reactions using procedures known in the art. For example, an antisense nucleic acid (*e.g.*, an antisense oligonucleotide) can be chemically synthesized using naturally occurring nucleotides or variously modified nucleotides designed to increase the biological stability of the molecules or to increase the physical stability of the duplex formed between the antisense and sense nucleic acids, *e.g.*, phosphorothioate derivatives and acridine substituted nucleotides can be used. Examples of modified nucleotides which can be used to generate the antisense nucleic acid include 5-fluorouracil, 5-bromouracil, 5-chlorouracil, 5-iodouracil, hypoxanthine, xanthine, 4-acetylcytosine, 5-(carboxyhydroxylmethyl) uracil, 5-carboxymethylaminomethyl-2-thiouridine, 5-carboxymethylaminomethyluracil, dihydrouracil, beta-D-galactosylqueosine, inosine, N6-isopentenyladenine, 1-methylguanine, 1-methylinosine, 2,2-dimethylguanine, 2-methyladenine, 2-methylguanine, 3-methylcytosine, 5-methylcytosine, N6-adenine, 7-methylguanine, 5-methylaminomethyluracil, 5-methoxyaminomethyl-2-thiouracil, beta-D-mannosylqueosine, 5'-methoxycarboxymethyluracil, 5-methoxyuracil, 2-methylthio-N6-isopentenyladenine, uracil-5-oxyacetic acid (v), wybutoxosine, pseudouracil, queosine,

2-thiocytosine, 5-methyl-2-thiouracil, 2-thiouracil, 4-thiouracil, 5-methyluracil, uracil-5-oxyacetic acid methylester, uracil-5-oxyacetic acid (v), 5-methyl-2-thiouracil, 3-(3-amino-3-N-2-carboxypropyl) uracil, (acp3)w, and 2,6-diaminopurine. Alternatively, the antisense nucleic acid can be produced biologically using an expression vector into which a nucleic acid has been subcloned in an antisense orientation (*i.e.*, RNA transcribed from the inserted nucleic acid will be of an antisense orientation to a target nucleic acid of interest, described further in the following subsection).

The antisense nucleic acid molecules of the invention are typically administered to a cell or generated *in situ* such that they hybridize with or bind to cellular mRNA and/or genomic DNA encoding an HA protein to thereby inhibit expression of the protein, *e.g.*, by inhibiting transcription and/or translation. The hybridization can be by conventional nucleotide complementarity to form a stable duplex, or, for example, in the case of an antisense nucleic acid molecule which binds to DNA duplexes, through specific interactions in the major groove of the double helix. The antisense molecule can be modified such that it specifically binds to a receptor or an antigen expressed on a selected cell surface, *e.g.*, by linking the antisense nucleic acid molecule to a peptide or an antibody which binds to a cell surface receptor or antigen. The antisense nucleic acid molecule can also be delivered to cells using the vectors described herein. To achieve sufficient intracellular concentrations of the antisense molecules, vector constructs in which the antisense nucleic acid molecule is placed under the control of a strong prokaryotic, viral, or eukaryotic promoter are preferred.

In yet another embodiment, the antisense nucleic acid molecule of the invention is an α-anomeric nucleic acid molecule. An α-anomeric nucleic acid molecule forms specific double-stranded hybrids with complementary RNA in which, contrary to the usual β-units, the strands run parallel to each other (Gaultier *et al.* (1987) *Nucleic Acids. Res.* 15:6625-6641). The antisense nucleic acid molecule can also comprise a 2'-o-methylribonucleotide (Inoue *et al.* (1987) *Nucleic Acids Res.* 15:6131-6148) or a chimeric RNA-DNA analogue (Inoue *et al.* (1987) *FEBS Lett.* 215:327-330).

In still another embodiment, an antisense nucleic acid of the invention is a ribozyme. Ribozymes are catalytic RNA molecules with ribonuclease activity which are capable of cleaving a single-stranded nucleic acid, such as an mRNA, to which they have a complementary region. Thus, ribozymes (*e.g.*, hammerhead ribozymes (described in Haselhoff and Gerlach (1988) *Nature* 334:585-591)) can be used to catalytically cleave HA mRNA transcripts to thereby inhibit translation of HA mRNA. A ribozyme having specificity for an HA-encoding nucleic acid can be designed based upon the nucleotide sequence of an HA DNA molecule disclosed herein (*i.e.*, SEQ ID NO. 3 (RXA02705) Appendix A). For example, a derivative of a *Tetrahymena* L-19

IVS RNA can be constructed in which the nucleotide sequence of the active site is complementary to the nucleotide sequence to be cleaved in an HA-encoding mRNA. See, *e.g.*, Cech *et al.* U.S. Patent No. 4,987,071 and Cech *et al.* U.S. Patent No. 5,116,742. Alternatively, HA mRNA can be used to select a catalytic RNA having a specific ribonuclease activity from a pool of RNA molecules. See, *e.g.*, Bartel, D. and Szostak, J.W. (1993) *Science* 261:1411-1418.

Alternatively, HA gene expression can be inhibited by targeting nucleotide sequences complementary to the regulatory region of an HA nucleotide sequence (*e.g.*, an HA promoter and/or enhancers) to form triple helical structures that prevent transcription of an HA gene in target cells. See generally, Helene, C. (1991) *Anticancer Drug Des.* 6(6):569-84; Helene, C. *et al.* (1992) *Ann. N.Y. Acad. Sci.* 660:27-36; and Maher, L.J. (1992) *Bioassays* 14(12):807-15.

B. Recombinant Expression Vectors and Host Cells

Another aspect of the invention pertains to vectors, preferably expression vectors, containing a nucleic acid encoding an HA protein (or a portion thereof). As used herein, the term "vector" refers to a nucleic acid molecule capable of transporting another nucleic acid to which it has been linked. One type of vector is a "plasmid", which refers to a circular double stranded DNA loop into which additional DNA segments can be ligated. Another type of vector is a viral vector, wherein additional DNA segments can be ligated into the viral genome. Certain vectors are capable of autonomous replication in a host cell into which they are introduced (*e.g.*, bacterial vectors having a bacterial origin of replication and episomal mammalian vectors). Other vectors (*e.g.*, non-episomal mammalian vectors) are integrated into the genome of a host cell upon introduction into the host cell, and thereby are replicated along with the host genome. Moreover, certain vectors are capable of directing the expression of genes to which they are operatively linked. Such vectors are referred to herein as "expression vectors". In general, expression vectors of utility in recombinant DNA techniques are often in the form of plasmids. In the present specification, "plasmid" and "vector" can be used interchangeably as the plasmid is the most commonly used form of vector. However, the invention is intended to include such other forms of expression vectors, such as viral vectors (*e.g.*, replication defective retroviruses, adenoviruses and adeno-associated viruses), which serve equivalent functions.

The recombinant expression vectors of the invention comprise a nucleic acid of the invention in a form suitable for expression of the nucleic acid in a host cell, which means that the recombinant expression vectors include one or more regulatory sequences, selected on the basis of the host cells to be used for expression, which are

operatively linked to the nucleic acid sequence to be expressed. Within a recombinant expression vector, "operably linked" is intended to mean that the nucleotide sequence of interest is linked to the regulatory sequence(s) in a manner which allows for expression of the nucleotide sequence (*e.g.*, in an *in vitro* transcription/translation system or in a host cell when the vector is introduced into the host cell). The term "regulatory sequence" is intended to include promoters, enhancers and other expression control elements (*e.g.*, polyadenylation signals). Such regulatory sequences are described, for example, in Goeddel; *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, CA (1990). Regulatory sequences include those which direct constitutive expression of a nucleotide sequence in many types of host cell and those which direct expression of the nucleotide sequence only in certain host cells. Preferred regulatory sequences are, for example, promoters such as cos-, tac-, trp-, tet-, trp-tet-, lpp-, lac-, lpp-lac-, lacI^q-, T7-, T5-, T3-, gal-, trc-, ara-, SP6-, arny, SPO2, λ-P_R- or λ P_L, which are used preferably in bacteria. Additional regulatory sequences are, for example, promoters from yeasts and fungi, such as ADC1, MFα, AC, P-60, CYC1, GAPDH, TEF, rp28, ADH, promoters from plants such as CaMV/35S, SSU, OCS, lib4, usp, STLS1, B33, nos or ubiquitin- or phaseolin-promoters. It is also possible to use artificial promoters. It will be appreciated by those of ordinary skill in the art that the design of the expression vector can depend on such factors as the choice of the host cell to be transformed, the level of expression of protein desired, etc. The expression vectors of the invention can be introduced into host cells to thereby produce proteins or peptides, including fusion proteins or peptides, encoded by nucleic acids as described herein (*e.g.*, HA proteins, mutant forms of HA proteins, fusion proteins, etc.).

The recombinant expression vectors of the invention can be designed for expression of HA proteins in prokaryotic or eukaryotic cells. For example, HA genes can be expressed in bacterial cells such as *C. glutamicum*, insect cells (using baculovirus expression vectors), yeast and other fungal cells (see Romanos, M.A. *et al.* (1992) "Foreign gene expression in yeast: a review", *Yeast* 8: 423-488; van den Hondel, C.A.M.J.J. *et al.* (1991) "Heterologous gene expression in filamentous fungi" in: More Gene Manipulations in Fungi, J.W. Bennet & L.L. Lasure, eds., p. 396-428: Academic Press: San Diego; and van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, Peberdy, J.F. *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge), algae and multicellular plant cells (see Schmidt, R. and Willmitzer, L. (1988) High efficiency *Agrobacterium tumefaciens* –mediated transformation of *Arabidopsis thaliana* leaf and cotyledon explants" *Plant Cell Rep.*: 583-586), or mammalian cells. Suitable host cells are discussed further in Goeddel, *Gene Expression Technology:*

Methods in Enzymology 185, Academic Press, San Diego, CA (1990). Alternatively, the recombinant expression vector can be transcribed and translated *in vitro*, for example using T7 promoter regulatory sequences and T7 polymerase.

Expression of proteins in prokaryotes is most often carried out with vectors containing constitutive or inducible promoters directing the expression of either fusion or non-fusion proteins. Fusion vectors add a number of amino acids to a protein encoded therein, usually to the amino terminus of the recombinant protein but also to the C-terminus or fused within suitable regions in the proteins. Such fusion vectors typically serve three purposes: 1) to increase expression of recombinant protein; 2) to increase the solubility of the recombinant protein; and 3) to aid in the purification of the recombinant protein by acting as a ligand in affinity purification. Often, in fusion expression vectors, a proteolytic cleavage site is introduced at the junction of the fusion moiety and the recombinant protein to enable separation of the recombinant protein from the fusion moiety subsequent to purification of the fusion protein. Such enzymes, and their cognate recognition sequences, include Factor Xa, thrombin and enterokinase.

Typical fusion expression vectors include pGEX (Pharmacia Biotech Inc; Smith, D.B. and Johnson, K.S. (1988) *Gene* 67:31-40), pMAL (New England Biolabs, Beverly, MA) and pRIT5 (Pharmacia, Piscataway, NJ) which fuse glutathione S-transferase (GST), maltose E binding protein, or protein A, respectively, to the target recombinant protein. In one embodiment, the coding sequence of the HA protein is cloned into a pGEX expression vector to create a vector encoding a fusion protein comprising, from the N-terminus to the C-terminus, GST-thrombin cleavage site-X protein. The fusion protein can be purified by affinity chromatography using glutathione-agarose resin. Recombinant HA protein unfused to GST can be recovered by cleavage of the fusion protein with thrombin.

Examples of suitable inducible non-fusion *E. coli* expression vectors include pTrc (Amann *et al.*, (1988) *Gene* 69:301-315) pLG338, pACYC184, pBR322, pUC18, pUC19, pKC30, pRep4, pHS1, pHS2, pPLc236, pMBL24, pLG200, pUR290, pIN-III113-B1, λgt11, pBdCl, and pET 11d (Studier *et al.*, *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 60-89 ; and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018). Target gene expression from the pTrc vector relies on host RNA polymerase transcription from a hybrid trp-lac fusion promoter. Target gene expression from the pET 11d vector relies on transcription from a T7 gn10-lac fusion promoter mediated by a coexpressed viral RNA polymerase (T7 gn1). This viral polymerase is supplied by host strains BL21(DE3) or HMS174(DE3) from a resident λ prophage harboring a T7 gn1 gene under the transcriptional control of the lacUV 5 promoter. For transformation

of other varieties of bacteria, appropriate vectors may be selected. For example, the plasmids pIJ101, pIJ364, pIJ702 and pIJ361 are known to be useful in transforming Streptomyces, while plasmids pUB110, pC194, or pBD214 are suited for transformation of Bacillus species. Several plasmids of use in the transfer of genetic information into Corynebacterium include pHM1519, pBL1, pSA77, or pAJ667 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

One strategy to maximize recombinant protein expression is to express the protein in a host bacteria with an impaired capacity to proteolytically cleave the recombinant protein (Gottesman, S., *Gene Expression Technology: Methods in Enzymology* 185, Academic Press, San Diego, California (1990) 119-128). Another strategy is to alter the nucleic acid sequence of the nucleic acid to be inserted into an expression vector so that the individual codons for each amino acid are those preferentially utilized in the bacterium chosen for expression, such as *C. glutamicum* (Wada *et al.* (1992) *Nucleic Acids Res.* 20: 2111-2118). Such alteration of nucleic acid sequences of the invention can be carried out by standard DNA synthesis techniques.

In another embodiment, the HA protein expression vector is a yeast expression vector. Examples of vectors for expression in yeast *S. cerevisiae* include pYepSec1 (Baldari, *et al.*, (1987) *Embo J.* 6:229-234), 2 μ, pAG-1, Yep6, Yep13, pEMBLYe23, pMFa (Kurjan and Herskowitz, (1982) *Cell* 30:933-943), pJRY88 (Schultz *et al.*, (1987) *Gene* 54:113-123), and pYES2 (Invitrogen Corporation, San Diego, CA). Vectors and methods for the construction of vectors appropriate for use in other fungi, such as the filamentous fungi, include those detailed in: van den Hondel, C.A.M.J.J. & Punt, P.J. (1991) "Gene transfer systems and vector development for filamentous fungi, in: Applied Molecular Genetics of Fungi, J.F. Peberdy, *et al.*, eds., p. 1-28, Cambridge University Press: Cambridge, and Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York (IBSN 0 444 904018).

Alternatively, the HA proteins of the invention can be expressed in insect cells using baculovirus expression vectors. Baculovirus vectors available for expression of proteins in cultured insect cells (*e.g.*, Sf 9 cells) include the pAc series (Smith *et al.* (1983) *Mol. Cell Biol.* 3:2156-2165) and the pVL series (Lucklow and Summers (1989) *Virology* 170:31-39).

In another embodiment, the HA proteins of the invention may be expressed in unicellular plant cells (such as algae) or in plant cells from higher plants (*e.g.*, the spermatophytes, such as crop plants). Examples of plant expression vectors include those detailed in: Becker, D., Kemper, E., Schell, J. and Masterson, R. (1992) "New plant binary vectors with selectable markers located proximal to the left border", *Plant Mol. Biol.* 20: 1195-1197; and Bevan, M.W. (1984) "Binary *Agrobacterium* vectors for

plant transformation", *Nucl. Acid. Res.* 12: 8711-8721, and include pLGV23, pGHlac+, pBIN19, pAK2004, and pDH51 (Pouwels *et al.*, eds. (1985) Cloning Vectors. Elsevier: New York IBSN 0 444 904018).

In yet another embodiment, a nucleic acid of the invention is expressed in mammalian cells using a mammalian expression vector. Examples of mammalian expression vectors include pCDM8 (Seed, B. (1987) *Nature* 329:840) and pMT2PC (Kaufman *et al.* (1987) *EMBO J.* 6:187-195). When used in mammalian cells, the expression vector's control functions are often provided by viral regulatory elements. For example, commonly used promoters are derived from polyoma, Adenovirus 2, cytomegalovirus and Simian Virus 40. For other suitable expression systems for both prokaryotic and eukaryotic cells see chapters 16 and 17 of Sambrook, J., Fritsh, E. F., and Maniatis, T. *Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989.

In another embodiment, the recombinant mammalian expression vector is capable of directing expression of the nucleic acid preferentially in a particular cell type (*e.g.*, tissue-specific regulatory elements are used to express the nucleic acid). Tissue-specific regulatory elements are known in the art. Non-limiting examples of suitable tissue-specific promoters include the albumin promoter (liver-specific; Pinkert *et al.* (1987) *Genes Dev.* 1:268-277), lymphoid-specific promoters (Calame and Eaton (1988) *Adv. Immunol.* 43:235-275), in particular promoters of T cell receptors (Winoto and Baltimore (1989) *EMBO J.* 8:729-733) and immunoglobulins (Banerji *et al.* (1983) *Cell* 33:729-740; Queen and Baltimore (1983) *Cell* 33:741-748), neuron-specific promoters (*e.g.*, the neurofilament promoter; Byrne and Ruddle (1989) *PNAS* 86:5473-5477), pancreas-specific promoters (Edlund *et al.* (1985) *Science* 230:912-916), and mammary gland-specific promoters (*e.g.*, milk whey promoter; U.S. Patent No. 4,873,316 and European Application Publication No. 264,166). Developmentally-regulated promoters are also encompassed, for example the murine hox promoters (Kessel and Gruss (1990) *Science* 249:374-379) and the α-fetoprotein promoter (Campes and Tilghman (1989) *Genes Dev.* 3:537-546).

The invention further provides a recombinant expression vector comprising a DNA molecule of the invention cloned into the expression vector in an antisense orientation. That is, the DNA molecule is operatively linked to a regulatory sequence in a manner which allows for expression (by transcription of the DNA molecule) of an RNA molecule which is antisense to HA mRNA. Regulatory sequences operatively linked to a nucleic acid cloned in the antisense orientation can be chosen which direct the continuous expression of the antisense RNA molecule in a variety of cell types, for

instance viral promoters and/or enhancers, or regulatory sequences can be chosen which direct constitutive, tissue specific or cell type specific expression of antisense RNA. The antisense expression vector can be in the form of a recombinant plasmid, phagemid or attenuated virus in which antisense nucleic acids are produced under the control of a high efficiency regulatory region, the activity of which can be determined by the cell type into which the vector is introduced. For a discussion of the regulation of gene expression using antisense genes see Weintraub, H. *et al.*, Antisense RNA as a molecular tool for genetic analysis, *Reviews - Trends in Genetics*, Vol. 1(1) (1986).

Another aspect of the invention pertains to host cells into which a recombinant expression vector of the invention has been introduced. The terms "host cell" and "recombinant host cell" are used interchangeably herein. It is understood that such terms refer not only to the particular subject cell but to the progeny or potential progeny of such a cell. Because certain modifications may occur in succeeding generations due to either mutation or environmental influences, such progeny may not, in fact, be identical to the parent cell, but are still included within the scope of the term as used herein.

A host cell can be any prokaryotic or eukaryotic cell. For example, an HA protein can be expressed in bacterial cells such as *C. glutamicum*, insect cells, yeast or mammalian cells (such as Chinese hamster ovary cells (CHO) or COS cells). Other suitable host cells are known to those of ordinary skill in the art. Microorganisms related to *Corynebacterium glutamicum* which may be conveniently used as host cells for the nucleic acid and protein molecules of the invention are set forth in Table 3.

Vector DNA can be introduced into prokaryotic or eukaryotic cells via conventional transformation or transfection techniques. As used herein, the terms "transformation" and "transfection", "conjugation" and "transduction" are intended to refer to a variety of art-recognized techniques for introducing foreign nucleic acid (*e.g.*, linear DNA or RNA (*e.g.*, a linearized vector or a gene construct alone without a vector) or nucleic acid in the form of a vector (*e.g.*, a plasmid, phage, phasmid, phagemid, transposon or other DNA) into a host cell, including calcium phosphate or calcium chloride co-precipitation, DEAE-dextran-mediated transfection, lipofection, natural competence, chemical-mediated transfer, or electroporation. Suitable methods for transforming or transfecting host cells can be found in Sambrook, *et al.* (*Molecular Cloning: A Laboratory Manual. 2nd, ed., Cold Spring Harbor Laboratory,* Cold Spring Harbor Laboratory Press, Cold Spring Harbor, NY, 1989), and other laboratory manuals.

For stable transfection of mammalian cells, it is known that, depending upon the expression vector and transfection technique used, only a small fraction of cells may integrate the foreign DNA into their genome. In order to identify and select these

integrants, a gene that encodes a selectable marker (*e.g.*, resistance to antibiotics) is generally introduced into the host cells along with the gene of interest. Preferred selectable markers include those which confer resistance to drugs, such as G418, hygromycin and methotrexate. Nucleic acid encoding a selectable marker can be introduced into a host cell on the same vector as that encoding an HA protein or can be introduced on a separate vector. Cells stably transfected with the introduced nucleic acid can be identified by, for example, drug selection (*e.g.*, cells that have incorporated the selectable marker gene will survive, while the other cells die).

To create a homologous recombinant microorganism, a vector is prepared which contains at least a portion of an HA gene into which a deletion, addition or substitution has been introduced to thereby alter, *e.g.*, functionally disrupt, the HA gene. Preferably, this HA gene is a *Corynebacterium glutamicum* HA gene, but it can be a homologue from a related bacterium or even from a mammalian, yeast, or insect source. In a preferred embodiment, the vector is designed such that, upon homologous recombination, the endogenous HA gene is functionally disrupted (*i.e.*, no longer encodes a functional protein; also referred to as a "knock out" vector). Alternatively, the vector can be designed such that, upon homologous recombination, the endogenous HA gene is mutated or otherwise altered but still encodes functional protein (*e.g.*, the upstream regulatory region can be altered to thereby alter the expression of the endogenous HA protein). In the homologous recombination vector, the altered portion of the HA gene is flanked at its 5' and 3' ends by additional nucleic acid of the HA gene to allow for homologous recombination to occur between the exogenous HA gene carried by the vector and an endogenous HA gene in a microorganism. The additional flanking HA nucleic acid is of sufficient length for successful homologous recombination with the endogenous gene. Typically, several kilobases of flanking DNA (both at the 5' and 3' ends) are included in the vector (see *e.g.*, Thomas, K.R., and Capecchi, M.R. (1987) Cell 51: 503 for a description of homologous recombination vectors). The vector is introduced into a microorganism (*e.g.*, by electroporation) and cells in which the introduced HA gene has homologously recombined with the endogenous HA gene are selected, using art-known techniques.

In another embodiment, recombinant microorganisms can be produced which contain selected systems which allow for regulated expression of the introduced gene. For example, inclusion of an HA gene on a vector placing it under control of the lac operon permits expression of the HA gene only in the presence of IPTG. Such regulatory systems are well known in the art.

In another embodiment, an endogenous HA gene in a host cell is disrupted (*e.g.*, by homologous recombination or other genetic means known in the art) such that

expression of its protein product does not occur. In another embodiment, an endogenous or introduced HA gene in a host cell has been altered by one or more point mutations, deletions, or inversions, but still encodes a functional HA protein. In still another embodiment, one or more of the regulatory regions (*e.g.*, a promoter, repressor, or inducer) of an HA gene in a microorganism has been altered (*e.g.*, by deletion, truncation, inversion, or point mutation) such that the expression of the HA gene is modulated. One of ordinary skill in the art will appreciate that host cells containing more than one of the described HA gene and protein modifications may be readily produced using the methods of the invention, and are meant to be included in the present invention.

A host cell of the invention, such as a prokaryotic or eukaryotic host cell in culture, can be used to produce (*i.e.*, express) an HA protein. Accordingly, the invention further provides methods for producing HA proteins using the host cells of the invention. In one embodiment, the method comprises culturing the host cell of invention (into which a recombinant expression vector encoding an HA protein has been introduced, or into which genome has been introduced a gene encoding a wild-type or altered HA protein) in a suitable medium until HA protein is produced. In another embodiment, the method further comprises isolating HA proteins from the medium or the host cell.

C. Isolated HA Proteins

Another aspect of the invention pertains to isolated HA proteins, and biologically active portions thereof. An "isolated" or "purified" protein or biologically active portion thereof is substantially free of cellular material when produced by recombinant DNA techniques, or chemical precursors or other chemicals when chemically synthesized. The language "substantially free of cellular material" includes preparations of HA protein in which the protein is separated from cellular components of the cells in which it is naturally or recombinantly produced. In one embodiment, the language "substantially free of cellular material" includes preparations of HA protein having less than about 30% (by dry weight) of non-HA protein (also referred to herein as a "contaminating protein"), more preferably less than about 20% of non-HA protein, still more preferably less than about 10% of non-HA protein, and most preferably less than about 5% non-HA protein. When the HA protein or biologically active portion thereof is recombinantly produced, it is also preferably substantially free of culture medium, *i.e.*, culture medium represents less than about 20%, more preferably less than about 10%, and most preferably less than about 5% of the volume of the protein preparation. The language "substantially free of chemical precursors or other chemicals" includes

preparations of HA protein in which the protein is separated from chemical precursors or other chemicals which are involved in the synthesis of the protein. In one embodiment, the language "substantially free of chemical precursors or other chemicals" includes preparations of HA protein having less than about 30% (by dry weight) of chemical precursors or non-HA chemicals, more preferably less than about 20% chemical precursors or non-HA chemicals, still more preferably less than about 10% chemical precursors or non-HA chemicals, and most preferably less than about 5% chemical precursors or non-HA chemicals. In preferred embodiments, isolated proteins or biologically active portions thereof lack contaminating proteins from the same organism from which the HA protein is derived. Typically, such proteins are produced by recombinant expression of, for example, a *C. glutamicum* HA protein in a microorganism such as *C. glutamicum.*

An isolated HA protein or a portion thereof of the invention can participate in the repair or recombination of DNA, in the transposition of genetic material, in gene expression (*i.e.*, the processes of transcription or translation), in protein folding, or in protein secretion in *Corynebacterium glutamicum*, or has one or more of the activities set forth in Table 1. In preferred embodiments, the protein or portion thereof comprises an amino acid sequence which is sufficiently homologous to an amino acid sequence of Appendix B such that the protein or portion thereof maintains the ability to participate in the maintenance of homeostasis in *C. glutamicum*, or to perform a function involved in the adaptation of this microorganism to different environmental conditions. The portion of the protein is preferably a biologically active portion as described herein. In another preferred embodiment, an HA protein of the invention has an amino acid sequence shown in Appendix B. In yet another preferred embodiment, the HA protein has an amino acid sequence which is encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A. In still another preferred embodiment, the HA protein has an amino acid sequence which is encoded by a nucleotide sequence that is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% % or more homologous to one of the nucleic acid sequences of Appendix A, or a portion thereof. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are

intended to be included. The preferred HA proteins of the present invention also preferably possess at least one of the HA activities described herein. For example, a preferred HA protein of the present invention includes an amino acid sequence encoded by a nucleotide sequence which hybridizes, *e.g.*, hybridizes under stringent conditions, to a nucleotide sequence of Appendix A, and which can participate in the maintenance of homeostasis in *C. glutamicum*, or can perform a function involved in the adaptation of this microorganism to different environmental conditions, or which has one or more of the activities set forth in Table 1.

In other embodiments, the HA protein is substantially homologous to an amino acid sequence of Appendix B and retains the functional activity of the protein of one of the sequences of Appendix B yet differs in amino acid sequence due to natural variation or mutagenesis, as described in detail in subsection I above. Accordingly, in another embodiment, the HA protein is a protein which comprises an amino acid sequence which is at least about 50%, 51%, 52%, 53%, 54%, 55%, 56%, 57%, 58%, 59%, or 60%, preferably at least about 61%, 62%, 63%, 64%, 65%, 66%, 67%, 68%, 69%, or 70%, more preferably at least about 71%, 72%, 73%, 74%, 75%, 76%, 77%, 78%, 79%, or 80%, 81%, 82%, 83%, 84%, 85%, 86%, 87%, 88%, 89%, or 90%, or 91%, 92%, 93%, 94%, and even more preferably at least about 95%, 96%, 97%, 98%, 99% or more homologous to an entire amino acid sequence of Appendix B and which has at least one of the HA activities described herein. Ranges and identity values intermediate to the above-recited values, (*e.g.*, 70-90% identical or 80-95% identical) are also intended to be encompassed by the present invention. For example, ranges of identity values using a combination of any of the above values recited as upper and/or lower limits are intended to be included. In another embodiment, the invention pertains to a full length *C. glutamicum* protein which is substantially homologous to an entire amino acid sequence of Appendix B.

Biologically active portions of an HA protein include peptides comprising amino acid sequences derived from the amino acid sequence of an HA protein, *e.g.*, the an amino acid sequence shown in Appendix B or the amino acid sequence of a protein homologous to an HA protein, which include fewer amino acids than a full length HA protein or the full length protein which is homologous to an HA protein, and exhibit at least one activity of an HA protein. Typically, biologically active portions (peptides, *e.g.*, peptides which are, for example, 5, 10, 15, 20, 30, 35, 36, 37, 38, 39, 40, 50, 100 or more amino acids in length) comprise a domain or motif with at least one activity of an HA protein. Moreover, other biologically active portions, in which other regions of the protein are deleted, can be prepared by recombinant techniques and evaluated for one or more of the activities described herein. Preferably, the biologically active portions of an

HA protein include one or more selected domains/motifs or portions thereof having biological activity.

HA proteins are preferably produced by recombinant DNA techniques. For example, a nucleic acid molecule encoding the protein is cloned into an expression vector (as described above), the expression vector is introduced into a host cell (as described above) and the HA protein is expressed in the host cell. The HA protein can then be isolated from the cells by an appropriate purification scheme using standard protein purification techniques. Alternative to recombinant expression, an HA protein, polypeptide, or peptide can be synthesized chemically using standard peptide synthesis techniques. Moreover, native HA protein can be isolated from cells (*e.g.*, endothelial cells), for example using an anti-HA antibody, which can be produced by standard techniques utilizing an HA protein or fragment thereof of this invention.

The invention also provides HA chimeric or fusion proteins. As used herein, an HA "chimeric protein" or "fusion protein" comprises an HA polypeptide operatively linked to a non-HA polypeptide. An "HA polypeptide" refers to a polypeptide having an amino acid sequence corresponding to an HA protein, whereas a "non-HA polypeptide" refers to a polypeptide having an amino acid sequence corresponding to a protein which is not substantially homologous to the HA protein, *e.g.*, a protein which is different from the HA protein and which is derived from the same or a different organism. Within the fusion protein, the term "operatively linked" is intended to indicate that the HA polypeptide and the non-HA polypeptide are fused in-frame to each other. The non-HA polypeptide can be fused to the N-terminus or C-terminus of the HA polypeptide. For example, in one embodiment the fusion protein is a GST-HA fusion protein in which the HA sequences are fused to the C-terminus of the GST sequences. Such fusion proteins can facilitate the purification of recombinant HA proteins. In another embodiment, the fusion protein is an HA protein containing a heterologous signal sequence at its N-terminus. In certain host cells (*e.g.*, mammalian host cells), expression and/or secretion of an HA protein can be increased through use of a heterologous signal sequence.

Preferably, an HA chimeric or fusion protein of the invention is produced by standard recombinant DNA techniques. For example, DNA fragments coding for the different polypeptide sequences are ligated together in-frame in accordance with conventional techniques, for example by employing blunt-ended or stagger-ended termini for ligation, restriction enzyme digestion to provide for appropriate termini, filling-in of cohesive ends as appropriate, alkaline phosphatase treatment to avoid undesirable joining, and enzymatic ligation. In another embodiment, the fusion gene can be synthesized by conventional techniques including automated DNA synthesizers. Alternatively, PCR amplification of gene fragments can be carried out using anchor

primers which give rise to complementary overhangs between two consecutive gene fragments which can subsequently be annealed and reamplified to generate a chimeric gene sequence (see, for example, *Current Protocols in Molecular Biology*, eds. Ausubel *et al.* John Wiley & Sons: 1992). Moreover, many expression vectors are commercially available that already encode a fusion moiety (*e.g.*, a GST polypeptide). An HA-encoding nucleic acid can be cloned into such an expression vector such that the fusion moiety is linked in-frame to the HA protein.

Homologues of the HA protein can be generated by mutagenesis, *e.g.*, discrete point mutation or truncation of the HA protein. As used herein, the term "homologue" refers to a variant form of the HA protein which acts as an agonist or antagonist of the activity of the HA protein. An agonist of the HA protein can retain substantially the same, or a subset, of the biological activities of the HA protein. An antagonist of the HA protein can inhibit one or more of the activities of the naturally occurring form of the HA protein, by, for example, competitively binding to a downstream or upstream member of a biochemical cascade which includes the HA protein, by binding to a target molecule with which the HA protein interacts, such that no functional interaction is possible, or by binding directly to the HA protein and inhibiting its normal activity.

In an alternative embodiment, homologues of the HA protein can be identified by screening combinatorial libraries of mutants, *e.g.*, truncation mutants, of the HA protein for HA protein agonist or antagonist activity. In one embodiment, a variegated library of HA variants is generated by combinatorial mutagenesis at the nucleic acid level and is encoded by a variegated gene library. A variegated library of HA variants can be produced by, for example, enzymatically ligating a mixture of synthetic oligonucleotides into gene sequences such that a degenerate set of potential HA sequences is expressible as individual polypeptides, or alternatively, as a set of larger fusion proteins (*e.g.*, for phage display) containing the set of HA sequences therein. There are a variety of methods which can be used to produce libraries of potential HA homologues from a degenerate oligonucleotide sequence. Chemical synthesis of a degenerate gene sequence can be performed in an automatic DNA synthesizer, and the synthetic gene then ligated into an appropriate expression vector. Use of a degenerate set of genes allows for the provision, in one mixture, of all of the sequences encoding the desired set of potential HA sequences. Methods for synthesizing degenerate oligonucleotides are known in the art (see, *e.g.*, Narang, S.A. (1983) *Tetrahedron* 39:3; Itakura *et al.* (1984) *Annu. Rev. Biochem.* 53:323; Itakura *et al.* (1984) *Science* 198:1056; Ike *et al.* (1983) *Nucleic Acid Res.* 11:477.

In addition, libraries of fragments of the HA protein coding can be used to generate a variegated population of HA fragments for screening and subsequent

selection of homologues of an HA protein. In one embodiment, a library of coding sequence fragments can be generated by treating a double stranded PCR fragment of an HA coding sequence with a nuclease under conditions wherein nicking occurs only about once per molecule, denaturing the double stranded DNA, renaturing the DNA to form double stranded DNA which can include sense/antisense pairs from different nicked products, removing single stranded portions from reformed duplexes by treatment with S1 nuclease, and ligating the resulting fragment library into an expression vector. By this method, an expression library can be derived which encodes N-terminal, C-terminal and internal fragments of various sizes of the HA protein.

Several techniques are known in the art for screening gene products of combinatorial libraries made by point mutations or truncation, and for screening cDNA libraries for gene products having a selected property. Such techniques are adaptable for rapid screening of the gene libraries generated by the combinatorial mutagenesis of HA homologues. The most widely used techniques, which are amenable to high through-put analysis, for screening large gene libraries typically include cloning the gene library into replicable expression vectors, transforming appropriate cells with the resulting library of vectors, and expressing the combinatorial genes under conditions in which detection of a desired activity facilitates isolation of the vector encoding the gene whose product was detected. Recursive ensemble mutagenesis (REM), a new technique which enhances the frequency of functional mutants in the libraries, can be used in combination with the screening assays to identify HA homologues (Arkin and Yourvan (1992) *PNAS* *89*:7811-7815; Delgrave *et al.* (1993) *Protein Engineering* 6(3):327-331).

In another embodiment, cell based assays can be exploited to analyze a variegated HA library, using methods well known in the art.

D. Uses and Methods of the Invention

The nucleic acid molecules, proteins, protein homologues, fusion proteins, primers, vectors, and host cells described herein can be used in one or more of the following methods: identification of *C. glutamicum* and related organisms; mapping of genomes of organisms related to *C. glutamicum*; identification and localization of *C. glutamicum* sequences of interest; evolutionary studies; determination of HA protein regions required for function; modulation of an HA protein activity; modulation of the metabolism of one or more inorganic compounds; modulation of the modification or degradation of one or more aromatic or aliphatic compounds; modulation of cell wall synthesis or rearrangements; modulation of enzyme activity or proteolysis; and modulation of cellular production of a desired compound, such as a fine chemical.

The HA nucleic acid molecules of the invention have a variety of uses. First,

they may be used to identify an organism as being *Corynebacterium glutamicum* or a close relative thereof. Also, they may be used to identify the presence of *C. glutamicum* or a relative thereof in a mixed population of microorganisms. The invention provides the nucleic acid sequences of a number of *C. glutamicum* genes; by probing the extracted genomic DNA of a culture of a unique or mixed population of microorganisms under stringent conditions with a probe spanning a region of a *C. glutamicum* gene which is unique to this organism, one can ascertain whether this organism is present. Although *Corynebacterium glutamicum* itself is nonpathogenic, it is related to pathogenic species, such as *Corynebacterium diphtheriae*. *Corynebacterium diphtheriae* is the causative agent of diphtheria, a rapidly developing, acute, febrile infection which involves both local and systemic pathology. In this disease, a local lesion develops in the upper respiratory tract and involves necrotic injury to epithelial cells; the bacilli secrete toxin which is disseminated through this lesion to distal susceptible tissues of the body. Degenerative changes brought about by the inhibition of protein synthesis in these tissues, which include heart, muscle, peripheral nerves, adrenals, kidneys, liver and spleen, result in the systemic pathology of the disease. Diphtheria continues to have high incidence in many parts of the world, including Africa, Asia, Eastern Europe and the independent states of the former Soviet Union. An ongoing epidemic of diphtheria in the latter two regions has resulted in at least 5,000 deaths since 1990.

In one embodiment, the invention provides a method of identifying the presence or activity of *Cornyebacterium diphtheriae* in a subject. This method includes detection of one or more of the nucleic acid or amino acid sequences of the invention (*e.g.*, the sequences set forth in Appendix A or Appendix B) in a subject, thereby detecting the presence or activity of *Corynebacterium diphtheriae* in the subject. *C. glutamicum* and *C. diphtheriae* are related bacteria, and many of the nucleic acid and protein molecules in C. *glutamicum* are homologous to *C. diphtheriae* nucleic acid and protein molecules, and can therefore be used to detect *C. diphtheriae* in a subject.

The nucleic acid and protein molecules of the invention may also serve as markers for specific regions of the genome. This has utility not only in the mapping of the genome, but also for functional studies of *C. glutamicum* proteins. For example, to identify the region of the genome to which a particular *C. glutamicum* DNA-binding protein binds, the *C. glutamicum* genome could be digested, and the fragments incubated with the DNA-binding protein. Those which bind the protein may be additionally probed with the nucleic acid molecules of the invention, preferably with readily detectable labels; binding of such a nucleic acid molecule to the genome fragment enables the localization of the fragment to the genome map of *C. glutamicum*, and, when performed multiple times with different enzymes, facilitates a rapid determination of the nucleic

acid sequence to which the protein binds. Further, the nucleic acid molecules of the invention may be sufficiently homologous to the sequences of related species such that these nucleic acid molecules may serve as markers for the construction of a genomic map in related bacteria, such as *Brevibacterium lactofermentum*.

The HA nucleic acid molecules of the invention are also useful for evolutionary and protein structural studies. The processes involved in adaptation and the maintenance of homeostasis in which the molecules of the invention participate are utilized by a wide variety of species; by comparing the sequences of the nucleic acid molecules of the present invention to those encoding similar enzymes from other organisms, the evolutionary relatedness of the organisms can be assessed. Similarly, such a comparison permits an assessment of which regions of the sequence are conserved and which are not, which may aid in determining those regions of the protein which are essential for the functioning of the enzyme. This type of determination is of value for protein engineering studies and may give an indication of what the protein can tolerate in terms of mutagenesis without losing function.

Manipulation of the HA nucleic acid molecules of the invention may result in the production of HA proteins having functional differences from the wild-type HA proteins. These proteins may be improved in efficiency or activity, may be present in greater numbers in the cell than is usual, or may be decreased in efficiency or activity.

The invention provides methods for screening molecules which modulate the activity of an HA protein, either by interacting with the protein itself or a substrate or binding partner of the HA protein, or by modulating the transcription or translation of an HA nucleic acid molecule of the invention. In such methods, a microorganism expressing one or more HA proteins of the invention is contacted with one or more test compounds, and the effect of each test compound on the activity or level of expression of the HA protein is assessed.

The modulation of activity or number of HA proteins involved in cell wall biosynthesis or rearrangements may impact the production, yield, and/or efficiency of production of one or more fine chemicals from *C. glutamicum* cells. For example, by altering the activity of these proteins, it may be possible to modulate the structure or thickness of the cell wall. The cell wall serves in large measure as a protective device against osmotic lysis and external sources of injury; by modifying the cell wall it may be possible to increase the ability of *C. glutamicum* to withstand the mechanical and shear force stresses encountered by this microorganism during large-scale fermentor culture. Further, each *C. glutamicum* cell is surrounded by a thick cell wall, and thus, a significant portion of the biomass present in large scale culture consists of cell wall. By increasing the rate at which the cell wall is synthesized or by activating cell wall

synthesis (through genetic engineering of the HA cell wall proteins of the invention) it may be possible to improve the growth rate of the microorganism. Similarly, by decreasing the activity or number of proteins involved in the degradation of cell wall or by decreasing the repression of cell wall biosynthesis, an overall increase in cell wall production may be achieved. An increase in the number of viable *C. glutamicum* cells (as may be accomplished by any of the foregoing described protein alterations) should result in increased numbers of cells producing the desired fine chemical in large-scale fermentor culture, which should permit increased yields or efficiency of production of these compounds from the culture.

The modulation of activity or number of *C. glutamicum* HA proteins that participate in the modification or degradation of aromatic or aliphatic compounds may also have direct or indirect impacts on the production of one or more fine chemicals from these cells. Certain aromatic or aliphatic modification or degradation products are desirable fine chemicals (*e.g.*, organic acids or modified aromatic and aliphatic compounds); thus, by modifying the enzymes which perform these modifications (*e.g.*, hydroxylation, methylation, or isomerization) or degradation reactions, it may be possible to increase the yields of these desired compounds. Similarly, by decreasing the activity or number of proteins involved in pathways which further degrade the modified or breakdown products of the aforementioned reactions it may be possible to improve the yields of these fine chemicals from *C. glutamicum* cells in culture.

These aromatic and aliphatic modification and degradative enzymes are themselves fine chemicals. In purified form, these enzymes may be used to degrade aromatic and aliphatic compounds (*e.g.*, toxic chemicals such as petroleum products), either for the bioremediation of polluted sites, for the engineered decomposition of wastes, or for the large-scale and economically feasible production of desired modified aromatic or aliphatic compounds or their breakdown products, some of which may be conveniently used as carbon or energy sources for other fine chemical-producing compounds in culture (see, *e.g.*, Faber, K. (1995) Biotransformations in Organic Chemistry, Springer: Berlin and references therein; and Roberts, S.M., ed. (1992-1996) Preparative Biotransformations, Wiley: Chichester, and references therein). By genetically altering these proteins such that their regulation by other cellular mechanisms is lessened or abolished, it may be possible to increase the overall number or activity of these proteins, thereby improving not only the yield of these fine chemicals but also the activity of these harvested proteins.

The modification of these aromatic and aliphatic modifying and degradation enzymes may also have an indirect effect on the production of one or more fine chemical. Many aromatic and aliphatic compounds (such as those that may be

encountered as impurities in culture media or as waste products from cellular metabolism) are toxic to cells; by modifying and/or degrading these compounds such that they may be readily removed or destroyed, cellular viability should be increased. Further, these enzymes may modify or degrade these compounds in such a manner that the resulting products may enter the normal carbon metabolism pathways of the cell, thus rendering the cell able to use these compounds as alternate carbon or energy sources. In large-scale culture situations, when there may be limiting amounts of optimal carbon sources, these enzymes provide a method by which cells may continue to grow and divide using aromatic or aliphatic compounds as nutrients. In either case, the resulting increase in the number of *C. glutamicum* cells in the culture producing the desired fine chemical should in turn result in increased yields or efficiency of production of the fine chemical(s).

Modifications in activity or number of HA proteins involved in the metabolism of inorganic compounds may also directly or indirectly affect the production of one or more fine chemicals from *C. glutamicum* or related bacterial cultures. For example, many desirable fine chemicals, such as nucleic acids, amino acids, cofactors and vitamins (*e.g.*, thiamine, biotin, and lipoic acid) cannot be synthesized without inorganic molecules such as phosphorous, nitrate, sulfate, and iron. The inorganic metabolism proteins of the invention permit the cell to obtain these molecules from a variety of inorganic compounds and to divert them into various fine chemical biosynthetic pathways. Therefore, by increasing the activity or number of enzymes involved in the metabolism of these inorganic compounds, it may be possible to increase the supply of these possibly limiting inorganic molecules, thereby directly increasing the production or efficiency of production of various fine chemicals from *C. glutamicum* cells containing such altered proteins. Modification of the activity or number of inorganic metabolism enzymes of the invention may also render *C. glutamicum* able to better utilize limited inorganic compound supplies, or to utilize nonoptimal inorganic compounds to synthesize amino acids, vitamins, cofactors, or nucleic acids, all of which are necessary for continued growth and replication of the cell. By improving the viability of these cells in large-scale culture, the number of *C. glutamicum* cells producing one or more fine chemicals in the culture may also be increased, in turn increasing the yields or efficiency of production of one or more fine chemicals.

C. *glutamicum* enzymes for general processes are themselves desirable fine chemicals. The specific properties of enzymes (*i.e.*, regio- and stereospecificity, among others) make them useful catalysts for chemical reactions *in vitro*. Either whole *C. glutamicum* cells may be incubated with an appropriate substrate such that the desired product is produced by enzymes in the cell, or the desired enzymes may be

overproduced and purified from *C. glutamicum* cultures (or those of a related bacterium) and subsequently utilized in *in vitro* reactions in an industrial setting (either in solution or immobilized on a suitable immobile phase). In either situation, the enzyme can either be a natural *C. glutamicum* protein, or it may be mutagenized to have an altered activity; typical industrial uses for such enzymes include as catalysts in the chemical industry (*e.g.*, for synthetic organic chemistry) as food additives, as feed components, for fruit processing, for leather preparation, in detergents, in analysis and medicine, and in the textile industry (see, *e.g.*,Yamada, H. (1993) "Microbial reactions for the production of useful organic compounds," *Chimica* 47: 5-10; Roberts, S.M. (1998) Preparative biotransformations: the employment of enzymes and whole-cells in synthetic chemistry," *J. Chem. Soc. Perkin Trans.* 1: 157-169; Zaks, A. and Dodds, D.R. (1997) "Application of biocatalysis and biotransformations to the synthesis of pharmaceuticals," *DDT* 2: 513-531; Roberts, S.M. and Williamson, N.M. (1997) "The use of enzymes for the preparation of biologically active natural products and analogues in optically active form," *Curr. Organ. Chemistry* 1: 1-20; Faber, K. (1995) Biotransformations in Organic Chemistry, Springer: Berlin; Roberts, S.M., ed. (1992-96) Preparative Biotransformations, Wiley: Chichester; Cheetham, P.S.J. (1995) "The applications of enzymes in industry" in : Handbook of Enzyme Biotechnology, 3rd ed., Wiseman, A., ed., Elis: Horwood, p. 419-552; and Ullmann's Encyclopedia of Industrial Chemistry (1987), vol. A9, Enzymes, p. 390-457). Thus, by increasing the activity or number of these enzymes, it may be possible to also increase the ability of the cell to convert supplied substrates to desired products, or to overproduce these enzymes for increased yields in large-scale culture. Further, by mutagenizing these proteins it may be possible to remove feedback inhibition or other repressive cellular regulatory controls such that greater numbers of these enzymes may be produced and activated by the cell, thereby leading to greater yields, production, or efficiency of production of these fine chemical proteins from large-scale cultures. Further, manipulation of these enzymes may alter the activity of one or more *C. glutamicum* metabolic pathways, such as those for the biosynthesis or secretion of one or more fine chemicals.

Mutagenesis of the proteolytic enzymes of the invention such that they are altered in activity or number may also directly or indirectly affect the yield, production, and/or efficiency of production of one or more fine chemicals from *C. glutamicum*. For example, by increasing the activity or number of these proteins, it may be possible to increase the ability of the bacterium to survive in large-scale culture, due to an increased ability of the cell to rapidly degrade proteins misfolded in response to the high temperatures, nonoptimal pH, and other stresses encountered during fermentor culture. Increased numbers of cells in these cultures may result in increased yields or efficiency

of production of one or more desired fine chemicals, due to the relatively larger number of cells producing these compounds in the culture. Also, *C. glutamicum* cells possess multiple cell-surface proteases which serve to break down external nutrients into molecules which may be more readily incorporated by the cells as carbon/energy sources or nutrients of other kinds. An increase in activity or number of these enzymes may improve this turnover and increase the levels of available nutrients, thereby improving cell growth or production. Thus, modifications of the proteases of the invention may indirectly impact *C. glutamicum* fine chemical production.

A more direct impact on fine chemical production in response to the modification of one or more of the proteases of the invention may occur when these proteases are involved in the production or degradation of a desired fine chemical. By decreasing the activity of a protease which degrades a fine chemical or a protein involved in the synthesis of a fine chemical it may be possible to increase the levels of that fine chemical (due to the decreased degradation or increased synthesis of the compound). Similarly, by increasing the activity of a protease which degrades a compound to result in a fine chemical or a protein involved in the degradation of a fine chemical, a similar result should be achieved: increased levels of the desired fine chemical from *C. glutamicum* cells containing these engineered proteins.

The aforementioned mutagenesis strategies for HA proteins to result in increased yields of a fine chemical from *C. glutamicum* are not meant to be limiting; variations on these strategies will be readily apparent to one of ordinary skill in the art. Using such strategies, and incorporating the mechanisms disclosed herein, the nucleic acid and protein molecules of the invention may be utilized to generate *C. glutamicum* or related strains of bacteria expressing mutated HA nucleic acid and protein molecules such that the yield, production, and/or efficiency of production of a desired compound is improved. This desired compound may be any product produced by *C. glutamicum*, which includes the final products of biosynthesis pathways and intermediates of naturally-occurring metabolic pathways, as well as molecules which do not naturally occur in the metabolism of *C. glutamicum*, but which are produced by a *C. glutamicum* strain of the invention.

This invention is further illustrated by the following examples which should not be construed as limiting. The contents of all references, patent applications, patents, published patent applications, Tables, Appendices, and the sequence listing cited throughout this application are hereby incorporated by reference.

Exemplification

Example 1: Preparation of total genomic DNA of *Corynebacterium glutamicum* ATCC 13032

A culture of *Corynebacterium glutamicum* (ATCC 13032) was grown overnight at 30°C with vigorous shaking in BHI medium (Difco). The cells were harvested by centrifugation, the supernatant was discarded and the cells were resuspended in 5 ml buffer-I (5% of the original volume of the culture — all indicated volumes have been calculated for 100 ml of culture volume). Composition of buffer-I: 140.34 g/l sucrose, 2.46 g/l $MgSO_4 \times 7H_2O$, 10 ml/l KH_2PO_4 solution (100 g/l, adjusted to pH 6.7 with KOH), 50 ml/l M12 concentrate (10 g/l $(NH_4)_2SO_4$, 1 g/l NaCl, 2 g/l $MgSO_4 \times 7H_2O$, 0.2 g/l $CaCl_2$, 0.5 g/l yeast extract (Difco), 10 ml/l trace-elements-mix (200 mg/l $FeSO_4 \times H_2O$, 10 mg/l $ZnSO_4 \times 7\ H_2O$, 3 mg/l $MnCl_2 \times 4\ H_2O$, 30 mg/l H_3BO_3 20 mg/l $CoCl_2 \times 6\ H_2O$, 1 mg/l $NiCl_2 \times 6\ H_2O$, 3 mg/l $Na_2MoO_4 \times 2\ H_2O$, 500 mg/l complexing agent (EDTA or critic acid), 100 ml/l vitamins-mix (0.2 mg/l biotin, 0.2 mg/l folic acid, 20 mg/l p-amino benzoic acid, 20 mg/l riboflavin, 40 mg/l ca-panthothenate, 140 mg/l nicotinic acid, 40 mg/l pyridoxole hydrochloride, 200 mg/l myo-inositol). Lysozyme was added to the suspension to a final concentration of 2.5 mg/ml. After an approximately 4 h incubation at 37°C, the cell wall was degraded and the resulting protoplasts are harvested by centrifugation. The pellet was washed once with 5 ml buffer-I and once with 5 ml TE-buffer (10 mM Tris-HCl, 1 mM EDTA, pH 8). The pellet was resuspended in 4 ml TE-buffer and 0.5 ml SDS solution (10%) and 0.5 ml NaCl solution (5 M) are added. After adding of proteinase K to a final concentration of 200 µg/ml, the suspension is incubated for ca.18 h at 37°C. The DNA was purified by extraction with phenol, phenol-chloroform-isoamylalcohol and chloroform-isoamylalcohol using standard procedures. Then, the DNA was precipitated by adding 1/50 volume of 3 M sodium acetate and 2 volumes of ethanol, followed by a 30 min incubation at -20°C and a 30 min centrifugation at 12,000 rpm in a high speed centrifuge using a SS34 rotor (Sorvall). The DNA was dissolved in 1 ml TE-buffer containing 20 µg/ml RNaseA and dialysed at 4°C against 1000 ml TE-buffer for at least 3 hours. During this time, the buffer was exchanged 3 times. To aliquots of 0.4 ml of the dialysed DNA solution, 0.4 ml of 2 M LiCl and 0.8 ml of ethanol are added. After a 30 min incubation at -20°C, the DNA was collected by centrifugation (13,000 rpm, Biofuge Fresco, Heraeus, Hanau, Germany). The DNA pellet was dissolved in TE-buffer. DNA prepared by this procedure could be used for all purposes, including southern blotting or construction of genomic libraries.

Example 2: Construction of genomic libraries in *Escherichia coli* of *Corynebacterium glutamicum* ATCC13032.

Using DNA prepared as described in Example 1, cosmid and plasmid libraries were constructed according to known and well established methods (*see e.g.,* Sambrook, J. *et al.* (1989) "Molecular Cloning : A Laboratory Manual", Cold Spring Harbor Laboratory Press, or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons.)

Any plasmid or cosmid could be used. Of particular use were the plasmids pBR322 (Sutcliffe, J.G. (1979) *Proc. Natl. Acad. Sci. USA*, 75:3737-3741); pACYC177 (Change & Cohen (1978) *J. Bacteriol* 134:1141-1156), plasmids of the pBS series (pBSSK+, pBSSK- and others; Stratagene, LaJolla, USA), or cosmids as SuperCos1 (Stratagene, LaJolla, USA) or Lorist6 (Gibson, T.J., Rosenthal A. and Waterson, R.H. (1987) *Gene* 53:283-286. Gene libraries specifically for use in *C. glutamicum* may be constructed using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Example 3: DNA Sequencing and Computational Functional Analysis

Genomic libraries as described in Example 2 were used for DNA sequencing according to standard methods, in particular by the chain termination method using ABI377 sequencing machines (see *e.g.*, Fleischman, R.D. *et al.* (1995) "Whole-genome Random Sequencing and Assembly of Haemophilus Influenzae Rd., Science, 269:496-512). Sequencing primers with the following nucleotide sequences were used: 5'-GGAAACAGTATGACCATG-3' or 5'-GTAAAACGACGGCCAGT-3'.

Example 4: *In vivo* Mutagenesis

In vivo mutagenesis of *Corynebacterium glutamicum* can be performed by passage of plasmid (or other vector) DNA through *E. coli* or other microorganisms (*e.g. Bacillus* spp. or yeasts such as *Saccharomyces cerevisiae*) which are impaired in their capabilities to maintain the integrity of their genetic information. Typical mutator strains have mutations in the genes for the DNA repair system (*e.g.*, mutHLS, mutD, mutT, etc.; for reference, see Rupp, W.D. (1996) DNA repair mechanisms, in: *Escherichia col*i and *Salmonella*, p. 2277-2294, ASM: Washington.) Such strains are well known to those of ordinary skill in the art. The use of such strains is illustrated, for example, in Greener, A. and Callahan, M. (1994) *Strategies* 7: 32-34.

Example 5: DNA Transfer Between *Escherichia coli* and *Corynebacterium glutamicum*

Several *Corynebacterium* and *Brevibacterium* species contain endogenous plasmids (as *e.g.*, pHM1519 or pBL1) which replicate autonomously (for review see, *e.g.*,

Martin, J.F. *et al.* (1987) *Biotechnology*, 5:137-146). Shuttle vectors for *Escherichia coli* and *Corynebacterium glutamicum* can be readily constructed by using standard vectors for *E. coli* (Sambrook, J. *et al.* (1989), "Molecular Cloning: A Laboratory Manual", Cold Spring Harbor Laboratory Press or Ausubel, F.M. *et al.* (1994) "Current Protocols in Molecular Biology", John Wiley & Sons) to which a origin or replication for and a suitable marker from *Corynebacterium glutamicum* is added. Such origins of replication are preferably taken from endogenous plasmids isolated from *Corynebacterium* and *Brevibacterium* species. Of particular use as transformation markers for these species are genes for kanamycin resistance (such as those derived from the Tn5 or Tn903 transposons) or chloramphenicol (Winnacker, E.L. (1987) "From Genes to Clones — Introduction to Gene Technology, VCH, Weinheim). There are numerous examples in the literature of the construction of a wide variety of shuttle vectors which replicate in both *E. coli and C. glutamicum*, and which can be used for several purposes, including gene over-expression (for reference, see *e.g.*, Yoshihama, M. *et al.* (1985) *J. Bacteriol.* 162:591-597, Martin J.F. *et al.* (1987) *Biotechnology*, 5:137-146 and Eikmanns, B.J. *et al.* (1991) *Gene*, 102:93-98).

Using standard methods, it is possible to clone a gene of interest into one of the shuttle vectors described above and to introduce such a hybrid vectors into strains of *Corynebacterium glutamicum*. Transformation of *C. glutamicum* can be achieved by protoplast transformation (Kastsumata, R. *et al.* (1984) *J. Bacteriol.* 159306-311), electroporation (Liebl, E. *et al.* (1989) *FEMS Microbiol. Letters*, 53:399-303) and in cases where special vectors are used, also by conjugation (as described *e.g.* in Schäfer, A *et al.* (1990) *J. Bacteriol.* 172:1663-1666). It is also possible to transfer the shuttle vectors for *C. glutamicum* to *E. coli* by preparing plasmid DNA from *C. glutamicum* (using standard methods well-known in the art) and transforming it into *E. coli*. This transformation step can be performed using standard methods, but it is advantageous to use an Mcr-deficient *E. coli* strain, such as NM522 (Gough & Murray (1983) *J. Mol. Biol.* 166:1-19).

Genes may be overexpressed in *C. glutamicum* strains using plasmids which comprise pCG1 (U.S. Patent No. 4,617,267) or fragments thereof, and optionally the gene for kanamycin resistance from TN903 (Grindley, N.D. and Joyce, C.M. (1980) *Proc. Natl. Acad. Sci. USA* 77(12): 7176-7180). In addition, genes may be overexpressed in *C. glutamicum* strains using plasmid pSL109 (Lee, H.-S. and A. J. Sinskey (1994) *J. Microbiol. Biotechnol.* 4: 256-263).

Aside from the use of replicative plasmids, gene overexpression can also be achieved by integration into the genome. Genomic integration in *C. glutamicum* or other Corynebacterium or Brevibacterium species may be accomplished by well-known methods, such as homologous recombination with genomic region(s), restriction

endonuclease mediated integration (REMI) (see, *e.g.*, DE Patent 19823834), or through the use of transposons. It is also possible to modulate the activity of a gene of interest by modifying the regulatory regions (*e.g.*, a promoter, a repressor, and/or an enhancer) by sequence modification, insertion, or deletion using site-directed methods (such as homologous recombination) or methods based on random events (such as transposon mutagenesis or REMI). Nucleic acid sequences which function as transcriptional terminators may also be inserted 3' to the coding region of one or more genes of the invention; such terminators are well-known in the art and are described, for example, in Winnacker, E.L. (1987) From Genes to Clones – Introduction to Gene Technology. VCH: Weinheim.

Example 6: Assessment of the Expression of the Mutant Protein

Observations of the activity of a mutated protein in a transformed host cell rely on the fact that the mutant protein is expressed in a similar fashion and in a similar quantity to that of the wild-type protein. A useful method to ascertain the level of transcription of the mutant gene (an indicator of the amount of mRNA available for translation to the gene product) is to perform a Northern blot (for reference see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York), in which a primer designed to bind to the gene of interest is labeled with a detectable tag (usually radioactive or chemiluminescent), such that when the total RNA of a culture of the organism is extracted, run on gel, transferred to a stable matrix and incubated with this probe, the binding and quantity of binding of the probe indicates the presence and also the quantity of mRNA for this gene. This information is evidence of the degree of transcription of the mutant gene. Total cellular RNA can be prepared from *Corynebacterium glutamicum* by several methods, all well-known in the art, such as that described in Bormann, E.R. *et al.* (1992) *Mol. Microbiol.* 6: 317-326.

To assess the presence or relative quantity of protein translated from this mRNA, standard techniques, such as a Western blot, may be employed (see, for example, Ausubel *et al.* (1988) Current Protocols in Molecular Biology, Wiley: New York). In this process, total cellular proteins are extracted, separated by gel electrophoresis, transferred to a matrix such as nitrocellulose, and incubated with a probe, such as an antibody, which specifically binds to the desired protein. This probe is generally tagged with a chemiluminescent or colorimetric label which may be readily detected. The presence and quantity of label observed indicates the presence and quantity of the desired mutant protein present in the cell.

Example 7: Growth of Genetically Modified *Corynebacterium glutamicum* — Media and Culture Conditions

Genetically modified *Corynebacteria* are cultured in synthetic or natural growth media. A number of different growth media for Corynebacteria are both well-known and readily available (Lieb *et al.* (1989) *Appl. Microbiol. Biotechnol.*, 32:205-210; von der Osten *et al.* (1998) *Biotechnology Letters*, 11:11-16; Patent DE 4,120,867; Liebl (1992) "The Genus *Corynebacterium*, in: The Procaryotes, Volume II, Balows, A. *et al.*, eds. Springer-Verlag). These media consist of one or more carbon sources, nitrogen sources, inorganic salts, vitamins and trace elements. Preferred carbon sources are sugars, such as mono-, di-, or polysaccharides. For example, glucose, fructose, mannose, galactose, ribose, sorbose, ribulose, lactose, maltose, sucrose, raffinose, starch or cellulose serve as very good carbon sources. It is also possible to supply sugar to the media via complex compounds such as molasses or other by-products from sugar refinement. It can also be advantageous to supply mixtures of different carbon sources. Other possible carbon sources are alcohols and organic acids, such as methanol, ethanol, acetic acid or lactic acid. Nitrogen sources are usually organic or inorganic nitrogen compounds, or materials which contain these compounds. Exemplary nitrogen sources include ammonia gas or ammonia salts, such as NH_4Cl or $(NH_4)_2SO_4$, NH_4OH, nitrates, urea, amino acids or complex nitrogen sources like corn steep liquor, soy bean flour, soy bean protein, yeast extract, meat extract and others.

Inorganic salt compounds which may be included in the media include the chloride-, phosphorous- or sulfate- salts of calcium, magnesium, sodium, cobalt, molybdenum, potassium, manganese, zinc, copper and iron. Chelating compounds can be added to the medium to keep the metal ions in solution. Particularly useful chelating compounds include dihydroxyphenols, like catechol or protocatechuate, or organic acids, such as citric acid. It is typical for the media to also contain other growth factors, such as vitamins or growth promoters, examples of which include biotin, riboflavin, thiamin, folic acid, nicotinic acid, pantothenate and pyridoxin. Growth factors and salts frequently originate from complex media components such as yeast extract, molasses, corn steep liquor and others. The exact composition of the media compounds depends strongly on the immediate experiment and is individually decided for each specific case. Information about media optimization is available in the textbook "Applied Microbiol. Physiology, A Practical Approach (*eds.* P.M. Rhodes, P.F. Stanbury, IRL Press (1997) pp. 53-73, ISBN 0 19 963577 3). It is also possible to select growth media from commercial suppliers, like standard 1 (Merck) or BHI (grain heart infusion, DIFCO) or others.

All medium components are sterilized, either by heat (20 minutes at 1.5 bar and 121°C) or by sterile filtration. The components can either be sterilized together or, if

necessary, separately. All media components can be present at the beginning of growth, or they can optionally be added continuously or batchwise.

Culture conditions are defined separately for each experiment. The temperature should be in a range between 15°C and 45°C. The temperature can be kept constant or can be altered during the experiment. The pH of the medium should be in the range of 5 to 8.5, preferably around 7.0, and can be maintained by the addition of buffers to the media. An exemplary buffer for this purpose is a potassium phosphate buffer. Synthetic buffers such as MOPS, HEPES, ACES and others can alternatively or simultaneously be used. It is also possible to maintain a constant culture pH through the addition of NaOH or NH_4OH during growth. If complex medium components such as yeast extract are utilized, the necessity for additional buffers may be reduced, due to the fact that many complex compounds have high buffer capacities. If a fermentor is utilized for culturing the micro-organisms, the pH can also be controlled using gaseous ammonia.

The incubation time is usually in a range from several hours to several days. This time is selected in order to permit the maximal amount of product to accumulate in the broth. The disclosed growth experiments can be carried out in a variety of vessels, such as microtiter plates, glass tubes, glass flasks or glass or metal fermentors of different sizes. For screening a large number of clones, the microorganisms should be cultured in microtiter plates, glass tubes or shake flasks, either with or without baffles. Preferably 100 ml shake flasks are used, filled with 10% (by volume) of the required growth medium. The flasks should be shaken on a rotary shaker (amplitude 25 mm) using a speed-range of 100 – 300 rpm. Evaporation losses can be diminished by the maintenance of a humid atmosphere; alternatively, a mathematical correction for evaporation losses should be performed.

If genetically modified clones are tested, an unmodified control clone or a control clone containing the basic plasmid without any insert should also be tested. The medium is inoculated to an OD_{600} of 0.5 – 1.5 using cells grown on agar plates, such as CM plates (10 g/l glucose, 2,5 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l NaCl, 2 g/l urea, 10 g/l polypeptone, 5 g/l yeast extract, 5 g/l meat extract, 22 g/l agar, pH 6.8 with 2M NaOH) that had been incubated at 30°C. Inoculation of the media is accomplished by either introduction of a saline suspension of *C. glutamicum* cells from CM plates or addition of a liquid preculture of this bacterium.

Example 8 – *In vitro* Analysis of the Function of Mutant Proteins

The determination of activities and kinetic parameters of enzymes is well established in the art. Experiments to determine the activity of any given altered enzyme must be tailored to the specific activity of the wild-type enzyme, which is well

within the ability of one of ordinary skill in the art. Overviews about enzymes in general, as well as specific details concerning structure, kinetics, principles, methods, applications and examples for the determination of many enzyme activities may be found, for example, in the following references: Dixon, M., and Webb, E.C., (1979) Enzymes. Longmans: London; Fersht, (1985) Enzyme Structure and Mechanism. Freeman: New York; Walsh, (1979) Enzymatic Reaction Mechanisms. Freeman: San Francisco; Price, N.C., Stevens, L. (1982) Fundamentals of Enzymology. Oxford Univ. Press: Oxford; Boyer, P.D., ed. (1983) The Enzymes, 3rd ed. Academic Press: New York; Bisswanger, H., (1994) Enzymkinetik, 2nd ed. VCH: Weinheim (ISBN 3527300325); Bergmeyer, H.U., Bergmeyer, J., Graßl, M., eds. (1983-1986) Methods of Enzymatic Analysis, 3rd ed., vol. I-XII, Verlag Chemie: Weinheim; and Ullmann's Encyclopedia of Industrial Chemistry (1987) vol. A9, "Enzymes". VCH: Weinheim, p. 352-363.

The activity of proteins which bind to DNA can be measured by several well-established methods, such as DNA band-shift assays (also called gel retardation assays). The effect of such proteins on the expression of other molecules can be measured using reporter gene assays (such as that described in Kolmar, H. *et al.* (1995) *EMBO J.* 14: 3895-3904 and references cited therein). Reporter gene test systems are well known and established for applications in both pro- and eukaryotic cells, using enzymes such as beta-galactosidase, green fluorescent protein, and several others.

The determination of activity of membrane-transport proteins can be performed according to techniques such as those described in Gennis, R.B. (1989) "Pores, Channels and Transporters", in Biomembranes, Molecular Structure and Function, Springer: Heidelberg, p. 85-137; 199-234; and 270-322.

Example 9: Analysis of Impact of Mutant Protein on the Production of the Desired Product

The effect of the genetic modification in *C. glutamicum* on production of a desired compound (such as an amino acid) can be assessed by growing the modified microorganism under suitable conditions (such as those described above) and analyzing the medium and/or the cellular component for increased production of the desired product (*i.e.*, an amino acid). Such analysis techniques are well known to one of ordinary skill in the art, and include spectroscopy, thin layer chromatography, staining methods of various kinds, enzymatic and microbiological methods, and analytical chromatography such as high performance liquid chromatography (see, for example, Ullman, Encyclopedia of Industrial Chemistry, vol. A2, p. 89-90 and p. 443-613, VCH: Weinheim (1985); Fallon, A. *et al.*, (1987) "Applications of HPLC in Biochemistry" in:

Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17; Rehm *et al.* (1993) Biotechnology, vol. 3, Chapter III: "Product recovery and purification", page 469-714, VCH: Weinheim; Belter, P.A. *et al.* (1988) Bioseparations: downstream processing for biotechnology, John Wiley and Sons; Kennedy, J.F. and Cabral, J.M.S. (1992) Recovery processes for biological materials, John Wiley and Sons; Shaeiwitz, J.A. and Henry, J.D. (1988) Biochemical separations, in: Ulmann's Encyclopedia of Industrial Chemistry, vol. B3, Chapter 11, page 1-27, VCH: Weinheim; and Dechow, F.J. (1989) Separation and purification techniques in biotechnology, Noyes Publications.)

In addition to the measurement of the final product of fermentation, it is also possible to analyze other components of the metabolic pathways utilized for the production of the desired compound, such as intermediates and side-products, to determine the overall efficiency of production of the compound. Analysis methods include measurements of nutrient levels in the medium (*e.g.*, sugars, hydrocarbons, nitrogen sources, phosphate, and other ions), measurements of biomass composition and growth, analysis of the production of common metabolites of biosynthetic pathways, and measurement of gasses produced during fermentation. Standard methods for these measurements are outlined in Applied Microbial Physiology, A Practical Approach, P.M. Rhodes and P.F. Stanbury, eds., IRL Press, p. 103-129; 131-163; and 165-192 (ISBN: 0199635773) and references cited therein.

Example 10: Purification of the Desired Product from *C. glutamicum* Culture

Recovery of the desired product from the *C. glutamicum* cells or supernatant of the above-described culture can be performed by various methods well known in the art. If the desired product is not secreted from the cells, the cells can be harvested from the culture by low-speed centrifugation, the cells can be lysed by standard techniques, such as mechanical force or sonication. The cellular debris is removed by centrifugation, and the supernatant fraction containing the soluble proteins is retained for further purification of the desired compound. If the product is secreted from the *C. glutamicum* cells, then the cells are removed from the culture by low-speed centrifugation, and the supernate fraction is retained for further purification.

The supernatant fraction from either purification method is subjected to chromatography with a suitable resin, in which the desired molecule is either retained on a chromatography resin while many of the impurities in the sample are not, or where the impurities are retained by the resin while the sample is not. Such chromatography steps may be repeated as necessary, using the same or different chromatography resins. One of ordinary skill in the art would be well-versed in the selection of appropriate

chromatography resins and in their most efficacious application for a particular molecule to be purified. The purified product may be concentrated by filtration or ultrafiltration, and stored at a temperature at which the stability of the product is maximized.

There are a wide array of purification methods known to the art and the preceding method of purification is not meant to be limiting. Such purification techniques are described, for example, in Bailey, J.E. & Ollis, D.F. Biochemical Engineering Fundamentals, McGraw-Hill: New York (1986).

The identity and purity of the isolated compounds may be assessed by techniques standard in the art. These include high-performance liquid chromatography (HPLC), spectroscopic methods, staining methods, thin layer chromatography, NIRS, enzymatic assay, or microbiologically. Such analysis methods are reviewed in: Patek *et al.* (1994) *Appl. Environ. Microbiol.* 60: 133-140; Malakhova *et al.* (1996) *Biotekhnologiya* 11: 27-32; and Schmidt *et al.* (1998) *Bioprocess Engineer.* 19: 67-70. Ulmann's Encyclopedia of Industrial Chemistry, (1996) vol. A27, VCH: Weinheim, p. 89-90, p. 521-540, p. 540-547, p. 559-566, 575-581 and p. 581-587; Michal, G. (1999) Biochemical Pathways: An Atlas of Biochemistry and Molecular Biology, John Wiley and Sons; Fallon, A. *et al.* (1987) Applications of HPLC in Biochemistry in: Laboratory Techniques in Biochemistry and Molecular Biology, vol. 17.

Example 11: Analysis of the Gene Sequences of the Invention

The comparison of sequences and determination of percent homology between two sequences are art-known techniques, and can be accomplished using a mathematical algorithm, such as the algorithm of Karlin and Altschul (1990) *Proc. Natl. Acad. Sci.* USA 87:2264-68, modified as in Karlin and Altschul (1993) *Proc. Natl. Acad. Sci.* USA 90:5873-77. Such an algorithm is incorporated into the NBLAST and XBLAST programs (version 2.0) of Altschul, *et al.* (1990) *J. Mol. Biol.* 215:403-10. BLAST nucleotide searches can be performed with the NBLAST program, score = 100, wordlength = 12 to obtain nucleotide sequences homologous to HA nucleic acid molecules of the invention. BLAST protein searches can be performed with the XBLAST program, score = 50, wordlength = 3 to obtain amino acid sequences homologous to HA protein molecules of the invention. To obtain gapped alignments for comparison purposes, Gapped BLAST can be utilized as described in Altschul *et al.*, (1997) *Nucleic Acids Res.* 25(17):3389-3402. When utilizing BLAST and Gapped BLAST programs, one of ordinary skill in the art will know how to optimize the parameters of the program (*e.g.*, XBLAST and NBLAST) for the specific sequence being analyzed.

Another example of a mathematical algorithm utilized for the comparison of sequences is the algorithm of Meyers and Miller ((1988) *Comput. Appl. Biosci.* 4: 11-17). Such an algorithm is incorporated into the ALIGN program (version 2.0) which is part of the GCG sequence alignment software package. When utilizing the ALIGN program for comparing amino acid sequences, a PAM120 weight residue table, a gap length penalty of 12, and a gap penalty of 4 can be used. Additional algorithms for sequence analysis are known in the art, and include ADVANCE and ADAM. described in Torelli and Robotti (1994) *Comput. Appl. Biosci.* 10:3-5; and FASTA, described in Pearson and Lipman (1988) *P.N.A.S.* 85:2444-8.

The percent homology between two amino acid sequences can also be accomplished using the GAP program in the GCG software package (available at http://www.gcg.com), using either a Blosum 62 matrix or a PAM250 matrix, and a gap weight of 12, 10, 8, 6, or 4 and a length weight of 2, 3, or 4. The percent homology between two nucleic acid sequences can be accomplished using the GAP program in the GCG software package, using standard parameters, such as a gap weight of 50 and a length weight of 3.

A comparative analysis of the gene sequences of the invention with those present in Genbank has been performed using techniques known in the art (see, *e.g.*, Bexevanis and Ouellette, eds. (1998) Bioinformatics: A Practical Guide to the Analysis of Genes and Proteins. John Wiley and Sons: New York). The gene sequences of the invention were compared to genes present in Genbank in a three-step process. In a first step, a BLASTN analysis (*e.g.*, a local alignment analysis) was performed for each of the sequences of the invention against the nucleotide sequences present in Genbank, and the top 500 hits were retained for further analysis. A subsequent FASTA search (*e.g.*, a combined local and global alignment analysis, in which limited regions of the sequences are aligned) was performed on these 500 hits. Each gene sequence of the invention was subsequently globally aligned to each of the top three FASTA hits, using the GAP program in the GCG software package (using standard parameters). In order to obtain correct results, the length of the sequences extracted from Genbank were adjusted to the length of the query sequences by methods well-known in the art. The results of this analysis are set forth in Table 4. The resulting data is identical to that which would have been obtained had a GAP (global) analysis alone been performed on each of the genes of the invention in comparison with each of the references in Genbank, but required significantly reduced computational time as compared to such a database-wide GAP (global) analysis. Sequences of the invention for which no alignments above the cutoff values were obtained are indicated on Table 4 by the absence of alignment information. It will further be understood by one of ordinary skill in the art that the GAP alignment

homology percentages set forth in Table 4 under the heading "% homology (GAP)" are listed in the European numerical format, wherein a ',' represents a decimal point. For example, a value of "40,345" in this column represents "40.345%".

Example 12: Construction and Operation of DNA Microarrays

The sequences of the invention may additionally be used in the construction and application of DNA microarrays (the design, methodology, and uses of DNA arrays are well known in the art, and are described, for example, in Schena, M. *et al.* (1995) *Science* 270: 467-470; Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367; DeSaizieu, A. *et al.* (1998) *Nature Biotechnology* 16: 45-48; and DeRisi, J.L. *et al.* (1997) *Science* 278: 680-686).

DNA microarrays are solid or flexible supports consisting of nitrocellulose, nylon, glass, silicone, or other materials. Nucleic acid molecules may be attached to the surface in an ordered manner. After appropriate labeling, other nucleic acids or nucleic acid mixtures can be hybridized to the immobilized nucleic acid molecules, and the label may be used to monitor and measure the individual signal intensities of the hybridized molecules at defined regions. This methodology allows the simultaneous quantification of the relative or absolute amount of all or selected nucleic acids in the applied nucleic acid sample or mixture. DNA microarrays, therefore, permit an analysis of the expression of multiple (as many as 6800 or more) nucleic acids in parallel (see, *e.g.*, Schena, M. (1996) *BioEssays* 18(5): 427-431).

The sequences of the invention may be used to design oligonucleotide primers which are able to amplify defined regions of one or more *C. glutamicum* genes by a nucleic acid amplification reaction such as the polymerase chain reaction. The choice and design of the 5' or 3' oligonucleotide primers or of appropriate linkers allows the covalent attachment of the resulting PCR products to the surface of a support medium described above (and also described, for example, Schena, M. *et al.* (1995) *Science* 270: 467-470).

Nucleic acid microarrays may also be constructed by *in situ* oligonucleotide synthesis as described by Wodicka, L. *et al.* (1997) *Nature Biotechnology* 15: 1359-1367. By photolithographic methods, precisely defined regions of the matrix are exposed to light. Protective groups which are photolabile are thereby activated and undergo nucleotide addition, whereas regions that are masked from light do not undergo any modification. Subsequent cycles of protection and light activation permit the synthesis of different oligonucleotides at defined positions. Small, defined regions of the genes of the invention may be synthesized on microarrays by solid phase oligonucleotide synthesis.

The nucleic acid molecules of the invention present in a sample or mixture of nucleotides may be hybridized to the microarrays. These nucleic acid molecules can be labeled according to standard methods. In brief, nucleic acid molecules (*e.g.*, mRNA molecules or DNA molecules) are labeled by the incorporation of isotopically or fluorescently labeled nucleotides, *e.g.*, during reverse transcription or DNA synthesis. Hybridization of labeled nucleic acids to microarrays is described (*e.g.*, in Schena, M. *et al.* (1995) *supra*; Wodicka, L. *et al.* (1997), *supra*; and DeSaizieu A. *et al.* (1998), *supra*). The detection and quantification of the hybridized molecule are tailored to the specific incorporated label. Radioactive labels can be detected, for example, as described in Schena, M. *et al.* (1995) *supra*) and fluorescent labels may be detected, for example, by the method of Shalon *et al.* (1996) *Genome Research* 6: 639-645).

The application of the sequences of the invention to DNA microarray technology, as described above, permits comparative analyses of different strains of *C. glutamicum* or other Corynebacteria. For example, studies of inter-strain variations based on individual transcript profiles and the identification of genes that are important for specific and/or desired strain properties such as pathogenicity, productivity and stress tolerance are facilitated by nucleic acid array methodologies. Also, comparisons of the profile of expression of genes of the invention during the course of a fermentation reaction are possible using nucleic acid array technology.

Example 13: Analysis of the Dynamics of Cellular Protein Populations (Proteomics)

The genes, compositions, and methods of the invention may be applied to study the interactions and dynamics of populations of proteins, termed 'proteomics'. Protein populations of interest include, but are not limited to, the total protein population of *C. glutamicum* (*e.g.*, in comparison with the protein populations of other organisms), those proteins which are active under specific environmental or metabolic conditions (*e.g.*, during fermentation, at high or low temperature, or at high or low pH), or those proteins which are active during specific phases of growth and development.

Protein populations can be analyzed by various well-known techniques, such as gel electrophoresis. Cellular proteins may be obtained, for example, by lysis or extraction, and may be separated from one another using a variety of electrophoretic techniques. Sodium dodecyl sulfate polyacrylamide gel electrophoresis (SDS-PAGE) separates proteins largely on the basis of their molecular weight. Isoelectric focusing polyacrylamide gel electrophoresis (IEF-PAGE) separates proteins by their isoelectric point (which reflects not only the amino acid sequence but also posttranslational modifications of the protein). Another, more preferred method of protein analysis is the

consecutive combination of both IEF-PAGE and SDS-PAGE, known as 2-D-gel electrophoresis (described, for example, in Hermann *et al.* (1998) *Electrophoresis* 19: 3217-3221; Fountoulakis *et al.* (1998) *Electrophoresis* 19: 1193-1202; Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192; Antelmann *et al.* (1997) *Electrophoresis* 18: 1451-1463). Other separation techniques may also be utilized for protein separation, such as capillary gel electrophoresis; such techniques are well known in the art.

Proteins separated by these methodologies can be visualized by standard techniques, such as by staining or labeling. Suitable stains are known in the art, and include Coomassie Brilliant Blue, silver stain, or fluorescent dyes such as Sypro Ruby (Molecular Probes). The inclusion of radioactively labeled amino acids or other protein precursors (*e.g.*, ^{35}S-methionine, ^{35}S-cysteine, ^{14}C-labelled amino acids, ^{15}N-amino acids, $^{15}NO_3$ or $^{15}NH_4^+$ or ^{13}C-labelled amino acids) in the medium of *C. glutamicum* permits the labeling of proteins from these cells prior to their separation. Similarly, fluorescent labels may be employed. These labeled proteins can be extracted, isolated and separated according to the previously described techniques.

Proteins visualized by these techniques can be further analyzed by measuring the amount of dye or label used. The amount of a given protein can be determined quantitatively using, for example, optical methods and can be compared to the amount of other proteins in the same gel or in other gels. Comparisons of proteins on gels can be made, for example, by optical comparison, by spectroscopy, by image scanning and analysis of gels, or through the use of photographic films and screens. Such techniques are well-known in the art.

To determine the identity of any given protein, direct sequencing or other standard techniques may be employed. For example, N- and/or C-terminal amino acid sequencing (such as Edman degradation) may be used, as may mass spectrometry (in particular MALDI or ESI techniques (see, *e.g.*, Langen *et al.* (1997) *Electrophoresis* 18: 1184-1192)). The protein sequences provided herein can be used for the identification of *C. glutamicum* proteins by these techniques.

The information obtained by these methods can be used to compare patterns of protein presence, activity, or modification between different samples from various biological conditions (*e.g.*, different organisms, time points of fermentation, media conditions, or different biotopes, among others). Data obtained from such experiments alone, or in combination with other techniques, can be used for various applications, such as to compare the behavior of various organisms in a given (*e.g.*, metabolic) situation, to increase the productivity of strains which produce fine chemicals or to increase the efficiency of the production of fine chemicals.

Equivalents

Those of ordinary skill in the art will recognize, or will be able to ascertain using no more than routine experimentation, many equivalents to the specific embodiments of the invention described herein. Such equivalents are intended to be encompassed by the following claims.

What is claimed:

1. An isolated nucleic acid molecule from *Corynebacterium glutamicum* encoding an HA protein, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

2. The isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes an HA protein involved in the production of a fine chemical.

3. An isolated *Corynebacterium glutamicum* nucleic acid molecule selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

4. An isolated nucleic acid molecule which encodes a polypeptide sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

5. An isolated nucleic acid molecule which encodes a naturally occurring allelic variant of a polypeptide selected from the group of amino acid sequences consisting of those sequences set forth in Appendix B, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

6. An isolated nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, or a portion thereof, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

7. An isolated nucleic acid molecule comprising a fragment of at least 15 nucleotides of a nucleic acid comprising a nucleotide sequence selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated genes set forth in Table 1.

8. An isolated nucleic acid molecule which hybridizes to the nucleic acid molecule of any one of claims 1-7 under stringent conditions.

9. An isolated nucleic acid molecule comprising the nucleic acid molecule of claim 1 or a portion thereof and a nucleotide sequence encoding a heterologous polypeptide.

10. A vector comprising the nucleic acid molecule of claim 1.

11. The vector of claim 10, which is an expression vector.

12. A host cell transfected with the expression vector of claim 11.

13. The host cell of claim 12, wherein said cell is a microorganism.

14. The host cell of claim 13, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

15. The host cell of claim 12, wherein the expression of said nucleic acid molecule results in the modulation in production of a fine chemical from said cell.

16. The host cell of claim 15, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

17. A method of producing a polypeptide comprising culturing the host cell of claim 12 in an appropriate culture medium to, thereby, produce the polypeptide.

18. An isolated HA polypeptide from *Corynebacterium glutamicum*, or a portion thereof.

19. The polypeptide of claim 18, wherein said polypeptide is involved in the production of a fine chemical production.

20. An isolated polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

21. An isolated polypeptide comprising a naturally occurring allelic variant of a polypeptide comprising an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, or a portion thereof, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

22. The isolated polypeptide of claim 18, further comprising heterologous amino acid sequences.

23. An isolated polypeptide which is encoded by a nucleic acid molecule comprising a nucleotide sequence which is at least 50% homologous to a nucleic acid selected from the group consisting of those sequences set forth in Appendix A, provided that the nucleic acid molecule does not consist of any of the F-designated nucleic acid molecules set forth in Table 1.

24. An isolated polypeptide comprising an amino acid sequence which is at least 50% homologous to an amino acid sequence selected from the group consisting of those sequences set forth in Appendix B, provided that the amino acid sequence is not encoded by any of the F-designated genes set forth in Table 1.

25. A method for producing a fine chemical, comprising culturing a cell containing a vector of claim 12 such that the fine chemical is produced.

26. The method of claim 25, wherein said method further comprises the step of recovering the fine chemical from said culture.

27. The method of claim 25, wherein said method further comprises the step of transfecting said cell with the vector of claim 11 to result in a cell containing said vector.

28. The method of claim 25, wherein said cell belongs to the genus *Corynebacterium* or *Brevibacterium.*

29. The method of claim 25, wherein said cell is selected from the group consisting of: *Corynebacterium glutamicum, Corynebacterium herculis, Corynebacterium lilium, Corynebacterium acetoacidophilum, Corynebacterium acetoglutamicum, Corynebacterium acetophilum, Corynebacterium ammoniagenes, Corynebacterium fujiokense, Corynebacterium nitrilophilus, Brevibacterium ammoniagenes, Brevibacterium butanicum, Brevibacterium divaricatum, Brevibacterium flavum, Brevibacterium healii, Brevibacterium ketoglutamicum, Brevibacterium ketosoreductum, Brevibacterium lactofermentum, Brevibacterium linens, Brevibacterium paraffinolyticum,* and those strains set forth in Table 3.

30. The method of claim 25, wherein expression of the nucleic acid molecule from said vector results in modulation of production of said fine chemical.

31. The method of claim 25, wherein said fine chemical is selected from the group consisting of: organic acids, proteinogenic and nonproteinogenic amino acids, purine and pyrimidine bases, nucleosides, nucleotides, lipids, saturated and unsaturated fatty acids, diols, carbohydrates, aromatic compounds, vitamins, cofactors, polyketides, and enzymes.

32. The method of claim 25, wherein said fine chemical is an amino acid.

33. The method of claim 32, wherein said amino acid is drawn from the group consisting of: lysine, glutamate, glutamine, alanine, aspartate, glycine, serine, threonine, methionine, cysteine, valine, leucine, isoleucine, arginine, proline, histidine, tyrosine, phenylalanine, and tryptophan.

34. A method for producing a fine chemical, comprising culturing a cell whose genomic DNA has been altered by the inclusion of a nucleic acid molecule of any one of claims 1-9.

35. A method for diagnosing the presence or activity of *Corynebacterium diphtheriae* in a subject, comprising detecting the presence of one or more of the sequences set forth in Appendix A or Appendix B in the subject, provided that the sequences are not or are not encoded by any of the F-designated sequences set forth in Table 1, thereby diagnosing the presence or activity of *Corynebacterium diphtheriae* in the subject.

36. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule is disrupted.

37. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the nucleic acid molecule comprises one or more nucleic acid modifications from the sequence set forth in Appendix A.

38. A host cell comprising a nucleic acid molecule selected from the group consisting of the nucleic acid molecules set forth in Appendix A, wherein the regulatory region of the nucleic acid molecule is modified relative to the wild-type regulatory region of the molecule.

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CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION

Abstract of the Disclosure

Isolated nucleic acid molecules, designated HA nucleic acid molecules, which encode novel HA proteins from *Corynebacterium glutamicum* are described. The invention also provides antisense nucleic acid molecules, recombinant expression vectors containing HA nucleic acid molecules, and host cells into which the expression vectors have been introduced. The invention still further provides isolated HA proteins, mutated HA proteins, fusion proteins, antigenic peptides and methods for the improvement of production of a desired compound from *C. glutamicum* based on genetic engineering of HA genes in this organism.

Table 1: Genes in the Application

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
1	2	RXA02702	GR00758	1572	115	UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8)
3	4	RXA02705	GR00758	5803	4388	UDP-N-ACETYLMURAMOYLALANINE--D-GLUTAMATE LIGASE (EC 6.3.2.9)
5	6	RXA01254	GR00365	3807	2539	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (EC 6.3.2.13)
7	8	RXN02707	VV0017	20110	18581	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D- ALANYL LIGASE
9	10	F RXA02707	GR00758	7264	6920	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D- ALANYL LIGASE (EC 6.3.2.15)
11	12	F RXA02708	GR00758	7694	7260	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D- ALANYL LIGASE (EC 6.3.2.15)
13	14	F RXA02709	GR00758	8451	7723	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMYL-2,6-DIAMINOPIMELATE--D-ALANYL-D- ALANYL LIGASE (EC 6.3.2.15)
15	16	RXA02710	GR00758	10035	8473	UDP-N-ACETYLMURAMOYLALANYL-D-GLUTAMATE--2,6-DIAMINOPIMELATE LIGASE (EC 6.3.2.13)
17	18	RXN00531	VV0079	19063	19557	FINE TANGLED PILI MAJOR SUBUNIT
19	20	RXA00944	GR00259	1573	602	NADPH DEHYDROGENASE 3 (EC 1.6.99.1)
21	22	RXS02560	VV0101	9922	10788	NADPH-FLAVIN OXIDOREDUCTASE (EC 1.6.99.-)
23	24	RXS03119	VV0098	86877	87008	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)
25	26	RXS03120	VV0098	87351	87476	SUPEROXIDE DISMUTASE [MN] (EC 1.15.1.1)

Cell wall biosynthesis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
27	28	RXA01430	GR00417	7458	6271	N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28)
29	30	RXA02641	GR00749	5097	3022	N-ACETYLMURAMOYL-L-ALANINE AMIDASE (EC 3.5.1.28)
31	32	RXA00135	GR00021	1709	2962	UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
33	34	RXA02706	GR00758	6910	5813	PHOSPHO-N-ACETYLMURAMOYL-PENTAPEPTIDE-TRANSFERASE (EC 2.7.8.13)
35	36	RXA02411	GR00703	1845	997	GLUTAMATE RACEMASE (EC 5.1.1.3)
37	38	RXN01022	VV0143	4460	3381	D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4)
39	40	F RXA01022	GR00292	3	806	D-ALANINE--D-ALANINE LIGASE (EC 6.3.2.4)
41	42	RXA02703	GR00758	2698	1610	UDP-N-ACETYLGLUCOSAMINE--N-ACETYLMURAMYL-(PENTAPEPTIDE) PYROPHOSPHORYL- UNDECAPRENOL N-ACETYLGLUCOSAMINE TRANSFERASE (EC 2.4.1.-)
43	44	RXA02711	GR00758	12273	10162	PENICILLIN-BINDING PROTEIN 2

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
45	46	RXA02859	GR10005	846	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
47	48	RXA00569	GR00152	3928	4953	PENICILLIN-BINDING PROTEIN 4
49	50	RXN03092	VV0054	10445	9561	PENICILLIN-BINDING PROTEIN 1A
51	52	F RXA00594	GR00158	3525	4457	PENICILLIN-BINDING PROTEIN 1A
53	54	RXA01828	GR00516	7736	6315	PENICILLIN-BINDING PROTEIN 3
55	56	RXA00612	GR00162	3	1187	PENICILLIN-BINDING PROTEIN 1A
57	58	RXA01510	GR00424	15370	16650	PENICILLIN-BINDING PROTEIN 4 PRECURSOR (PBP-4) (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4) / D-ALANYL-D-ALANINE-ENDOPEPTIDASE (EC 3.4.99.-)
59	60	RXN01608	VV0139	3536	5374	PENICILLIN-BINDING PROTEIN 5 PRECURSOR
61	62	F RXA01608	GR00449	837	2675	(AL008883) penecillin binding protein [Mycobacterium tuberculosis]
63	64	RXA01270	GR00367	21652	20498	perosamine synthetase
65	66	RXN00549	VV0079	31746	33419	PENICILLIN-BINDING PROTEIN 1A
67	68	RXN00550	VV0079	33457	33777	PENICILLIN-BINDING PROTEIN 1A
69	70	RXN03091	VV0054	9515	8970	PENICILLIN-BINDING PROTEIN 1A
71	72	RXN03178	VV0334	921	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
73	74	F RXA02859	GR10005	846	121	PENICILLIN-BINDING PROTEIN 5* PRECURSOR (D-ALANYL-D-ALANINE CARBOXYPEPTIDASE) (EC 3.4.16.4)
75	76	RXN01267	VV0009	17895	16582	UDP-N-ACETYLGLUCOSAMINE 1-CARBOXYVINYLTRANSFERASE (EC 2.5.1.7)
77	78	RXN00045	VV0119	4409	5317	UDP-N-acetylglucosamine-2-epimerase (EC 5.1.3.14) /N-acetylmannosamine kinase (EC 2.7.1.60)

Cell division

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
79	80	RXN02704	VV0017	16043	14355	CELL DIVISIN PROTEIN FTSW
81	82	F RXA02704	GR00758	4382	2694	CELL DIVISIN PROTEIN FTSW
83	84	RXA02722	GR00759	2729	1404	CELL DIVISION PROTEIN FTSZ
85	86	RXA00009	GR00002	1545	646	CELL DIVISION PROTEIN FTSX
87	88	RXA00010	GR00002	2248	1562	CELL DIVISION ATP-BINDING PROTEIN FTSE
89	90	RXA00143	GR00022	6328	4847	CELL DIVISION INHIBITOR
91	92	RXA00277	GR00043	1588	5	CELL DIVISION CONTROL PROTEIN 15 (EC 2.7.1.-)
93	94	RXA00857	GR00233	2	1291	CELL DIVISION PROTEIN FTSK
95	96	RXA01435	GR00418	2	871	CELL DIVISION CONTROL PROTEIN 15 (EC 2.7.1.-)
97	98	RXA01511	GR00424	16655	17596	CELL CYCLE PROTEIN MESJ
99	100	RXA01513	GR00424	18368	20926	CELL DIVISION PROTEIN FTSH (EC 3.4.24.-)
101	102	RXA02098	GR00630	4161	5906	CELL DIVISION PROTEIN FTSY
103	104	RXA02713	GR00758	14077	13067	Hypothetical Cell Division Protein mraW
105	106	RXN02723	VV0017	11745	11080	FTSQ
107	108	F RXA02723	GR00759	3460	2984	FTSQ
109	110	RXA01426	GR00417	2777	3403	GLUCOSE INHIBITED DIVISION PROTEIN B

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
111	112	RXA01428	GR00417	4495	5631	STAGE 0 SPORULATION PROTEIN J
113	114	RXA01640	GR00456	4661	1344	STAGE III SPORULATION PROTEIN E
115	116	RXA01829	GR00516	9058	7736	STAGE V SPORULATION PROTEIN E
117	118	RXA01427	GR00417	3512	4432	SOJ PROTEIN
119	120	RXN02973	VV0229	657	4	SOJ PROTEIN
121	122	F RXA01603	GR00447	14043	14663	SOJ PROTEIN
123	124	RXN00818	VV0054	28524	27685	INHIBITION OF MORPHOLOGICAL DIFFERENTIATION

Proteolysis

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
125	126	RXN03028	VV0008	41156	43930	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
127	128	F RXA02470	GR00715	2216	3196	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
129	130	F RXA02471	GR00715	3159	4991	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
131	132	RXN03094	VV0057	1794	43	CLPB PROTEIN
133	134	F RXA01668	GR00464	2205	3920	CLPB PROTEIN
135	136	RXN02937	VV0098	85783	85382	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1 14)
137	138	RXN03077	VV0043	1729	2913	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5.1.14)
139	140	F RXA02855	GR10002	1693	2877	N-ACYL-L-AMINO ACID AMIDOHYDROLASE (EC 3.5 1 14), hippurate hydrolase
141	142	RXN00982	VV0149	7596	6091	(L42758) proteinase [Streptomyces lividans]
143	144	F RXA00977	GR00275	1647	2660	(L42758) proteinase [Streptomyces lividans]
145	146	F RXA00982	GR00276	5194	4949	(L42758) proteinase [Streptomyces lividans]
147	148	RXN01181	VV0065	1	957	AMINOPEPTIDASE A/I (EC 3.4.11.1)
149	150	F RXA01181	GR00337	1	957	AMINOPEPTIDASE
151	152	RXN01014	VV0209	13328	10728	AMINOPEPTIDASE N (EC 3.4.11 2)
153	154	F RXA01014	GR00289	3	1580	AMINOPEPTIDASE N (EC 3 4.11.2)
155	156	F RXA01018	GR00290	2289	3152	AMINOPEPTIDASE N (EC 3.4.11.2)
157	158	RXN01046	VV0015	47863	49641	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
159	160	RXN01974	VV0218	3793	5577	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPA
161	162	RXN01120	VV0182	5678	4401	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
163	164	F RXA01120	GR00310	2349	1072	ATP-DEPENDENT CLP PROTEASE ATP-BINDING SUBUNIT CLPX
165	166	RXN00397	VV0025	3803	4603	XAA-PRO AMINOPEPTIDASE (EC 3.4.11.9)
167	168	RXN01868	VV0127	9980	11905	ZINC METALLOPROTEASE (EC 3.4.24.-)
169	170	F RXA01868	GR00534	1640	30	ZINC METALLOPROTEASE (EC 3.4.24.-)
171	172	F RXA01869	GR00534	1954	1652	ZINC METALLOPROTEASE (EC 3.4.24.-)
173	174	RXN00499	VV0086	8158	9438	PROLINE IMINOPEPTIDASE (EC 3.4.11.5)
175	176	F RXA00499	GR00125	3	959	PROLINE IMINOPEPTIDASE
177	178	RXN01277	VV0009	32155	34158	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
179	180	F RXA01277	GR00368	1738	50	PROLYL ENDOPEPTIDASE (EC 3.4.21.26)
181	182	RXN00675	VV0005	33258	34049	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
183	184	F RXA00675	GR00178	2	484	METHIONINE AMINOPEPTIDASE (EC 3.4.11.18)
185	186	RXN00877	VV0099	2221	3885	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)
187	188	F RXA00877	GR00242	3	1067	PEPTIDYL-DIPEPTIDASE DCP (EC 3.4.15.5)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
189	190	RXN01226	VV0064	4172	4711	PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29)
191	192	RXN01963	VV0200	689	6	Hypothetical Secretory Serine Protease (EC 3.4.21.-)
193	194	RXN00621	VV0135	5853	5071	PROTEASE II (EC 3.4.21.83)
195	196	F RXA00621	GR00163	4075	4857	PTRB periplasmic protease
197	198	RXN00622	VV0135	5150	3735	PROTEASE II (EC 3.4.21.83)
199	200	F RXA00622	GR00163	4778	6193	PTRB periplasmic protease
201	202	RXN02146	VV0300	14742	15368	PROTEIN P60 PRECURSOR
203	204	RXN03133	VV0127	39393	40076	HYDROGENASE 1 MATURATION PROTEASE (EC 3.4.-.-)
205	206	RXN02820	VV0131	4799	6109	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
207	208	F RXA02820	GR00801	1	507	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
209	210	F RXA02000	GR00589	3430	3933	GAMMA-GLUTAMYLTRANSPEPTIDASE (EC 2.3.2.2)
211	212	RXN02944	VV0169	12751	12074	GAMMA-GLUTAMYLTRANSPEPTIDASE PRECURSOR (EC 2.3.2.2)
213	214	RXS00197	VV0115	2733	1522	Membrane Spanning Protease
215	216	RXS01223	VV0064	7528	8139	PEPTIDYL-TRNA HYDROLASE (EC 3.1.1.29)
217	218	RXS01642	VV0005	49423	48182	Serine protease

Enzymes in general

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
219	220	RXA01728	GR00489	2452	1478	BETA C-S LYASE (EC 3.-.-.-) PUTATIVE AMINOTRANSFERASE
221	222	RXA02214	GR00650	954	1562	Acetyltransferases
223	224	RXA02716	GR00758	16827	17387	Acetyltransferases
225	226	RXN01499	VV0008	7034	3213	ENTEROBACTIN SYNTHETASE COMPONENT F
227	228	FRXA01499	GR00424	7034	3213	Acetyltransferases (the isoleucine patch superfamily)
229	230	RXN00787	VV0321	3736	5637	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
231	232	F RXA00787	GR00209	598	5	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
233	234	F RXA00791	GR00210	831	4	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
235	236	RXA01057	GR00296	7548	6046	D-AMINO ACID DEHYDROGENASE LARGE SUBUNIT (EC 1.4.99.1)
237	238	RXA01055	GR00296	4821	4720	D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT (EC 1.4.99.1)
239	240	RXA01056	GR00296	5952	5053	D-AMINO ACID DEHYDROGENASE SMALL SUBUNIT (EC 1.4.99.1)
241	242	RXN02021	VV0160	2008	1061	2,3,4,5-tetrahydropyridine-2-carboxylate N-succinyltransferase (EC 2.3.1.117)
243	244	RXS00949				quinate dehydrogenase (pyrroloquinoline-quinone) (EC 1.1.99.25)
245	246	RXS00004	VV0196	6930	6460	NITRILASE REGULATOR
247	248	RXS00166	VV0232	3650	4309	Methyltransferase
249	250	RXS00288	VV0079	14586	15596	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
251	252	RXS01114	VV0182	9118	10341	3-KETOACYL-COA THIOLASE (EC 2.3.1.16)
253	254	RXS01205	VV0268	893	363	UNDECAPRENYL-PHOSPHATE ALPHA-N-ACETYLGLUCOSAMINYLTRANSFERASE (EC 2.4.1.-)
255	256	RXS01269	VV0009	21430	20990	UNDECAPRENYL-PHOSPHATE GALACTOSEPHOSPHOTRANSFERASE (EC 2.7.8.6)
257	258	RXS01421	VV0122	16024	15638	ACYLTRANSFERASE (EC 2.3.1.-)
259	260	RXS01491	VV0139	36800	37450	DNA FOR L-PROLINE 3-HYDROXYLASE, COMPLETE CDS
261	262	RXS01572	VV0009	43945	44436	ALCOHOL DEHYDROGENASE (EC 1.1.1.1)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
263	264	RXS02453	VV0107	7370	8122	ACETOIN(DIACETYL) REDUCTASE (EC 1.1.1.5)
265	266	RXS02474	VV0008	47021	46248	(S,S)-butane-2,3-diol dehydrogenase (EC 1.1.1.76)
267	268	RXS02485	VV0007	2359	3459	UDP-N-ACETYLENOLPYRUVOYLGLUCOSAMINE REDUCTASE (EC 1.1.1.158)
269	270	RXS02539	VV0057	17332	15815	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
271	272	RXS02578	VV0098	7668	6565	ACYLTRANSFERASE
273	274	RXS02741	VV0074	5768	6733	QUINONE OXIDOREDUCTASE (EC 1.6.5.5)
275	276	RXS03061	VV0034	108	437	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
277	278	RXS03150	VV0155	10678	10055	ALDEHYDE DEHYDROGENASE (EC 1.2.1.3)
279	280	RXS02554				Oxidoreductase (EC 1.1.1.-)
281	282	RXS03058				METHYLTRANSFERASE (EC 2.1.1.-)
283	284	RXS03218				CAFFEOYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
285	286	F RXA01918	GR00549	4644	5057	CAFFEOYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
287	288	RXC00110	VV0054	27517	26969	Protein involved in hydrolysis of epoxides
289	290	RXC01971	VV0105	4545	3715	Metal-Dependent Hydrolase

Genes encoding enzymes for the metabolism of inorganic compounds

Phosphate and Phosphonate metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
291	292	RXA02118	GR00636	2124	1783	PHNA PROTEIN
293	294	RXA00078	GR00012	6375	5962	PHNB PROTEIN
295	296	RXA02105	GR00632	294	4	PHNB PROTEIN
297	298	RXN00663	VV0142	10120	11493	PHOH PROTEIN HOMOLOG
299	300	F RXA00663	GR00173	1222	227	PHOH PROTEIN HOMOLOG
301	302	RXA00888	GR00242	14325	15341	PHOH PROTEIN HOMOLOG
303	304	RXA01437	GR00418	3932	2550	PHOSPHATE ACETYLTRANSFERASE (EC 2.3.1.8)
305	306	RXN00778	VV0103	18126	19250	PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
307	308	F RXA00778	GR00205	9079	8246	PHOSPHATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
309	310	RXA02497	GR00720	10059	10985	EXOPOLYPHOSPHATASE (EC 3.6.1.11)
311	312	RXA01477	GR00422	8469	10016	ALKALINE PHOSPHATASE D PRECURSOR (EC 3.1.3.1)
313	314	RXA01509	GR00424	15169	14696	INORGANIC PYROPHOSPHATASE (EC 3.6.1.1)
315	316	RXA00100	GR00014	9512	10111	DEDA PROTEIN, similar to alkaline phosphatase
317	318	RXA00615	GR00162	3355	2774	DEDA PROTEIN
319	320	RXN00250	VV0189	286	1032	DEDA PROTEIN - ALKALINE PHOSPHATASE LIKE PROTEIN
321	322	F RXA02010	GR00602	79	525	DEDA PROTEIN
323	324	RXA02120	GR00636	5021	4260	CARBOXYVINYL-CARBOXYPHOSPHONATE PHOSPHORYLMUTASE (EC 2.7.8.23)
325	326	RXS01000	VV0106	7252	6407	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
327	328	RXS01002	VV0106	8858	8055	PHOSPHONATES TRANSPORT ATP-BINDING PROTEIN PHNC
329	330	RXS01003	VV0106	8055	7252	PHOSPHONATES TRANSPORT SYSTEM PERMEASE PROTEIN PHNE
331	332	RXS01902	VV0098	84095	83037	alkaline phosphatase

Fe-Metabolism

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
333	334	RXA01967	GR00567	1848	706	FERRIC ENTEROCHELIN ESTERASE HOMOLOG
335	336	RXA00070	GR00011	3436	3867	FERRIC UPTAKE REGULATION PROTEIN
337	338	RXA01934	GR00555	7192	7749	FERRIPYOCHELIN BINDING PROTEIN
339	340	RXN01997	VV0084	33308	33793	FERRITIN
341	342	F RXA01997	GR00586	546	935	FERRITIN
343	344	RXA01082	GR00302	1486	827	IRON REPRESSOR
345	346	RXA01236	GR00358	2185	1241	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
347	348	RXA01354	GR00393	2692	1757	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
349	350	RXA01620	GR00451	2585	3532	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
351	352	RXA02052	GR00624	4586	3795	IRON(III) DICITRATE-BINDING PERIPLASMIC PROTEIN PRECURSOR
353	354	RXA00372	GR00078	1653	2729	PERIPLASMIC-IRON-BINDING PROTEIN SHIB
355	356	RXA00088	GR00013	4389	5402	FERRIC ANGUIBACTIN-BINDING PROTEIN PRECURSOR
357	358	RXS00156	VV0167	1342	2451	FERROCHELATASE (EC 4.99.1.1)
359	360	RXS00624	VV0135	2018	1332	FERROCHELATASE (EC 4.99.1.1)

Modification and degradation of aromatic compounds

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
361	362	RXA00024	GR00003	938	1882	ARYL-ALCOHOL DEHYDROGENASE (NADP+) (EC 1.1.1.91)
363	364	RXA02526	GR00725	4109	5314	3-CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE (EC 5.5.1.2)
365	366	RXN02813	VV0128	13120	14118	3-CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE HOMOLOG (EC 5.5.1.2)
367	368	F RXA02813	GR00794	651	10	3-CARBOXY-CIS,CIS-MUCONATE CYCLOISOMERASE HOMOLOG (EC 5.5.1.2)
369	370	RXA01113	GR00307	1098	862	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
371	372	RXA02126	GR00637	1556	1876	4-CARBOXYMUCONOLACTONE DECARBOXYLASE (EC 4.1.1.44)
373	374	RXA01465	GR00421	4121	2961	MUCONATE CYCLOISOMERASE (EC 5.5.1.1)
375	376	RXA02316	GR00665	9038	8025	MUCONATE CYCLOISOMERASE (EC 5.5.1.1)
377	378	RXA01464	GR00421	2945	2655	MUCONOLACTONE ISOMERASE (EC 5.3.3.4)
379	380	RXA02603	GR00742	7742	8737	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
381	382	RXN02839	VV0362	3	449	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
383	384	F RXA02839	GR00832	3	419	4-HYDROXYBENZOATE OCTAPRENYLTRANSFERASE (EC 2.5.1.-)
385	386	RXA01502	GR00424	8385	9617	BENZENE 1,2-DIOXYGENASE SYSTEM FERREDOXIN--NAD(+) REDUCTASE COMPONENT (EC 1.18.1.3)
387	388	RXA02828	GR00813	15	572	BIPHENYL-2,3-DIOL 1,2-DIOXYGENASE III (EC 1.13.11.39)
389	390	RXA02064	GR00626	5223	4585	CAFFEOYL-COA O-METHYLTRANSFERASE (EC 2.1.1.104)
391	392	RXN00639	VV0128	7858	8712	CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
393	394	F RXA00639	GR00168	665	6	CATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
395	396	RXN01653	VV0321	12867	11407	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
397	398	F RXA00797	GR00212	445	804	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
399	400	F RXA01653	GR00458	1909	971	DIBENZOTHIOPHENE DESULFURIZATION ENZYME A
401	402	RXN02530	VV0057	5469	6125	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8)
403	404	F RXA02530	GR00726	20	469	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 1 (EC 1.14.13.8)
405	406	RXA02083	GR00629	1720	311	DIMETHYLANILINE MONOOXYGENASE (N-OXIDE FORMING) 2 (EC 1.14.13.8)

Nucleic Acid SEQ ID NO	Amino Acid SEQ ID NO	Identification Code	Contig.	NT Start	NT Stop	Function
407	408	RXA00892	GR00243	2188	1295	PARANITROBENZYL ESTERASE (EC 3 1.1.-)
409	410	RXA02092	GR00629	12153	10516	PARANITROBENZYL ESTERASE (EC 3.1.1.-)
411	412	RXN00658	VV0083	15705	16397	PHENOL 2-MONOOXYGENASE (EC 1.14.13.7)
413	414	F RXA00658	GR00170	321	4	PHENOL 2 MONOOXYGENASE (EC 1.14.13 7)
415	416	RXA01385	GR00406	5320	3440	PHENOL 2 MONOOXYGENASE (EC 1.14.13.7)
417	418	RXN01461	VV0128	12414	13025	PROTOCATECHUATE 3,4-DIOXYGENASE ALPHA CHAIN (EC 1.13.11.3)
419	420	F RXA01461	GR00421	463	5	PROTOCATECHUATE 3,4-DIOXYGENASE ALPHA CHAIN (EC 1.13.11.3)
421	422	RXA01462	GR00421	1167	478	PROTOCATECHUATE 3,4-DIOXYGENASE BETA CHAIN (EC 1 13.11.3)
423	424	RXN00641	VV0128	7440	5950	TOLUATE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12 -)
425	426	F RXA00640	GR00168	1083	1331	TOLUATE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12.-)
427	428	F RXA00641	GR00168	1533	2573	TOLUATE 1,2-DIOXYGENASE ALPHA SUBUNIT (EC 1.14.12.-)
429	430	RXA00642	GR00168	2616	3107	TOLUATE 1,2-DIOXYGENASE BETA SUBUNIT (EC 1.14.12.-)
431	432	RXA00643	GR00168	3122	4657	TOLUATE 1,2-DIOXYGENASE ELECTRON TRANSFER COMPONENT
433	434	RXN01993	VV0182	16	1143	VANILLATE DEMETHYLASE (EC 1.14 -.-)
435	436	F RXA01993	GR00584	1	366	VANILLATE DEMETHYLASE (EC 1.14 -.-)
437	438	F RXA02012	GR00604	2	670	VANILLATE DEMETHYLASE (EC 1 14.-.-)
439	440	RXA01994	GR00584	373	1347	VANILLATE DEMETHYLASE OXIDOREDUCTASE (EC 1 -.-.-)
441	442	RXA02535	GR00726	6599	7753	XYLENE MONOOXYGENASE ELECTRON TRANSFER COMPONENT
443	444	RXA00964	GR00269	1575	451	1-hydroxy-2-naphthoate 1,2-dioxygenase (EC 1.13.11 38)
445	446	RXN01466	VV0019	7050	6091	ARYLESTERASE (EC 3.1.1.2)
447	448	F RXA01466	GR00422	826	5	ARYLESTERASE (EC 3.1 1 2)
449	450	RXN03036	VV0014	671	6	PROTOCATECHUATE 3,4-DIOXYGENASE BETA CHAIN (EC 1 13.11.3)
451	452	F RXA02895	GR10037	671	6	CHLOROCATECHOL 1,2-DIOXYGENASE (EC 1.13.11.1)
453	454	RXA02449	GR00710	1458	2360	hydroxyquinol 1,2-dioxygenase (EC 1.13.11.37)
455	456	RXN00178	VV0174	14670	15554	hydroxyquinol 1,2-dioxygenase (EC 1.13 11.37)
457	458	F RXA00178	GR00028	304	1188	HYDROXYQUINOL-1, 2-DIOXYGENASE
459	460	RXA02111	GR00632	4310	5593	QUINOLINATE SYNTHETASE A
461	462	RXA00644		GR0016 8	4657	CIS-1,2-DIHYDROXYCYCLOHEXA-3,5-DIENE-1-CARBOXYLATE DEHYDROGENASE (EC 1.3.1.55)
463	464	RXN00177	VV0174	13589	14656	MALEYLACETATE REDUCTASE (EC 1.3.1.32)
465	466	F RXA00177	GR00028	3	290	MALEYLACETATE REDUCTASE (EC 1.3.1 32) metabolism of 2,4,5-trichlorophenoxyacetic acid
467	468	RXA02448	GR00710	340	1428	MALEYLACETATE REDUCTASE (EC 1.3.1.32)
469	470	RXA00048	GR00008	2185	527	3-(3-HYDROXYPHENYL) PROPIONATE HYDROXYLASE
471	472	RXA01126	GR00313	2	565	POSSIBLE 2-HYDROXYHEPTA-2,4-DIENE-1,7- DIOATE ISOMAERASE
473	474	RXA01117	GR00309	1713	973	SUCCINYL-COA:3-KETOACID-COENZYME A TRANSFERASE PRECURSOR (EC 2.8.3.5)
475	476	RXA00772	GR00205	2715	1210	SUCCINYL-COA:COENZYME A TRANSFERASE (EC 2.8.3.-)
477	478	RXA01288	GR00372	2018	1644	SUCCINYL-COA·COENZYME A TRANSFERASE (EC 2.8.3.-)

TABLE 2: GENES IDENTIFIED FROM GENBANK

GenBank™ Accession No.	Gene Name	Gene Function	Reference
A09073	ppg	Phosphoenol pyruvate carboxylase	Bachmann, B. et al. "DNA fragment coding for phosphoenolpyruvat corboxylase, recombinant DNA carrying said fragment, strains carrying the recombinant DNA and method for producing L-aminino acids using said strains," Patent: EP 0358940-A 3 03/21/90
A45579, A45581, A45583, A45585 A45587		Threonine dehydratase	Moeckel, B. et al. "Production of L-isoleucine by means of recombinant micro-organisms with deregulated threonine dehydratase," Patent: WO 9519442-A 5 07/20/95
AB003132	murC; ftsQ; ftsZ		Kobayashi, M. et al. "Cloning, sequencing, and characterization of the ftsZ gene from coryneform bacteria," *Biochem. Biophys. Res. Commun.*, 236(2):383-388 (1997)
AB015023	murC; ftsQ		Wachi, M. et al. "A murC gene from Coryneform bacteria," *Appl. Microbiol. Biotechnol.*, 51(2):223-228 (1999)
AB018530	dtsR		Kimura, E. et al. "Molecular cloning of a novel gene, dtsR, which rescues the detergent sensitivity of a mutant derived from *Brevibacterium lactofermentum*," *Biosci. Biotechnol. Biochem.*, 60(10):1565-1570 (1996)
AB018531	dtsR1; dtsR2		
AB020624	murI	D-glutamate racemase	
AB023377	tkt	transketolase	
AB024708	gltB; gltD	Glutamine 2-oxoglutarate aminotransferase large and small subunits	
AB025424	acn	aconitase	
AB027714	rep	Replication protein	
AB027715	rep; aad	Replication protein; aminoglycoside adenyltransferase	
AF005242	argC	N-acetylglutamate-5-semialdehyde dehydrogenase	
AF005635	glnA	Glutamine synthetase	
AF030405	hisF	cyclase	
AF030520	argG	Argininosuccinate synthetase	
AF031518	argF	Ornithine carbamolytransferase	
AF036932	aroD	3-dehydroquinate dehydratase	

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF038548	pyc	Pyruvate carboxylase	
AF038651	dciAE; apt; rel	Dipeptide-binding protein; adenine phosphoribosyltransferase; GTP pyrophosphokinase	Wehmeier, L. et al. "The role of the Corynebacterium glutamicum rel gene in (p)ppGpp metabolism," *Microbiology,* 144:1853-1862 (1998)
AF041436	argR	Arginine repressor	
AF045998	impA	Inositol monophosphate phosphatase	
AF048764	argH	Argininosuccinate lyase	
AF049897	argC; argJ; argB; argD; argF; argR; argG; argH	N-acetylglutamylphosphate reductase; ornithine acetyltransferase; N-acetylglutamate kinase; acetylornithine transminase; ornithine carbamoyltransferase; arginine repressor; argininosuccinate synthase; argininosuccinate lyase	
AF050109	inhA	Enoyl-acyl carrier protein reductase	
AF050166	hisG	ATP phosphoribosyltransferase	
AF051846	hisA	Phosphoribosylformimino-5-amino-1-phosphoribosyl-4-imidazolecarboxamide isomerase	
AF052652	metA	Homoserine O-acetyltransferase	Park, S. et al. "Isolation and analysis of metA, a methionine biosynthetic gene encoding homoserine acetyltransferase in Corynebacterium glutamicum," *Mol. Cells.,* 8(3):286-294 (1998)
AF053071	aroB	Dehydroquinate synthetase	
AF060558	hisH	Glutamine amidotransferase	
AF086704	hisE	Phosphoribosyl-ATP-pyrophosphohydrolase	
AF114233	aroA	5-enolpyruvylshikimate 3-phosphate synthase	
AF116184	panD	L-aspartate-alpha-decarboxylase precursor	Dusch, N. et al. "Expression of the Corynebacterium glutamicum panD gene encoding L-aspartate-alpha-decarboxylase leads to pantothenate overproduction in Escherichia coli," *Appl. Environ. Microbiol.,* 65(4)1530-1539 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
AF124518	aroD; aroE	3-dehydroquinase; shikimate dehydrogenase	
AF124600	aroC; aroK; aroB; pepQ	Chorismate synthase; shikimate kinase; 3-dehydroquinate synthase; putative cytoplasmic peptidase	
AF145897	inhA		
AF145898	inhA		
AJ001436	ectP	Transport of ectoine, glycine betaine, proline	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.*, 180(22):6005-6012 (1998)
AJ004934	dapD	Tetrahydrodipicolinate succinylase (incomplete[i])	Wehrmann, A. et al. "Different modes of diaminopimelate synthesis and their role in cell wall integrity: A study with Corynebacterium glutamicum," *J. Bacteriol.*, 180(12):3159-3165 (1998)
AJ007732	ppc; secG; amt; ocd; soxA	Phosphoenolpyruvate-carboxylase; ?; high affinity ammonium uptake protein; putative ornithine-cyclodecarboxylase; sarcosine oxidase	
AJ010319	ftsY, glnB, glnD; srp; amtP	Involved in cell division; PII protein; uridylyltransferase (uridylyl-removing enzmye); signal recognition particle; low affinity ammonium uptake protein	Jakoby, M. et al. "Nitrogen regulation in Corynebacterium glutamicum; Isolation of genes involved in biochemical characterization of corresponding proteins," *FEMS Microbiol.*, 173(2):303-310 (1999)
AJ132968	cat	Chloramphenicol aceteyl transferase	
AJ224946	mqo	L-malate: quinone oxidoreductase	Molenaar, D. et al. "Biochemical and genetic characterization of the membrane-associated malate dehydrogenase (acceptor) from Corynebacterium glutamicum," *Eur. J. Biochem.*, 254(2):395-403 (1998)
AJ238250	ndh	NADH dehydrogenase	
AJ238703	porA	Porin	Lichtinger, T. et al. "Biochemical and biophysical characterization of the cell wall porin of Corynebacterium glutamicum: The channel is formed by a low molecular mass polypeptide," *Biochemistry*, 37(43):15024-15032 (1998)
D17429		Transposable element IS31831	Vertes, A.A. et al. "Isolation and characterization of IS31831, a transposable element from Corynebacterium glutamicum," *Mol. Microbiol.*, 11(4):739-746 (1994)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
D84102	odhA	2-oxoglutarate dehydrogenase	Usuda, Y. et al. "Molecular cloning of the Corynebacterium glutamicum (Brevibacterium lactofermentum AJ12036) odhA gene encoding a novel type of 2-oxoglutarate dehydrogenase," *Microbiology,* 142:3347-3354 (1996)
E01358	hdh; hk	Homoserine dehydrogenase; homoserine kinase	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 1 10/12/87
E01359		Upstream of the start codon of homoserine kinase gene	Katsumata, R. et al. "Production of L-thereonine and L-isoleucine," Patent: JP 1987232392-A 2 10/12/87
E01375		Tryptophan operon	
E01376	trpL; trpE	Leader peptide; anthranilate synthase	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E01377		Promoter and operator regions of tryptophan operon	Matsui, K. et al. "Tryptophan operon, peptide and protein coded thereby, utilization of tryptophan operon gene expression and production of tryptophan," Patent: JP 1987244382-A 1 10/24/87
E03937		Biotin-synthase	Hatakeyama, K. et al. "DNA fragment containing gene capable of coding biotin synthetase and its utilization," Patent: JP 1992278088-A 1 10/02/92
E04040		Diamino pelargonic acid aminotransferase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04041		Desthiobiotinsynthetase	Kohama, K. et al. "Gene coding diaminopelargonic acid aminotransferase and desthiobiotin synthetase and its utilization," Patent: JP 1992330284-A 1 11/18/92
E04307		Flavum aspartase	Kurusu, Y. et al. "Gene DNA coding aspartase and utilization thereof," Patent: JP 1993030977-A 1 02/09/93
E04376		Isocitric acid lyase	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04377		Isocitric acid lyase N-terminal fragment	Katsumata, R. et al. "Gene manifestation controlling DNA," Patent: JP 1993056782-A 3 03/09/93
E04484		Prephenate dehydratase	Sotouchi, N. et al. "Production of L-phenylalanine by fermentation," Patent: JP 1993076352-A 2 03/30/93
E05108		Aspartokinase	Fugono, N. et al. "Gene DNA coding Aspartokinase and its use," Patent: JP 1993184366-A 1 07/27/93
E05112		Dihydro-dipichorinate synthetase	Hatakeyama, K. et al. "Gene DNA coding dihydrodipicolinic acid synthetase and its use," Patent: JP 1993184371-A 1 07/27/93

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E05776		Diaminopimelic acid dehydrogenase	Kobayashi, M. et al. "Gene DNA coding Diaminopimelic acid dehydrogenase and its use," Patent: JP 1993284970-A 1 11/02/93
E05779		Threonine synthase	Kohama, K. et al. "Gene DNA coding threonine synthase and its use," Patent: JP 1993284972-A 1 11/02/93
E06110		Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06111		Mutated Prephenate dehydratase	Kikuchi, T. et al. "Production of L-phenylalanine by fermentation method," Patent: JP 1993344881-A 1 12/27/93
E06146		Acetohydroxy acid synthetase	Inui, M. et al. "Gene capable of coding Acetohydroxy acid synthetase and its use," Patent: JP 1993344893-A 1 12/27/93
E06825		Aspartokinase	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06826		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E06827		Mutated aspartokinase alpha subunit	Sugimoto, M. et al. "Mutant aspartokinase gene," patent: JP 1994062866-A 1 03/08/94
E07701	secY		Honno, N. et al. "Gene DNA participating in integration of membraneous protein to membrane," Patent: JP 1994169780-A 1 06/21/94
E08177		Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08178, E08179, E08180, E08181, E08182		Feedback inhibition-released Aspartokinase	Sato, Y. et al. "Genetic DNA capable of coding Aspartokinase released from feedback inhibition and its utilization," Patent: JP 1994261766-A 1 09/20/94
E08232		Acetohydroxy-acid isomeroreductase	Inui, M. et al. "Gene DNA coding acetohydroxy acid isomeroreductase," Patent: JP 1994277067-A 1 10/04/94
E08234	secE		Asai, Y. et al. "Gene DNA coding for translocation machinery of protein," Patent: JP 1994277073-A 1 10/04/94
E08643		FT aminotransferase and desthiobiotin synthetase promoter region	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95
E08646		Biotin synthetase	Hatakeyama, K. et al. "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031476-A 1 02/03/95

GenBank™ Accession No.	Gene Name	Gene Function	Reference
E08649		Aspartase	Kohama, K. et al "DNA fragment having promoter function in coryneform bacterium," Patent: JP 1995031478-A 1 02/03/95
E08900		Dihydrodipicolinate reductase	Madori, M. et al. "DNA fragment containing gene coding Dihydrodipicolinate acid reductase and utilization thereof," Patent: JP 1995075578-A 1 03/20/95
E08901		Diaminopimelic acid decarboxylase	Madori, M. et al. "DNA fragment containing gene coding Diaminopimelic acid decarboxylase and utilization thereof," Patent: JP 1995075579-A 1 03/20/95
E12594		Serine hydroxymethyltransferase	Hatakeyama, K. et al. "Production of L-trypophan," Patent: JP 1997028391-A 1 02/04/97
E12760, E12759, E12758		transposase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12764		Arginyl-tRNA synthetase; diaminopimelic acid decarboxylase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12767		Dihydrodipicolinic acid synthetase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12770		aspartokinase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E12773		Dihydrodipicolinic acid reductase	Moriya, M. et al. "Amplification of gene using artificial transposon," Patent: JP 1997070291-A 03/18/97
E13655		Glucose-6-phosphate dehydrogenase	Hatakeyama, K. et al. "Glucose-6-phosphate dehydrogenase and DNA capable of coding the same," Patent: JP 1997224661-A 1 09/02/97
L01508	IlvA	Threonine dehydratase	Moeckel, B. et al. "Functional and structural analysis of the threonine dehydratase of Corynebacterium glutamicum," *J. Bacteriol.*, 174:8065-8072 (1992)
L07603	EC 4.2.1.15	3-deoxy-D-arabinoheptulosonate-7-phosphate synthase	Chen, C. et al. "The cloning and nucleotide sequence of Corynebacterium glutamicum 3-deoxy-D-arabinoheptulosonate-7-phosphate synthase gene," *FEMS Microbiol. Lett.*, 107:223-230 (1993)
L09232	IlvB; ilvN; ilvC	Acetohydroxy acid synthase large subunit; Acetohydroxy acid synthase small subunit; Acetohydroxy acid isomeroreductase	Keilhauer, C. et al. "Isoleucine synthesis in Corynebacterium glutamicum: molecular analysis of the ilvB-ilvN-ilvC operon," *J. Bacteriol.*, 175(17):5595-5603 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
L18874	PtsM	Phosphoenolpyruvate sugar phosphotransferase	Fouet, A et al. "Bacillus subtilis sucrose-specific enzyme II of the phosphotransferase system: expression in Escherichia coli and homology to enzymes II from enteric bacteria," *PNAS USA,* 84(24):8773-8777 (1987); Lee, J.K. et al. "Nucleotide sequence of the gene encoding the Corynebacterium glutamicum mannose enzyme II and analyses of the deduced protein sequence," *FEMS Microbiol. Lett.,* 119(1-2):137-145 (1994)
L27123	aceB	Malate synthase	Lee, H-S. et al. "Molecular characterization of aceB, a gene encoding malate synthase in Corynebacterium glutamicum," *J. Microbiol. Biotechnol.,* 4(4):256-263 (1994)
L27126		Pyruvate kinase	Jetten, M. S. et al. "Structural and functional analysis of pyruvate kinase from Corynebacterium glutamicum," *Appl. Environ. Microbiol.,* 60(7):2501-2507 (1994)
L28760	aceA	Isocitrate lyase	
L35906	dtxr	Diphtheria toxin repressor	Oguiza, J.A. et al. "Molecular cloning, DNA sequence analysis, and characterization of the Corynebacterium diphtheriae dtxR from Brevibacterium lactofermentum," *J. Bacteriol.,* 177(2):465-467 (1995)
M13774		Prephenate dehydratase	Follettie, M.T. et al. "Molecular cloning and nucleotide sequence of the Corynebacterium glutamicum pheA gene," *J. Bacteriol.,* 167:695-702 (1986)
M16175	5S rRNA		Park, Y-H. et al. "Phylogenetic analysis of the coryneform bacteria by 56 rRNA sequences," *J. Bacteriol.,* 169:1801-1806 (1987)
M16663	trpE	Anthranilate synthase, 5' end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M16664	trpA	Tryptophan synthase, 3'end	Sano, K. et al. "Structure and function of the trp operon control regions of Brevibacterium lactofermentum, a glutamic-acid-producing bacterium," *Gene,* 52:191-200 (1987)
M25819		Phosphoenolpyruvate carboxylase	O'Regan, M. et al. "Cloning and nucleotide sequence of the Phosphoenolpyruvate carboxylase-coding gene of Corynebacterium glutamicum ATCC13032," *Gene,* 77(2):237-251 (1989)
M85106		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.,* 138:1167-1175 (1992)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
M85107, M85108		23S rRNA gene insertion sequence	Roller, C. et al. "Gram-positive bacteria with a high DNA G+C content are characterized by a common insertion within their 23S rRNA genes," *J. Gen. Microbiol.*, 138:1167-1175 (1992)
M89931	aecD; brnQ; yhbw	Beta C-S lyase; branched-chain amino acid uptake carrier; hypothetical protein yhbw	Rossol, I. et al. "The Corynebacterium glutamicum aecD gene encodes a C-S lyase with alpha, beta-elimination activity that degrades aminoethylcysteine," *J. Bacteriol.*, 174(9):2968-2977 (1992); Tauch, A. et al. "Isoleucine uptake in Corynebacterium glutamicum ATCC 13032 is directed by the brnQ gene product," *Arch. Microbiol.*, 169(4):303-312 (1998)
S59299	trp	Leader gene (promoter)	Herry, D.M. et al. "Cloning of the trp gene cluster from a tryptophan-hyperproducing strain of Corynebacterium glutamicum: identification of a mutation in the trp leader sequence," *Appl. Environ. Microbiol.*, 59(3):791-799 (1993)
U11545	trpD	Anthranilate phosphoribosyltransferase	O'Gara, J.P. and Dunican, L.K. (1994) Complete nucleotide sequence of the Corynebacterium glutamicum ATCC 21850 tpD gene." Thesis, Microbiology Department, University College Galway, Ireland.
U13922	cglIM; cglIR; clgIIR	Putative type II 5-cytosoine methyltransferase; putative type II restriction endonuclease; putative type I or type III restriction endonuclease	Schafer, A. et al. "Cloning and characterization of a DNA region encoding a stress-sensitive restriction system from Corynebacterium glutamicum ATCC 13032 and analysis of its role in intergeneric conjugation with Escherichia coli," *J. Bacteriol.*, 176(23):7309-7319 (1994); Schafer, A. et al. "The Corynebacterium glutamicum cglIM gene encoding a 5-cytosine in an McrBC-deficient Escherichia coli strain," *Gene,* 203(2):95-101 (1997)
U14965	recA		
U31224	ppx		Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31225	proC	L-proline: NADP+ 5-oxidoreductase	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)
U31230	obg; proB; unkdh	?;gamma glutamyl kinase;similar to D-isomer specific 2-hydroxyacid dehydrogenases	Ankri, S. et al. "Mutations in the Corynebacterium glutamicumproline biosynthetic pathway: A natural bypass of the proA step," *J. Bacteriol.*, 178(15):4412-4419 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
U31281	bioB	Biotin synthase	Serebriiskii, I.G., "Two new members of the bio B superfamily: Cloning, sequencing and expression of bio B genes of Methylobacillus flagellatum and Corynebacterium glutamicum," *Gene,* 175:15-22 (1996)
U35023	thtR; accBC	Thiosulfate sulfurtransferase; acyl CoA carboxylase	Jager, W. et al. "A Corynebacterium glutamicum gene encoding a two-domain protein similar to biotin carboxylases and biotin-carboxyl-carrier proteins," *Arch. Microbiol.,* 166(2);76-82 (1996)
U43535	cmr	Multidrug resistance protein	Jager, W. et al. "A Corynebacterium glutamicum gene conferring multidrug resistance in the heterologous host Escherichia coli," *J. Bacteriol.,* 179(7):2449-2451 (1997)
U43536	clpB	Heat shock ATP-binding protein	
U53587	aphA-3	3'5''-aminoglycoside phosphotransferase	
U89648		Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	
X04960	trpA; trpB; trpC; trpD; trpE; trpG; trpL	Tryptophan operon	Matsui, K. et al. "Complete nucleotide and deduced amino acid sequences of the Brevibacterium lactofermentum tryptophan operon," *Nucleic Acids Res.,* 14(24):10113-10114 (1986)
X07563	lys A	DAP decarboxylase (meso-diaminopimelate decarboxylase, EC 4.1.1.20)	Yeh, P. et al. "Nucleic sequence of the lysA gene of Corynebacterium glutamicum and possible mechanisms for modulation of its expression," *Mol. Gen. Genet.,* 212(1):112-119 (1988)
X14234	EC 4.1.1.31	Phosphoenolpyruvate carboxylase	Eikmanns, B.J. et al. "The Phosphoenolpyruvate carboxylase gene of Corynebacterium glutamicum: Molecular cloning, nucleotide sequence, and expression," *Mol. Gen. Genet.,* 218(2):330-339 (1989); Lepiniec, L. et al. "Sorghum Phosphoenolpyruvate carboxylase gene family: structure, function and molecular evolution," *Plant. Mol. Biol.,* 21 (3):487-502 (1993)
X17313	fda	Fructose-bisphosphate aldolase	Von der Osten, C.H. et al. "Molecular cloning, nucleotide sequence and fine-structural analysis of the Corynebacterium glutamicum fda gene: structural comparison of C. glutamicum fructose-1, 6-biphosphate aldolase to class I and class II aldolases," *Mol. Microbiol.,*
X53993	dapA	L-2, 3-dihydrodipicolinate synthetase (EC 4.2.1.52)	Bonnassie, S. et al. "Nucleic sequence of the dapA gene from Corynebacterium glutamicum," *Nucleic Acids Res.,* 18(21):6421 (1990)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X54223		AttB-related site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X54740	argS; lysA	Arginyl-tRNA synthetase; Diaminopimelate decarboxylase	Marcel, T. et al. "Nucleotide sequence and organization of the upstream region of the Corynebacterium glutamicum lysA gene," *Mol. Microbiol.,* 4(11):1819-1830 (1990)
X55994	trpL; trpE	Putative leader peptide; anthranilate synthase component 1	Heery, D.M. et al. "Nucleotide sequence of the Corynebacterium glutamicum trpE gene," *Nucleic Acids Res.,* 18(23):7138 (1990)
X56037	thrC	Threonine synthase	Han, K.S. et al. "The molecular structure of the Corynebacterium glutamicum threonine synthase gene," *Mol. Microbiol.,* 4(10):1693-1702 (1990)
X56075	attB-related site	Attachment site	Cianciotto, N. et al. "DNA sequence homology between att B-related sites of Corynebacterium diphtheriae, Corynebacterium ulcerans, Corynebacterium glutamicum , and the attP site of lambdacorynephage," *FEMS. Microbiol, Lett.,* 66:299-302 (1990)
X57226	lysC-alpha; lysC-beta; asd	Aspartokinase-alpha subunit; Aspartokinase-beta subunit; aspartate beta semialdehyde dehydrogenase	Kalinowski, J. et al. "Genetic and biochemical analysis of the Aspartokinase from Corynebacterium glutamicum," *Mol. Microbiol.,* 5(5):1197-1204 (1991); Kalinowski, J. et al. "Aspartokinase genes lysC alpha and lysC beta overlap and are adjacent to the aspertate beta-semialdehyde dehydrogenase gene asd in Corynebacterium glutamicum," *Mol. Gen. Genet.,* 224(3):317-324 (1990)
X59403	gap;pgk; tpi	Glyceraldehyde-3-phosphate; phosphoglycerate kinase; triosephosphate isomerase	Eikmanns, B.J. "Identification, sequence analysis, and expression of a Corynebacterium glutamicum gene cluster encoding the three glycolytic enzymes glyceraldehyde-3-phosphate dehydrogenase, 3-phosphoglycerate kinase, and triosephosphate isomeras," *J. Bacteriol.,* 174(19):6076-6086 (1992)
X59404	gdh	Glutamate dehydrogenase	Bormann, E.R. et al. "Molecular analysis of the Corynebacterium glutamicum gdh gene encoding glutamate dehydrogenase," *Mol. Microbiol.,* 6(3):317-326 (1992)
X60312	lysI	L-lysine permease	Seep-Feldhaus, A.H. et al. "Molecular analysis of the Corynebacterium glutamicum lysI gene involved in lysine uptake," *Mol. Microbiol.,* 5(12):2995-3005 (1991)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X66078	cop1	Ps1 protein	Joliff, G. et al. "Cloning and nucleotide sequence of the csp1 gene encoding PS1, one of the two major secreted proteins of Corynebacterium glutamicum: The deduced N-terminal region of PS1 is similar to the Mycobacterium antigen 85 complex," *Mol. Microbiol.,* 6(16):2349-2362 (1992)
X66112	glt	Citrate synthase	Eikmanns, B.J. et al. "Cloning sequence, expression and transcriptional analysis of the Corynebacterium glutamicum gltA gene encoding citrate synthase," *Microbiol.,* 140:1817-1828 (1994)
X67737	dapB	Dihydrodipicolinate reductase	
X69103	csp2	Surface layer protein PS2	Peyret, J.L. et al. "Characterization of the cspB gene encoding PS2, an ordered surface-layer protein in Corynebacterium glutamicum," *Mol. Microbiol.,* 9(1):97-109 (1993)
X69104		IS3 related insertion element	Bonamy, C. et al. "Identification of IS1206, a Corynebacterium glutamicum IS3-related insertion sequence and phylogenetic analysis," *Mol. Microbiol.,* 14(3):571-581 (1994)
X70959	leuA	Isopropylmalate synthase	Patek, M. et al. "Leucine synthesis in Corynebacterium glutamicum: enzyme activities, structure of leuA, and effect of leuA inactivation on lysine synthesis," *Appl. Environ. Microbiol.,* 60(1):133-140 (1994)
X71489	icd	Isocitrate dehydrogenase (NADP+)	Eikmanns, B.J. et al. "Cloning sequence analysis, expression, and inactivation of the Corynebacterium glutamicum icd gene encoding isocitrate dehydrogenase and biochemical characterization of the enzyme," *J. Bacteriol.,* 177(3):774-782 (1995)
X72855	GDHA	Glutamate dehydrogenase (NADP+)	
X75083, X70584	mtrA	5-methyltryptophan resistance	Heery, D.M. et al. "A sequence from a tryptophan-hyperproducing strain of Corynebacterium glutamicum encoding resistance to 5-methyltryptophan," *Biochem. Biophys. Res. Commun.,* 201(3):1255-1262 (1994)
X75085	recA		Fitzpatrick, R. et al. "Construction and characterization of recA mutant strains of Corynebacterium glutamicum and Brevibacterium lactofermentum," *Appl. Microbiol. Biotechnol.,* 42(4):575-580 (1994)
X75504	aceA; thiX	Partial Isocitrate lyase; ?	Reinscheid, D.J. et al. "Characterization of the isocitrate lyase gene from Corynebacterium glutamicum and biochemical analysis of the enzyme," *J. Bacteriol.,* 176(12):3474-3483 (1994)
X76875		ATPase beta-subunit	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X77034	tuf	Elongation factor Tu	Ludwig, W. et al. "Phylogenetic relationships of bacteria based on comparative sequence analysis of elongation factor Tu and ATP-synthase beta-subunit genes," *Antonie Van Leeuwenhoek,* 64:285-305 (1993)
X77384	recA		Billman-Jacobe, H. "Nucleotide sequence of a recA gene from Corynebacterium glutamicum," *DNA Seq.,* 4(6):403-404 (1994)
X78491	aceB	Malate synthase	Reinscheid, D.J. et al. "Malate synthase from Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase: sequence analysis," *Microbiology,* 140:3099-3108 (1994)
X80629	16S rDNA	16S ribosomal RNA	Rainey, F.A. et al. "Phylogenetic analysis of the genera Rhodococcus and Norcardia and evidence for the evolutionary origin of the genus Norcardia from within the radiation of Rhodococcus species," *Microbiol.,* 141:523-528 (1995)
X81191	gluA; gluB; gluC; gluD	Glutamate uptake system	Kronemeyer, W. et al. "Structure of the gluABCD cluster encoding the glutamate uptake system of Corynebacterium glutamicum," *J. Bacteriol.*, 177(5):1152-1158 (1995)
X81379	dapE	Succinyldiaminopimelate desuccinylase	Wehrmann, A. et al. "Analysis of different DNA fragments of Corynebacterium glutamicum complementing dapE of Escherichia coli," *Microbiology*, 40:3349-56 (1994)
X82061	16S rDNA	16S ribosomal RNA	Ruimy, R. et al. "Phylogeny of the genus Corynebacterium deduced from analyses of small-subunit ribosomal DNA sequences," *Int. J. Syst. Bacteriol.,* 45(4):740-746 (1995)
X82928	asd; lysC	Aspartate-semialdehyde dehydrogenase; ?	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X82929	proA	Gamma-glutamyl phosphate reductase	Serebrijski, I. et al. "Multicopy suppression by asd gene and osmotic stress-dependent complementation by heterologous proA in proA mutants," *J. Bacteriol.,* 177(24):7255-7260 (1995)
X84257	16S rDNA	16S ribosomal RNA	Pascual, C. et al. "Phylogenetic analysis of the genus Corynebacterium based on 16S rRNA gene sequences," *Int. J. Syst. Bacteriol.,* 45(4):724-728 (1995)
X85965	aroP; dapE	Aromatic amino acid permease; ?	Wehrmann, A. et al. "Functional analysis of sequences adjacent to dapE of Corynebacterium glutamicumproline reveals the presence of aroP, which encodes the aromatic amino acid transporter," *J. Bacteriol.,* 177(20):5991-5993 (1995)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X86157	argB; argC; argD; argF; argJ	Acetylglutamate kinase; N-acetyl-gamma-glutamyl-phosphate reductase; acetylornithine aminotransferase; ornithine carbamoyltransferase; glutamate N-acetyltransferase	Sakanyan, V. et al. "Genes and enzymes of the acetyl cycle of arginine biosynthesis in Corynebacterium glutamicum: enzyme evolution in the early steps of the arginine pathway," *Microbiology,* 142:99-108 (1996)
X89084	pta; ackA	Phosphate acetyltransferase; acetate kinase	Reinscheid, D.J. et al. "Cloning, sequence analysis, expression and inactivation of the Corynebacterium glutamicum pta-ack operon encoding phosphotransacetylase and acetate kinase," *Microbiology,* 145:503-513 (1999)
X89850	attB	Attachment site	Le Marrec, C. et al. "Genetic characterization of site-specific integration functions of phi AAU2 infecting "Arthrobacter aureus C70," *J. Bacteriol.,* 178(7):1996-2004 (1996)
X90356		Promoter fragment F1	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90357		Promoter fragment F2	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90358		Promoter fragment F10	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90359		Promoter fragment F13	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90360		Promoter fragment F22	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90361		Promoter fragment F34	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)
X90362		Promoter fragment F37	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology,* 142:1297-1309 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X90363		Promoter fragment F45	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90364		Promoter fragment F64	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90365		Promoter fragment F75	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90366		Promoter fragment PF101	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90367		Promoter fragment PF104	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X90368		Promoter fragment PF109	Patek, M. et al. "Promoters from Corynebacterium glutamicum: cloning, molecular analysis and search for a consensus motif," *Microbiology*, 142:1297-1309 (1996)
X93513	amt	Ammonium transport system	Siewe, R.M. et al. "Functional and genetic characterization of the (methyl) ammonium uptake carrier of Corynebacterium glutamicum," *J. Biol. Chem.*, 271(10):5398-5403 (1996)
X93514	betP	Glycine betaine transport system	Peter, H. et al. "Isolation, characterization, and expression of the Corynebacterium glutamicum betP gene, encoding the transport system for the compatible solute glycine betaine," *J. Bacteriol.*, 178(17):5229-5234 (1996)
X95649	orf4		Patek, M. et al. "Identification and transcriptional analysis of the dapB-ORF2-dapA-ORF4 operon of Corynebacterium glutamicum, encoding two enzymes involved in L-lysine synthesis," *Biotechnol. Lett.*, 19:1113-1117 (1997)
X96471	lysE; lysG	Lysine exporter protein; Lysine export regulator protein	Vrljic, M. et al. "A new type of transporter with a new type of cellular function: L-lysine export from Corynebacterium glutamicum," *Mol. Microbiol.*, 22(5):815-826 (1996)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
X96580	panB; panC; xylB	3-methyl-2-oxobutanoate hydroxymethyltransferase; pantoate-beta-alanine ligase; xylulokinase	Sahm, H. et al. "D-pantothenate synthesis in Corynebacterium glutamicum and use of panBC and genes encoding L-valine synthesis for D-pantothenate overproduction," *Appl. Environ. Microbiol.*, 65(5):1973-1979 (1999)
X96962		Insertion sequence IS1207 and transposase	
X99289		Elongation factor P	Ramos, A. et al. "Cloning, sequencing and expression of the gene encoding elongation factor P in the amino-acid producer Brevibacterium lactofermentum (Corynebacterium glutamicum ATCC 13869)," *Gene*, 198:217-222 (1997)
Y00140	thrB	Homoserine kinase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine kinase (thrB) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(9):3922 (1987)
Y00151	ddh	Meso-diaminopimelate D-dehydrogenase (EC 1.4.1.16)	Ishino, S. et al. "Nucleotide sequence of the meso-diaminopimelate D-dehydrogenase gene from Corynebacterium glutamicum," *Nucleic Acids Res.*, 15(9):3917 (1987)
Y00476	thrA	Homoserine dehydrogenase	Mateos, L.M. et al. "Nucleotide sequence of the homoserine dehydrogenase (thrA) gene of the Brevibacterium lactofermentum," *Nucleic Acids Res.*, 15(24):10598 (1987)
Y00546	hom; thrB	Homoserine dehydrogenase; homoserine kinase	Peoples, O.P. et al. "Nucleotide sequence and fine structural analysis of the Corynebacterium glutamicum hom-thrB operon," *Mol. Microbiol.*, 2(1):63-72 (1988)
Y08964	murC; ftsQ/divD; ftsZ	UPD-N-acetylmuramate-alanine ligase; division initiation protein or cell division protein; cell division protein	Honrubia, M.P. et al. "Identification, characterization, and chromosomal organization of the ftsZ gene from Brevibacterium lactofermentum," *Mol. Gen. Genet.*, 259(1):97-104 (1998)
Y09163	putP	High affinity proline transport system	Peter, H. et al. "Isolation of the putP gene of Corynebacterium glutamicumproline and characterization of a low-affinity uptake system for compatible solutes," *Arch. Microbiol.*, 168(2):143-151 (1997)
Y09548	pyc	Pyruvate carboxylase	Peters-Wendisch, P.G. et al. "Pyruvate carboxylase from Corynebacterium glutamicum: characterization, expression and inactivation of the pyc gene," *Microbiology*, 144:915-927 (1998)
Y09578	leuB	3-isopropylmalate dehydrogenase	Patek, M. et al. "Analysis of the leuB gene from Corynebacterium glutamicum," *Appl. Microbiol. Biotechnol.*, 50(1):42-47 (1998)
Y12472		Attachment site bacteriophage Phi-16	Moreau, S. et al. "Site-specific integration of corynephage Phi-16: The construction of an integration vector," *Microbiol.*, 145:539-548 (1999)

GenBank™ Accession No.	Gene Name	Gene Function	Reference
Y12537	proP	Proline/ectoine uptake system protein	Peter, H. et al. "Corynebacterium glutamicum is equipped with four secondary carriers for compatible solutes: Identification, sequencing, and characterization of the proline/ectoine uptake system, ProP, and the ectoine/proline/glycine betaine carrier, EctP," *J. Bacteriol.,* 180(22):6005-6012 (1998)
Y13221	glnA	Glutamine synthetase I	Jakoby, M. et al. "Isolation of Corynebacterium glutamicum glnA gene encoding glutamine synthetase I," *FEMS Microbiol. Lett.,* 154(1):81-88 (1997)
Y16642	lpd	Dihydrolipoamide dehydrogenase	
Y18059		Attachment site Corynephage 304L	Moreau, S. et al. "Analysis of the integration functions of φ304L: An integrase module among corynephages," *Virology*, 255(1):150-159 (1999)
Z21501	argS; lysA	Arginyl-tRNA synthetase; diaminopimelate decarboxylase (partial)	Oguiza, J.A. et al. "A gene encoding arginyl-tRNA synthetase is located in the upstream region of the lysA gene in Brevibacterium lactofermentum: Regulation of argS-lysA cluster expression by arginine," *J. Bacteriol.*,175(22):7356-7362 (1993)
Z21502	dapA; dapB	Dihydrodipicolinate synthase; dihydrodipicolinate reductase	Pisabarro, A. et al. "A cluster of three genes (dapA, orf2, and dapB) of Brevibacterium lactofermentum encodes dihydrodipicolinate reductase, and a third polypeptide of unknown function," *J. Bacteriol.,* 175(9):2743-2749 (1993)
Z29563	thrC	Threonine synthase	Malumbres, M. et al. "Analysis and expression of the thrC gene of the encoded threonine synthase," *Appl. Environ. Microbiol.,* 60(7)2209-2219 (1994)
Z46753	16S rDNA	Gene for 16S ribosomal RNA	
Z49822	sigA	SigA sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.,* 178(2):550-553 (1996)
Z49823	galE; dtxR	Catalytic activity UDP-galactose 4-epimerase; diphtheria toxin regulatory protein	Oguiza, J.A. et al "The galE gene encoding the UDP-galactose 4-epimerase of Brevibacterium lactofermentum is coupled transcriptionally to the dmdR gene," *Gene,* 177:103-107 (1996)
Z49824	orf1; sigB	?; SigB sigma factor	Oguiza, J.A. et al "Multiple sigma factor genes in Brevibacterium lactofermentum: Characterization of sigA and sigB," *J. Bacteriol.,* 178(2):550-553 (1996)
Z66534		Transposase	Correia, A. et al. "Cloning and characterization of an IS-like element present in the genome of Brevibacterium lactofermentum ATCC 13869," *Gene,* 170(1):91-94 (1996)

[1] A sequence for this gene was published in the indicated reference. However, the sequence obtained by the inventors of the present application is significantly longer than the published version. It is believed that the published version relied on an incorrect start codon, and thus represents only a fragment of the actual coding region.

TABLE 3: Corynebacterium and Brevibacterium Strains Which May be Used in the Practice of the Invention

Genus	species	ATCC	FERM	NRRL	CECT	NCIMB	CBS	NCTC	DSMZ
Brevibacterium	ammoniagenes	21054							
Brevibacterium	ammoniagenes	19350							
Brevibacterium	ammoniagenes	19351							
Brevibacterium	ammoniagenes	19352							
Brevibacterium	ammoniagenes	19353							
Brevibacterium	ammoniagenes	19354							
Brevibacterium	ammoniagenes	19355							
Brevibacterium	ammoniagenes	19356							
Brevibacterium	ammoniagenes	21055							
Brevibacterium	ammoniagenes	21077							
Brevibacterium	ammoniagenes	21553							
Brevibacterium	ammoniagenes	21580							
Brevibacterium	ammoniagenes	39101							
Brevibacterium	butanicum	21196							
Brevibacterium	divaricatum	21792	P928						
Brevibacterium	flavum	21474							
Brevibacterium	flavum	21129							
Brevibacterium	flavum	21518							
Brevibacterium	flavum			B11474					
Brevibacterium	flavum			B11472					
Brevibacterium	flavum	21127							
Brevibacterium	flavum	21128							
Brevibacterium	flavum	21427							
Brevibacterium	flavum	21475							
Brevibacterium	flavum	21517							
Brevibacterium	flavum	21528							
Brevibacterium	flavum	21529							

Brevibacterium	flavum			B11477					
Brevibacterium	flavum			B11478					
Brevibacterium	flavum	21127							
Brevibacterium	flavum			B11474					
Brevibacterium	healii	15527							
Brevibacterium	ketoglutamicum	21004							
Brevibacterium	ketoglutamicum	21089							
Brevibacterium	ketosoreductum	21914							
Brevibacterium	lactofermentum				70				
Brevibacterium	lactofermentum				74				
Brevibacterium	lactofermentum				77				
Brevibacterium	lactofermentum	21798							
Brevibacterium	lactofermentum	21799							
Brevibacterium	lactofermentum	21800							
Brevibacterium	lactofermentum	21801							
Brevibacterium	lactofermentum			B11470					
Brevibacterium	lactofermentum			B11471					
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	21420							
Brevibacterium	lactofermentum	21086							
Brevibacterium	lactofermentum	31269							
Brevibacterium	linens	9174							
Brevibacterium	linens	19391							
Brevibacterium	linens	8377							
Brevibacterium	paraffinolyticum					11160			
Brevibacterium	spec.						717.73		
Brevibacterium	spec.						717.73		
Brevibacterium	spec.	14604							
Brevibacterium	spec.	21860							
Brevibacterium	spec.	21864							
Brevibacterium	spec.	21865							

Brevibacterium	spec.	21866							
Brevibacterium	spec.	19240							
Corynebacterium	acetoacidophilum	21476							
Corynebacterium	acetoacidophilum	13870							
Corynebacterium	acetoglutamicum			B11473					
Corynebacterium	acetoglutamicum			B11475					
Corynebacterium	acetoglutamicum	15806							
Corynebacterium	acetoglutamicum	21491							
Corynebacterium	acetoglutamicum	31270							
Corynebacterium	acetophilum			B3671					
Corynebacterium	ammoniagenes	6872						2399	
Corynebacterium	ammoniagenes	15511							
Corynebacterium	fujiokense	21496							
Corynebacterium	glutamicum	14067							
Corynebacterium	glutamicum	39137							
Corynebacterium	glutamicum	21254							
Corynebacterium	glutamicum	21255							
Corynebacterium	glutamicum	31830							
Corynebacterium	glutamicum	13032							
Corynebacterium	glutamicum	14305							
Corynebacterium	glutamicum	15455							
Corynebacterium	glutamicum	13058							
Corynebacterium	glutamicum	13059							
Corynebacterium	glutamicum	13060							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum	21513							
Corynebacterium	glutamicum	21526							
Corynebacterium	glutamicum	21543							
Corynebacterium	glutamicum	13287							
Corynebacterium	glutamicum	21851							
Corynebacterium	glutamicum	21253							

Corynebacterium	glutamicum	21514							
Corynebacterium	glutamicum	21516							
Corynebacterium	glutamicum	21299							
Corynebacterium	glutamicum	21300							
Corynebacterium	glutamicum	39684							
Corynebacterium	glutamicum	21488							
Corynebacterium	glutamicum	21649							
Corynebacterium	glutamicum	21650							
Corynebacterium	glutamicum	19223							
Corynebacterium	glutamicum	13869							
Corynebacterium	glutamicum	21157							
Corynebacterium	glutamicum	21158							
Corynebacterium	glutamicum	21159							
Corynebacterium	glutamicum	21355							
Corynebacterium	glutamicum	31808							
Corynebacterium	glutamicum	21674							
Corynebacterium	glutamicum	21562							
Corynebacterium	glutamicum	21563							
Corynebacterium	glutamicum	21564							
Corynebacterium	glutamicum	21565							
Corynebacterium	glutamicum	21566							
Corynebacterium	glutamicum	21567							
Corynebacterium	glutamicum	21568							
Corynebacterium	glutamicum	21569							
Corynebacterium	glutamicum	21570							
Corynebacterium	glutamicum	21571							
Corynebacterium	glutamicum	21572							
Corynebacterium	glutamicum	21573							
Corynebacterium	glutamicum	21579							
Corynebacterium	glutamicum	19049							
Corynebacterium	glutamicum	19050							

Corynebacterium	glutamicum	19051							
Corynebacterium	glutamicum	19052							
Corynebacterium	glutamicum	19053							
Corynebacterium	glutamicum	19054							
Corynebacterium	glutamicum	19055							
Corynebacterium	glutamicum	19056							
Corynebacterium	glutamicum	19057							
Corynebacterium	glutamicum	19058							
Corynebacterium	glutamicum	19059							
Corynebacterium	glutamicum	19060							
Corynebacterium	glutamicum	19185							
Corynebacterium	glutamicum	13286							
Corynebacterium	glutamicum	21515							
Corynebacterium	glutamicum	21527							
Corynebacterium	glutamicum	21544							
Corynebacterium	glutamicum	21492							
Corynebacterium	glutamicum			B8183					
Corynebacterium	glutamicum			B8182					
Corynebacterium	glutamicum			B12416					
Corynebacterium	glutamicum			B12417					
Corynebacterium	glutamicum			B12418					
Corynebacterium	glutamicum			B11476					
Corynebacterium	glutamicum	21608							
Corynebacterium	lilium		P973						
Corynebacterium	nitrilophilus	21419				11594			
Corynebacterium	spec.		P4445						
Corynebacterium	spec.		P4446						
Corynebacterium	spec.	31088							
Corynebacterium	spec.	31089							
Corynebacterium	spec.	31090							
Corynebacterium	spec.	31090							

Corynebacterium	spec.	31090							
Corynebacterium	spec.	15954							20145
Corynebacterium	spec.	21857							
Corynebacterium	spec.	21862							
Corynebacterium	spec.	21863							

ATCC: American Type Culture Collection, Rockville, MD, USA

FERM: Fermentation Research Institute, Chiba, Japan

NRRL: ARS Culture Collection, Northern Regional Research Laboratory, Peoria, IL, USA

CECT: Coleccion Espanola de Cultivos Tipo, Valencia, Spain

NCIMB: National Collection of Industrial and Marine Bacteria Ltd., Aberdeen, UK

CBS: Centraalbureau voor Schimmelcultures, Baarn, NL

NCTC: National Collection of Type Cultures, London, UK

DSMZ: Deutsche Sammlung von Mikroorganismen und Zellkulturen, Braunschweig, Germany

For reference see Sugawara, H. et al. (1993) World directory of collections of cultures of microorganisms: Bacteria, fungi and yeasts (4th edn), World federation for culture collections world data center on microorganisms, Saimata, Japen.

TABLE 4: ALIGNMENT RESULTS

ID #	length (NT)	Genbank Hit	Length	Accession	Name of Genbank Hit	Source of Genbank Hit	% homology (GAP)	Date of Deposit
rxa00009	1023	GB_IN1:CELZK563	29655	U40061	Caenorhabditis elegans cosmid ZK563.	Caenorhabditis elegans	33,694	9-Nov-95
		GB_IN1:CELZK563	29655	U40061	Caenorhabditis elegans cosmid ZK563.	Caenorhabditis elegans	36,040	9-Nov-95
rxa00010	810	GB_BA1:MTCY164	39150	Z95150	Mycobacterium tuberculosis H37Rv complete genome; segment 135/162.	Mycobacterium tuberculosis	38,442	19-Jun-98
		GB_BA1:MTFTSX	4068	X70031	M.tuberculosis ftsX and ftsE (partial) genes.	Mycobacterium tuberculosis	63,158	06-MAR-1997
		GB_BA1:SHGCPIR	107379	X86780	S.hygroscopicus gene cluster for polyketide immunosuppressant rapamycin.	Streptomyces hygroscopicus	38,875	16-Aug-96
rxa00024	1068	GB_HTG1:CEY113G7_3	110000	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,217	12-Jan-99
		GB_HTG1:CEY113G7_3	110000	AL031113	Caenorhabditis elegans chromosome V clone Y113G7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	36,217	12-Jan-99
		GB_PL2:ATF1C12	111945	AL022224	Arabidopsis thaliana DNA chromosome 4, BAC clone F1C12 (ESSA project).	Arabidopsis thaliana	35,824	20-Sep-99
rxa00048	1782	GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259I14, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	38,826	3-Aug-99
		GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259I14, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	38,826	3-Aug-99
		GB_HTG3:AC008905	129915	AC008905	Homo sapiens chromosome 5 clone CITB-H1_2259I14, *** SEQUENCING IN PROGRESS ***, 40 unordered pieces.	Homo sapiens	37,379	3-Aug-99
rxa00070	555	GB_BA2:BPEFUR	1003	L31851	Bordetella pertussis DNA repair protein (recN) gene, partial cds; iron regulatory protein (fur) gene, complete cds.	Bordetella pertussis	45,756	17-Apr-95
		GB_BA2:BPU11699	537	U11699	Bordetella pertussis ferric uptake regulator (fur) gene, complete cds.	Bordetella pertussis	47,119	14-Jan-95
		GB_BA1:BTFURRECN	1106	Z48227	B.pertussis fur gene for ferric uptake regulator and partial recN gene.	Bordetella pertussis	45,756	10-Feb-95
rxa00078	537	GB_PR3:HUMCOL2A1Z	31001	L10347	Human pro-alpha1 type II collagen (COL2A1) gene exons 1-54, complete cds.	Homo sapiens	39,010	3-Aug-95
		GB_HTG2:AC006721	135550	AC006721	Caenorhabditis elegans clone Y18H1, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	40,661	23-Feb-99
		GB_HTG2:AC006721	135550	AC006721	Caenorhabditis elegans clone Y18H1, *** SEQUENCING IN PROGRESS ***, 5 unordered pieces.	Caenorhabditis elegans	40,661	23-Feb-99
rxa00088	899	GB_RO:MMCGT6	3009	U48896	Mus musculus UDP-galactose:ceramide galactosyltransferase (Cgt) gene, exon 6 and complete cds.	Mus musculus	35,455	1-Nov-96
		GB_RO:MMCGT6	3009	U48896	Mus musculus UDP-galactose:ceramide galactosyltransferase (Cgt) gene, exon 6 and complete cds.	Mus musculus	34,439	1-Nov-96
rxa00100	723	GB_PL1:CAC41C10	38874	AL033501	C.albicans cosmid Ca41C10.	Candida albicans	36,222	10-Nov-98
		GB_PR4:AC007115	180821	AC007115	Homo sapiens chromosome 12 clone 917O5, complete sequence.	Homo sapiens	33,050	17-Aug-99
		GB_PR4:AC007115	180821	AC007115	Homo sapiens chromosome 12 clone 917O5, complete sequence.	Homo sapiens	34,993	17-Aug-99
rxa00135	1377	GB_BA1:MTCY373	35516	Z73419	Mycobacterium tuberculosis H37Rv complete genome; segment 57/162.	Mycobacterium tuberculosis	60,639	17-Jun-98
		GB_BA1:MLU15186	36241	U15186	Mycobacterium leprae cosmid L471.	Mycobacterium leprae	38,377	09-MAR-1995
		GB_BA1:MTMURAGEN	1257	X96711	M.tuberculosis murA gene.	Mycobacterium tuberculosis	61,575	22-MAR-1996
rxa00143	1605	GB_PAT:I92051	1107	I92051	Sequence 18 from patent US 5726299.	Unknown.	37,773	01-DEC-1998

TABLE 4: ALIGNMENT RESULTS

		GB_PAT:I78761	1107	I78761	Sequence 17 from patent US 5693781.	Unknown.	37,773	3-Apr-98
		GB_BA1:MTCY28	40163	Z95890	Mycobacterium tuberculosis H37Rv complete genome; segment 79/162.	Mycobacterium tuberculosis	36,984	18-Jun-98
rxa00177	1191	GB_GSS14:AQ543786	345	AQ543786	RPCI-11-365L6.TV RPCI-11 Homo sapiens genomic clone RPCI-11-365L6, genomic survey sequence.	Homo sapiens	38,551	19-MAY-1999
		GB_PL2:AF017646	3394	AF017646	Schizosaccharomyces pombe TFIIH subunit p47 (tfh47) gene, complete cds.	Schizosaccharomyces pombe	38,122	17-MAR-1999
		GB_PL1:SPCC1682	37404	AL031525	S.pombe chromosome III cosmid c1682.	Schizosaccharomyces pombe	33,983	14-DEC-1998
rxa00178	1008	GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	65,182	8-Sep-99
		GB_BA1:CGPUTP	3791	Y09163	C.glutamicum putP gene.	Corynebacterium glutamicum	38,806	8-Sep-97
		GB_STS:G05495	271	G05495	human STS WI-5918.	Homo sapiens	39,925	8-Jun-95
rxa00277	1684	GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	39,976	17-Jun-98
		GB_IN1:CELT03F1	38643	U88169	Caenorhabditis elegans cosmid T03F1.	Caenorhabditis elegans	35,127	7-Feb-97
		GB_IN2:CELK02A2	38261	U23171	Caenorhabditis elegans cosmid K02A2.	Caenorhabditis elegans	36,166	21-MAY-1999
rxa00372	1200	GB_IN2:AC005452	79333	AC005452	Drosophila melanogaster, chromosome 2R, region 43B2-43C2, P1 clone DS07185, complete sequence.	Drosophila melanogaster	37,006	26-Nov-98
		GB_IN2:AC005452	79333	AC005452	Drosophila melanogaster, chromosome 2R, region 43B2-43C2, P1 clone DS07185, complete sequence.	Drosophila melanogaster	34,907	26-Nov-98
		GB_IN1:CELW03F8	34766	AF039041	Caenorhabditis elegans cosmid W03F8.	Caenorhabditis elegans	40,712	1-Jan-98
rxa00389	1683	GB_IN1:AB010703	772	AB010703	Theileria sp. gene for major piroplasm surface protein, partial cds, isolate Kamphaeng Saen.	Theileria sp.	40,285	18-Apr-98
		GB_BA1:LLU08911	619	U08911	Lactobacillus leichmannii putative D-alanine:D-alanine ligase (ddl) gene, partial cds.	Lactobacillus leichmannii	40,194	16-Feb-96
		GB_IN1:TPMS1	822	Z48740	T.parva Tpms1 gene for merozoite surface glycoprotein.	Theileria parva	38,902	15-MAY-1995
rxa00467	792	GB_PR4:DJ293M10	202267	AF111167	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene.	Homo sapiens	37,995	7-Apr-99
		GB_PR4:DJ293M10	202267	AF111167	Homo sapiens jun dimerization protein gene, partial cds; cfos gene, complete cds; and unknown gene.	Homo sapiens	36,639	7-Apr-99
		GB_IN1:CEW01C9	21493	Z49969	Caenorhabditis elegans cosmid W01C9, complete sequence.	Caenorhabditis elegans	37,980	23-Nov-98
rxa00499	1404	GB_PR4:AC007206	42732	AC007206	Homo sapiens chromosome 19, cosmid R27370, complete sequence.	Homo sapiens	34,982	4-Apr-99
		GB_EST26:AI344735	462	AI344735	qp05a10.x1 NCI_CGAP_Kid5 Homo sapiens cDNA clone IMAGE:1917114 3' similar to gb:M15800 T-LYMPHOCYTE MATURATION-ASSOCIATED PROTEIN (HUMAN);, mRNA sequence.	Homo sapiens	42,675	2-Feb-99
		GB_PR4:AC006479	161837	AC006479	Homo sapiens clone DJ1051J04, complete sequence.	Homo sapiens	38,462	11-Nov-99
rxa00508	1206	GB_HTG2:AC007111	84245	AC007111	Homo sapiens chromosome 16 clone 1-8F, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,931	18-MAR-1999
		GB_HTG2:AC007111	84245	AC007111	Homo sapiens chromosome 16 clone 1-8F, *** SEQUENCING IN PROGRESS ***, 2 ordered pieces.	Homo sapiens	37,931	18-MAR-1999
		GB_VI:AF141890	1791	AF141890	Columbid herpesvirus 1 DNA-dependent DNA polymerase gene, partial cds.	columbid herpesvirus 1	39,401	7-Jul-99
rxa00569	1149	GB_PAT:I15213	3728	I15213	Sequence 1 from patent US 5460951.	Unknown.	41,244	2-Apr-96
		GB_PAT:E07353	3728	E07353	cDNA encoding bone-related carboxypeptidase-like protein,OSF-5.	Mus sp.	41,244	29-Sep-97

TABLE 4: ALIGNMENT RESULTS

		GB_HTG1:CEY70G10	152184	AL020987	Caenorhabditis elegans chromosome III clone Y70G10, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Caenorhabditis elegans	34,148	12-DEC-1997
rxa00612	1077	GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	34,551	12-Jun-98
		GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	34,551	12-Jun-98
		GB_HTG2:AC005020	177756	AC005020	Homo sapiens clone GS259H13, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Homo sapiens	37,628	12-Jun-98
rxa00615	705	GB_GSS15:AQ622921	517	AQ622921	HS_5351_A1_A08_T7A RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=927 Col=15 Row=A, genomic survey sequence.	Homo sapiens	38,254	16-Jun-99
		GB_GSS3:B36703	432	B36703	HS-1041-B1-B12-MR.abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 823 Col=23 Row=D, genomic survey sequence.	Homo sapiens	44,981	17-OCT-1997
		GB_EST25:AI245926	572	AI245926	qk33c08.x1 NCI_CGAP_Co8 Homo sapiens cDNA clone IMAGE:1870766 3' similar to SW:COPG_BOVIN P53620 COATOMER GAMMA SUBUNIT ;, mRNA sequence.	Homo sapiens	38,902	28-Jan-99
rxa00621	906	GB_EST1:D36491	360	D36491	CELK033GYF Yuji Kohara unpublished cDNA Caenorhabditis elegans cDNA clone yk33g11 5', mRNA sequence.	Caenorhabditis elegans	40,390	8-Aug-94
		GB_IN2:CELC16A3	34968	U41534	Caenorhabditis elegans cosmid C16A3.	Caenorhabditis elegans	35,477	18-MAY-1999
		GB_HTG3:AC009311	160198	AC009311	Homo sapiens clone NH0311L03, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,636	13-Aug-99
rxa00622	1539	GB_BA1:AB004795	3039	AB004795	Pseudomonas sp. gene for dipeptidyl aminopeptidase, complete cds.	Pseudomonas sp.	54,721	5-Feb-99
		GB_BA1:MBOPII	2392	D38405	Moraxella lacunata gene for protease II, complete cds.	Moraxella lacunata	50,167	8-Feb-99
		GB_IN2:AF078916	2960	AF078916	Trypanosoma brucei brucei oligopeptidase B (opb) gene, complete cds.	Trypanosoma brucei brucei	48,076	08-OCT-1999
rxa00639	978	GB_BA2:AF043741	1223	AF043741	Rhodococcus rhodochrous catechol 1,2-dioxygenase (catA) gene, complete cds.	Rhodococcus rhodochrous	66,940	27-Aug-98
		GB_BA1:D83237	1626	D83237	Rhodococcus erythropolis DNA for catechol 1,2-dioxgenase, complete cds.	Rhodococcus erythropolis	65,440	1-Sep-99
		GB_BA1:ROX99622	7224	X99622	Rhodococcus opacus catR, catA, catB, catC genes and five ORFs.	Rhodococcus opacus	63,617	24-Sep-97
rxa00641	1614	GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	59,863	20-MAY-1999
		GB_BA1:PWWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	59,588	26-Apr-93
		GB_BA1:PCCBDABC	3548	X79076	P.cepacia (2CBS) cbdA, cbdB and cbdC genes.	Burkholderia cepacia	55,410	3-Apr-97
rxa00642	615	GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	60,920	20-MAY-1999
		GB_BA1:PWWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	58,756	26-Apr-93
		GB_GSS11:AQ274007	637	AQ274007	nbxb0032l07f CUGI Rice BAC Library Oryza sativa genomic clone nbxb0032l07f, genomic survey sequence.	Oryza sativa	41,390	3-Nov-98

TABLE 4: ALIGNMENT RESULTS

rxa00643	1659	GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	53,871	20-MAY-1999
		GB_BA1:PWWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	52,603	26-Apr-93
		GB_EST22:AI020666	328	AI020666	ua97f07.r1 Soares mouse mammary gland NbMMG Mus musculus cDNA clone IMAGE:1365445 5' similar to SW:DUS7_RAT Q63340 DUAL SPECIFICITY PROTEIN PHOSPHATASE 7 ;, mRNA sequence.	Mus musculus	43,865	16-Jun-98
rxa00644	951	GB_BA1:PWWXYL	9037	M64747	Pseudomonas putida plasmid pWW0 meta operon, 5' genes.	Plasmid pWW0	55,626	26-Apr-93
		GB_BA2:AF134348	5000	AF134348	Pseudomonas putida plasmid pDK1 toluate 1,2 dioxygenase subunit (xylX), toluate 1,2 dioxygenase subunit (xylY), and toluate 1,2 dioxygenase subunit (xylZ) genes, complete cds; and 1,2-dihydroxycyclohexa-3,5-diene carboxylate dehydrogenase (xylL) gene, partial cds.	Pseudomonas putida	50,410	20-MAY-1999
		GB_EST22:AI038396	438	AI038396	ox21g10.x1 Soares_fetal_liver_spleen_1NFLS_S1 Homo sapiens cDNA clone IMAGE:1657026 3' similar to contains Alu repetitive element;contains element L1 repetitive element ;, mRNA sequence.	Homo sapiens	40,138	28-Aug-98
rxa00658	816	GB_EST16:C26090	414	C26090	C26090 Rice callus cDNA Oryza sativa cDNA clone C11617_1A, mRNA sequence.	Oryza sativa	40,636	6-Aug-97
		GB_EST16:C26090	414	C26090	C26090 Rice callus cDNA Oryza sativa cDNA clone C11617_1A, mRNA sequence.	Oryza sativa	38,406	6-Aug-97
rxa00663	1497	GB_BA1:MTV017	67200	AL021897	Mycobacterium tuberculosis H37Rv complete genome; segment 48/162.	Mycobacterium tuberculosis	57,976	24-Jun-99
		GB_BA1:MLCB1222	34714	AL049491	Mycobacterium leprae cosmid B1222.	Mycobacterium leprae	39,669	27-Aug-99
		GB_HTG2:AC007482	155357	AC007482	Homo sapiens clone hRPK.56_A_1, *** SEQUENCING IN PROGRESS ***, 6 unordered pieces.	Homo sapiens	36,154	05-MAY-1999
rxa00675	915	GB_BA1:SC3C8	33095	AL023861	Streptomyces coelicolor cosmid 3C8.	Streptomyces coelicolor	36,836	15-Jan-99
		GB_PR3:AC005736	215441	AC005736	Homo sapiens chromosome 16, BAC clone 462G18 (LANL), complete sequence.	Homo sapiens	42,027	01-OCT-1998
		GB_IN2:AC005719	188357	AC005719	Drosophila melanogaster, chromosome 2L, region 38A5-38B4, BAC clone BACR48M05, complete sequence.	Drosophila melanogaster	35,531	27-OCT-1999
rxa00762	999	GB_HTG2:HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25.3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,295	03-DEC-1999
		GB_HTG2:HSJ473J16	203460	AL109942	Homo sapiens chromosome 6 clone RP3-473J16 map q25.3-26, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,295	03-DEC-1999
		GB_PR2:HSU91327	129252	U91327	Human chromosome 12p15 BAC clone CIT987SK-99D8 complete sequence.	Homo sapiens	35,650	21-Aug-97
rxa00772	1629	GB_BA2:AF010184	1494	AF010184	Pseudomonas aeruginosa coenzyme A transferase PsecoA (psecoA) gene, complete cds.	Pseudomonas aeruginosa	56,472	18-Jul-98
		GB_PAT:I92043	713	I92043	Sequence 10 from patent US 5726299.	Unknown.	92,701	01-DEC-1998
		GB_PAT:I78754	713	I78754	Sequence 10 from patent US 5693781.	Unknown.	92,701	3-Apr-98
rxa00778	1248	GB_BA1:MTPST2GN	1347	Z48056	M.tuberculosis PstS-2 gene.	Mycobacterium tuberculosis	47,791	24-Apr-99
		GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	35,536	7-Feb-99
		GB_BA1:D90907	132419	D90907	Synechocystis sp. PCC6803 complete genome, 9/27, 1056467-1188885.	Synechocystis sp.	38,006	7-Feb-99

TABLE 4: ALIGNMENT RESULTS

rxa00787	2025	GB_PL1:SCX11RA	36849	X91258	S.cerevisiae DNA from chromosome XII right arm including ACE2, CKI1, PDC5, SLS1, PUT1 and tRNA-Asp genes.	Saccharomyces cerevisiae	36,122	13-OCT-1995
		GB_PL2:YSCL9606	29154	U53881	Saccharomyces cerevisiae chromosome XII cosmid 9606.	Saccharomyces cerevisiae	36,122	25-OCT-1997
		GB_PL1:SCX11RA	36849	X91258	S.cerevisiae DNA from chromosome XII right arm including ACE2, CKI1, PDC5, SLS1, PUT1 and tRNA-Asp genes.	Saccharomyces cerevisiae	37,198	13-OCT-1995
rxa00792	1320	GB_PR4:AC004841	132072	AC004841	Homo sapiens PAC clone DJ0607J23 from 7q21.2-q31.1, complete sequence.	Homo sapiens	37,452	18-MAR-1999
		GB_HTG2.AC006706	180664	AC006706	Caenorhabditis elegans clone Y110A2, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Caenorhabditis elegans	34,824	23-Feb-99
		GB_HTG2:AC006706	180664	AC006706	Caenorhabditis elegans clone Y110A2, *** SEQUENCING IN PROGRESS ***, 4 unordered pieces.	Caenorhabditis elegans	34,824	23-Feb-99
rxa00857	1313	GB_BA1:MTV002	56414	AL008967	Mycobacterium tuberculosis H37Rv complete genome; segment 122/162.	Mycobacterium tuberculosis	38,080	17-Jun-98
		GB_BA1:MSGY154	40221	AD000002	Mycobacterium tuberculosis sequence from clone y154.	Mycobacterium tuberculosis	68,345	03-DEC-1996
		GB_BA1:MLCB33	42224	Z94723	Mycobacterium leprae cosmid B33.	Mycobacterium leprae	38,824	24-Jun-97
rxa00877	1788	GB_PAT.I92050	567	I92050	Sequence 17 from patent US 5726299.	Unknown.	62,787	01-DEC-1998
		GB_PAT:I78760	567	I78760	Sequence 16 from patent US 5693781.	Unknown.	62,787	3-Apr-98
		GB_BA2:AE000426	10240	AE000426	Escherichia coli K-12 MG1655 section 316 of 400 of the complete genome.	Escherichia coli	36,456	12-Nov-98
rxa00888	1140	GB_BA1:MTCY27	27548	Z95208	Mycobacterium tuberculosis H37Rv complete genome; segment 104/162.	Mycobacterium tuberculosis	40,165	17-Jun-98
		GB_BA1.U00016	42931	U00016	Mycobacterium leprae cosmid B1937.	Mycobacterium leprae	58,444	01-MAR-1994
		GB_BA1:ECU82598	136742	U82598	Escherichia coli genomic sequence of minutes 9 to 12	Escherichia coli	37,876	15-Jan-97
rxa00892	1017	GB_BA2:AE000817	13157	AE000817	Methanobacterium thermoautotrophicum from bases 251486 to 264642 (section 23 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	36,710	15-Nov-97
		GB_EST29:AI620549	239	AI620549	tu95b07.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:2258773 3' similar to gb:X60708_rna1 DIPEPTIDYL PEPTIDASE IV (HUMAN),, mRNA sequence.	Homo sapiens	38,075	21-Apr-99
		GB_BA2:AE000817	13157	AE000817	Methanobacterium thermoautotrophicum from bases 251486 to 264642 (section 23 of 148) of the complete genome.	Methanobacterium thermoautotrophicum	35,650	15-Nov-97
rxa00897	1128	GB_PR3:HS246D7	28011	AL031843	Human DNA sequence from clone 246D7 on chromosome 22q13.1-13.33. Contains ESTs, a GSS and an STS, complete sequence	Homo sapiens	38,724	23-Nov-99
		GB_PR3:HSDJ185D5	24387	AL118498	Human DNA sequence from clone 185D5 on chromosome 22, complete sequence.	Homo sapiens	37,021	23-Nov-99
		GB_PR3:HS246D7	28011	AL031843	Human DNA sequence from clone 246D7 on chromosome 22q13.1-13.33. Contains ESTs, a GSS and an STS, complete sequence.	Homo sapiens	36,054	23-Nov-99
rxa00944	1095	GB_BA1:ECU68759	1531	U68759	Enterobacter cloacae pentaerythritol tetranitrate reductase (onr) gene, complete cds.	Enterobacter cloacae	43,041	14-DEC-1996
		GB_PAT:A59288	1531	A59288	Sequence 1 from Patent WO9703201.	unidentified	43,041	06-MAR-1998
		GB_EST23:AI099394	601	AI099394	ue32a09.y1 Sugano mouse liver mlia Mus musculus cDNA clone IMAGE.1482040 5' similar to gb:U21301 Mus musculus c-mer tyrosine kinase receptor mRNA, complete (MOUSE),, mRNA sequence.	Mus musculus	37,225	20-Aug-98
rxa00964	1248	GB_HTG6:AC009794	152794	AC009794	Homo sapiens chromosome 4 clone RP11-343C10 map 4, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	34,762	03-DEC-1999
		GB_HTG6:AC009794	152794	AC009794	Homo sapiens chromosome 4 clone RP11-343C10 map 4, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	35,708	03-DEC-1999

TABLE 4: ALIGNMENT RESULTS

rxa00982	1629	GB_BA1:BLARGS	2501	Z21501	B lactofermentum argS and lysA genes for arginyl-tRNA synthetase and diaminopimelate decarboxylase (partial).	Corynebacterium glutamicum	39,003	28-DEC-1993
		GB_BA1:CGXLYSA	2344	X54740	Corynebacterium glutamicum argS-lysA operon gene for the upstream region of the arginyl-tRNA synthetase and diaminopimelate decarboxylase (EC 4.1.1.20).	Corynebacterium glutamicum	41,435	30-Jun-93
		GB_PAT:E14508	3579	E14508	DNA encoding Brevibacterium diaminopimelic acid decarboxylase and arginyl-tRNA synthase.	Corynebacterium glutamicum	40,566	28-Jul-99
rxa01014	2724	GB_BA1.MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162	Mycobacterium tuberculosis	56,167	17-Jun-98
		GB_BA1:STMAMPEPN	2849	L23172	Streptomyces lividans aminopeptidase N gene, complete cds.	Streptomyces lividans	57,067	18-MAY-1994
		GB_BA1:SC7H2	42655	AL109732	Streptomyces coelicolor cosmid 7H2	Streptomyces coelicolor A3(2)	37,551	2-Aug-99
rxa01022	1203	GB_PAT:A68384	1080	A68384	Sequence 1 from Patent WO9748809.	Mycobacterium avium	56,913	06-MAY-1999
		GB_BA2:AF077728	1346	AF077728	Mycobacterium smegmatis D-alanine:D-alanine ligase gene, complete cds.	Mycobacterium smegmatis	57,203	1-Jan-99
rxa01055		GB_BA1:MSGB1723CS	38477	L78825	Mycobacterium leprae cosmid B1723 DNA sequence.	Mycobacterium leprae	54,599	15-Jun-96
rxa01056	1023	GB_BA2:AE001715	11086	AE001715	Thermotoga maritima section 27 of 136 of the complete genome.	Thermotoga maritima	39,034	2-Jun-99
		GB_EST38:AW046857	161	AW046857	UI-M-BH1-akl-a-04-0-UI s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-akl-a-04-0-UI 3', mRNA sequence	Mus musculus	45,963	18-Sep-99
		GB_EST38:AW049435	244	AW049435	UI-M-BH1-ams-b-01-0-UI.s1 NIH_BMAP_M_S2 Mus musculus cDNA clone UI-M-BH1-ams-b-01-0-UI 3', mRNA sequence	Mus musculus	40,984	18-Sep-99
rxa01057	1626	GB_PL1:LPAJ5046	656	AJ225046	Lycopersicon peruvianum mRNA for Hsp20 1 protein	Lycopersicon peruvianum	37,117	22-Jul-98
		GB_PL2:SPAC806	22870	AL117212	S pombe chromosome I cosmid c806.	Schizosaccharomyces pombe	38,211	24-Nov-99
		GB_PL2:SPAC806	22870	AL117212	S pombe chromosome I cosmid c806	Schizosaccharomyces pombe	36,934	24-Nov-99
rxa01082	783	GB_BA2:AF112535	4363	AF112535	Corynebacterium glutamicum putative glutaredoxin NrdH (nrdH), NrdI (nrdI), and ribonucleotide reductase alpha-chain (nrdE) genes, complete cds.	Corynebacterium glutamicum	99,794	5-Aug-99
		GB_PL2:TAE237897	8020	AJ237897	Triticum aestivum sbe1 gene, exons 1-14.	Triticum aestivum	37,132	1-Nov-99
		GB_PL2:AF076680	10499	AF076680	Aegilops tauschii starch branching enzyme-I (SBE-I) gene, complete cds.	Aegilops tauschii	38,651	14-MAY-1999
rxa01113	260	GB_VI:ASU02468	11424	U02468	African swine fever virus BA71V (A489R, A280R, A505R, A498R, A528R, A506R, and A542R) genes, complete cds.	African swine fever virus	31,923	28-Apr-94
		GB_VI:ASU18466	170101	U18466	African swine fever virus, complete genome.	African swine fever virus	31,923	22-Apr-95
		GB_GSS5:AQ752779	1647	AQ752779	HS_5569_B1_D02_SP6 RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1145 Col=3 Row=H, genomic survey sequence.	Homo sapiens	37,154	19-Jul-99
rxa01115	876	GB_BA1:AB014757	6057	AB014757	Pseudomonas sp. 61-3 genes for PhbR, acetoacetyl-CoA reductase, beta-ketothiolase and PHB synthase, complete cds	Pseudomonas sp. 61-3	40,850	26-DEC-1998
		GB_IN2:DMU60591	5630	U60591	Drosophila melanogaster kuzbanian (kuz) mRNA, complete cds.	Drosophila melanogaster	37,326	10-Sep-96
		GB_RO:MMMMP10	1744	Y13185	Mus musculus mRNA for stromelysin-2.	Mus musculus	35,877	14-Jan-98
rxa01116	735	GB_BA1.SC4C6	30941	AL079355	Streptomyces coelicolor cosmid 4C6.	Streptomyces coelicolor	40,616	21-Jun-99
		GB_BA2:AF109386	6551	AF109386	Streptomyces sp. 2065 protocatechuaic acid catabolic gene cluster, complete sequence.	Streptomyces sp. 2065	64,099	06-DEC-1999
		GB_BA1:MTCY07A7	23967	Z95556	Mycobacterium tuberculosis H37Rv complete genome; segment 109/162.	Mycobacterium tuberculosis	41,716	17-Jun-98

TABLE 4: ALIGNMENT RESULTS

rxa01117	864	GB_BA2:AF109386	6551	AF109386	Streptomyces sp. 2065 protocatechuaic acid catabolic gene cluster, complete sequence.	Streptomyces sp. 2065	62,116	06-DEC-1999
		GB_BA2:AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis,cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	36,712	12-MAR-1998
		GB_BA1:XCLPSIJ	2578	Y11313	X.campestris lpsI, lpsJ, xanA genes and orfX.	Xanthomonas campestris	39,833	20-Jan-98
rxa01120	1401	GB_BA1:MTV008	63033	AL021246	Mycobacterium tuberculosis H37Rv complete genome; segment 108/162.	Mycobacterium tuberculosis	36,715	17-Jun-98
		GB_BA1:CAJ10321	6710	AJ010321	Caulobacter crescentus partial tig gene and clpP, cicA, clpX, lon genes.	Caulobacter crescentus	63,311	01-OCT-1998
		GB_BA2:AF150957	4440	AF150957	Azospirillum brasilense trigger factor (tig), heat-shock protein ClpP (clpP), and heat-shock protein ClpX (clpX) genes, complete cds; and Lon protease (lon) gene, partial cds.	Azospirillum brasilense	60,613	7-Jun-99
rxa01126	583	GB_HTG3:AC009199	66498	AC009199	Drosophila melanogaster chromosome 2 clone BACR10J23 (D1024) RPCI-98 10.J.23 map 37B-37B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	35,294	20-Sep-99
		GB_HTG3:AC009199	66498	AC009199	Drosophila melanogaster chromosome 2 clone BACR10J23 (D1024) RPCI-98 10.J.23 map 37B-37B strain y; cn bw sp, *** SEQUENCING IN PROGRESS ***, 79 unordered pieces.	Drosophila melanogaster	35,294	20-Sep-99
		GB_PL1:AB016880	81284	AB016880	Arabidopsis thaliana genomic DNA, chromosome 5, P1 clone: MTG10, complete sequence.	Arabidopsis thaliana	34,477	20-Nov-99
rxa01181	980	GB_BA1:MLCB22	40281	Z98741	Mycobacterium leprae cosmid B22.	Mycobacterium leprae	61,570	22-Aug-97
		GB_BA1:MTCY190	34150	Z70283	Mycobacterium tuberculosis H37Rv complete genome; segment 98/162.	Mycobacterium tuberculosis	60,434	17-Jun-98
		GB_BA1:SC5F7	40024	AL096872	Streptomyces coelicolor cosmid 5F7.	Streptomyces coelicolor A3(2)	57,011	22-Jul-99
rxa01236	1068	GB_EST3:H01832	381	H01832	yj28c11.s1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:150068 3', mRNA sequence.	Homo sapiens	41,406	19-Jun-95
		GB_PR4:AC004850	105891	AC004850	Homo sapiens PAC clone DJ0665C04 from 7p14-p13, complete sequence.	Homo sapiens	37,428	26-Feb-99
		GB_GSS11:AQ304150	528	AQ304150	HS_3208_A1_D12_T7 CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3208 Col=23 Row=G, genomic survey sequence.	Homo sapiens	37,421	16-DEC-1998
rxa01254	1392	GB_BA1:MTV025	121125	AL022121	Mycobacterium tuberculosis H37Rv complete genome; segment 155/162.	Mycobacterium tuberculosis	58,315	24-Jun-99
		GB_BA1:MSGB577COS	37770	L01263	M. leprae genomic dna sequence, cosmid b577.	Mycobacterium leprae	56,323	14-Jun-96
		GB_BA1:MLCB2407	35615	AL023596	Mycobacterium leprae cosmid B2407.	Mycobacterium leprae	37,645	27-Aug-99
rxa01270	1278	GB_BA1:BSPX91182	345	X91182	Bacterial sp. partial 16S rRNA gene (clone group G10).	unidentified bacterium	41,228	15-Jul-96
		GB_BA1:BSPJN12D	347	Z69277	Bacterial sp. partial 16S rRNA gene (clone group JN12d).	Bacteria	38,905	24-Jun-98
		GB_EST7:W93397	545	W93397	zd95b03.s1 Soares_fetal_heart_NbHH19W Homo sapiens cDNA clone IMAGE:357197 3', mRNA sequence.	Homo sapiens	40,516	25-Nov-96
rxa01277	2127	GB_PL2:AF111709	52684	AF111709	Oryza sativa subsp. indica Retrosat 1 retrotransposon and Ty3-Gypsy type Retrosat 2 retrotransposon, complete sequences; and unknown genes.	Oryza sativa subsp. indica	37,410	26-Apr-99
		GB_IN1:CELZC250	34372	AF003383	Caenorhabditis elegans cosmid ZC250.	Caenorhabditis elegans	35,506	14-MAY-1997

TABLE 4: ALIGNMENT RESULTS

		GB_EST1:Z14808	331	Z14808	CEL5E4 Chris Martin sorted cDNA library Caenorhabditis elegans cDNA clone cm5e4 5', mRNA sequence.	Caenorhabditis elegans	36,890	19-Jun-97
rxa01288	498	GB_VI:S62819	3348	S62819	F2L=putative RNA polymerase-associated transcription factor. . F4R=type I topoisomerase homolog [orf virus OV, NZ2, host=sheep, Genomic, 3 genes, 3348 nt].	orf virus	40,471	25-Aug-93
		GB_PR4 HUMCCLEC1	17079	AF077344	Homo sapiens cartilage-derived C-type lectin (CLECSF1) gene, exons 1 and 2	Homo sapiens	34,631	15-OCT-1999
		GB_PR4:HUMCCLEC1	17079	AF077344	Homo sapiens cartilage-derived C-type lectin (CLECSF1) gene, exons 1 and 2	Homo sapiens	39,300	15-OCT-1999
rxa01354	1059	GB_PR1:D87675	301692	D87675	Homo sapiens DNA for amyloid precursor protein, complete cds	Homo sapiens	37,984	22-Sep-97
		GB_PR1:D87675	301692	D87675	Homo sapiens DNA for amyloid precursor protein, complete cds.	Homo sapiens	35,140	22-Sep-97
		GB_RO:MMNUCLEO	11478	X07699	Mouse nucleolin gene.	Mus musculus	37,146	27-Aug-98
rxa01376	984	GB_BA1:MTCY71	42729	Z92771	Mycobacterium tuberculosis H37Rv complete genome; segment 141/162.	Mycobacterium tuberculosis	39,496	10-Feb-99
		GB_BA1:ACCPSXM	2748	X81320	A calcoaceticus epsX and epsM genes.	Acinetobacter calcoaceticus	40,353	19-OCT-1994
		GB_BA2:ECU05248	1781	U05248	Escherichia coli polysialic acid gene cluster region 2 (neuD and neuB) genes, complete cds	Escherichia coli	34,995	1-Feb-95
rxa01385	2004	GB_BA1:FVBPENTA	2519	M98557	Flavobacterium sp. pentachlorophenol 4-monooxygenase gene, complete mRNA.	Flavobacterium sp.	40,855	26-Apr-93
		GB_PAT:I19994	2516	I19994	Sequence 2 from patent US 5512478	Unknown	40,855	07-OCT-1996
		GB_BA2:AF059680	2410	AF059680	Sphingomonas sp UG30 pentachlorophenol 4-monooxygenase (pcpB) gene, complete cds; and pentachlorophenol 4-monooxygenase reductase (pcpD) gene, partial cds.	Sphingomonas sp. UG30	42,993	27-Apr-99
rxa01426	750	GB_GSS3.B35912	313	B35912	HS-1031-A2-D02-MR abi CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 811 Col=4 Row=G, genomic survey sequence.	Homo sapiens	38,019	17-OCT-1997
		GB_GSS1:FR0027767	497	AL020589	F.rubripes GSS sequence, clone 197B17aA3, genomic survey sequence.	Fugu rubripes	35,814	10-DEC-1997
		GB_GSS5:AQ774340	449	AQ774340	HS_3137_A2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3137 Col=22 Row=I, genomic survey sequence.	Homo sapiens	40,535	29-Jul-99
rxa01427	1044	GB_BA2:AF036766	3487	AF036766	Lactobacillus reuteri plasmid pTE15 replication-associated protein A (repA) and replication-associated protein B (repB) genes, complete cds.	Lactobacillus reuteri	39,101	19-Feb-98
		GB_PR4:AC007032	126803	AC007032	Homo sapiens clone NH0022N19, complete sequence.	Homo sapiens	34,180	17-Jul-99
		GB_PR4:AC007032	126803	AC007032	Homo sapiens clone NH0022N19, complete sequence.	Homo sapiens	36,858	17-Jul-99
rxa01428	1260	GB_BA1:SCH24	41625	AL049826	Streptomyces coelicolor cosmid H24.	Streptomyces coelicolor	51,278	11-MAY-1999
		GB_BA2:AF031590	6676	AF031590	Streptomyces coelicolor thioredoxin (trxA) gene, partial cds; SpoOJ-like, Soj-like, GidB-like, Jag-like, inner membrane protein, and 9-10kDa protein-like genes, complete cds; RNase P protein (rnpA) gene, partial cds; and unknown gene.	Streptomyces coelicolor	39,389	20-Feb-98
		GB_BA1.SCTRXARNP	6676	Y16311	Streptomyces coelicolor trxA & rnpA genes & ORFs 205, 344, 255, 239, 170, 341 & 124.	Streptomyces coelicolor	39,389	18-DEC-1998
rxa01430	1311	GB_EST30:AI643302	254	AI643302	vl39b08 y1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:974583 5' similar to SW:6PGD_HUMAN P52209 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;, mRNA sequence.	Mus musculus	38,627	29-Apr-99

TABLE 4: ALIGNMENT RESULTS

		GB_EST34:AI788121	490	AI788121	ul17f02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone IMAGE:2087835 5' similar to SW:6PGD_HUMAN P52209 6-PHOSPHOGLUCONATE DEHYDROGENASE, DECARBOXYLATING ;, mRNA sequence.	Mus musculus	40,583	2-Jul-99
		GB_EST16:AA560354	253	AA560354	vl39b08.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:974583 5' similar to TR:G984325 G984325 PHOSPHOGLUCONATE DEHYDROGENASE. ;, mRNA sequence.	Mus musculus	42,544	18-Aug-97
rxa01435	893	GB_EST22:AI069195	892	AI069195	mgae0005dF02f Magnaporthe grisea Appressorium Stage cDNA Library Pyricularia grisea cDNA clone mgae0005dF02f 5', mRNA sequence.	Pyricularia grisea	40,964	09-DEC-1999
		GB_EST26:AI392390	574	AI392390	NCSC1B12T7 Subtracted Conidial Neurospora crassa cDNA clone SC1B12 3' similar to adenylate kinase 2 (ATP-AMP transphosphorylase), mRNA sequence.	Neurospora crassa	40,127	3-Feb-99
		GB_HTG2:AC004845	140230	AC004845	Homo sapiens clone DJ0635O05, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Homo sapiens	36,437	12-Jun-98
rxa01437	1506	GB_BA1:CGPTAACKA	3657	X89084	C.glutamicum pta gene and ackA gene.	Corynebacterium glutamicum	100,000	23-MAR-1999
		GB_BA1:MTCY22G10	35420	Z84724	Mycobacterium tuberculosis H37Rv complete genome; segment 21/162.	Mycobacterium tuberculosis	54,867	17-Jun-98
		GB_HTG3:AC010254	114363	AC010254	Homo sapiens chromosome 5 clone CIT-HSPC_434O11, *** SEQUENCING IN PROGRESS ***, 58 unordered pieces.	Homo sapiens	35,547	15-Sep-99
rxa01461	735	GB_BA2:AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis,cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	57,939	12-MAR-1998
		GB_PR2:HSA535K18	182408	AL078638	Human DNA sequence from clone RP11-535K18 on chromosome Xq26.2-27.1, complete sequence.	Homo sapiens	37,123	22-Nov-99
		GB_EST33:AI764654	420	AI764654	UI-R-Y0-abw-e-02-0-UI.s2 UI-R-Y0 Rattus norvegicus cDNA clone UI-R-Y0-abw-e-02-0-UI 3', mRNA sequence.	Rattus norvegicus	35,885	25-Jun-99
rxa01462	813	GB_BA2:AF003947	5475	AF003947	Rhodococcus opacus succinyl CoA:3-oxoadipate CoA transferase subunit homolog (pcaI') gene, partial cds, protocatechuate dioxygenase beta subunit (pcaH), protocatechuate dioxygenase alpha subunit (pcaG), 3-carboxy-cis,cis-muconate cycloisomerase homolog (pcaB), 3-oxoadipate enol-lactone hydrolase/4-carboxymuconolactone decarboxylase (pcaL) and PcaR (pcaR) genes, complete cds, and 3-oxoadipyl CoA thiolase homolog (pcaF') gene, partial cds.	Rhodococcus opacus	66,667	12-MAR-1998
		GB_BA1:SC4C6	30941	AL079355	Streptomyces coelicolor cosmid 4C6.	Streptomyces coelicolor	40,822	21-Jun-99
		GB_BA2:AF109386	6551	AF109386	Streptomyces sp. 2065 protocatechuaic acid catabolic gene cluster, complete sequence.	Streptomyces sp. 2065	56,049	06-DEC-1999
rxa01464	414	GB_BA1:AB009343	6342	AB009343	Frateuria sp. ANA-18 ORFR2, catBI, catCI, catAI and catD genes, complete cds.	Frateuria sp. ANA-18	50,966	26-MAY-1999
		GB_GSS10:AQ241375	284	AQ241375	CITBI-E1-2505O7.TF.1 CITBI-E1 Homo sapiens genomic clone 2505O7, genomic survey sequence.	Homo sapiens	39,085	30-Sep-98

TABLE 4: ALIGNMENT RESULTS

		GB_HTG3.AC010363	174962	AC010363	Homo sapiens chromosome 5 clone CITB-H1_2039P12, *** SEQUENCING IN PROGRESS ***, 43 unordered pieces.	Homo sapiens	35,784	15-Sep-99
rxa01465	1284	GB_BA1:ROX99622	7224	X99622	Rhodococcus opacus catR, catA, catB, catC genes and five ORFs	Rhodococcus opacus	58,814	24-Sep-97
		GB_BA1:D83237	1626	D83237	Rhodococcus erythropolis DNA for catechol 1,2-dioxgenase, complete cds	Rhodococcus erythropolis	53,904	1-Sep-99
		GB_EST9.AA119571	445	AA119571	mp68d04.r1 Soares 2NbMT Mus musculus cDNA clone IMAGE:574375 5' similar to TR:G559375 G559375 RAS GTPASE-ACTIVATING PROTEIN. ,, mRNA sequence	Mus musculus	39,551	17-Feb-97
rxa01466	1083	GB_EST37:AI934978	425	AI934978	wd17b06.x1 Soares_NFL_T_GBC_S1 Homo sapiens cDNA clone IMAGE:2328371 3', mRNA sequence.	Homo sapiens	43,609	2-Sep-99
		GB_EST15.AA465729	289	AA465729	aa32g06.s1 NCI_CGAP_GCB1 Homo sapiens cDNA clone IMAGE.815002 3', mRNA sequence.	Homo sapiens	41,115	13-Aug-97
		GB_EST24.AI219091	633	AI219091	qg12a05.x1 Soares_placenta_8to9weeks_2NbHP8to9W Homo sapiens cDNA clone IMAGE.1759280 3' similar to TR.Q99988 Q99988 TGF-BETA SUPERFAMILY PROTEIN [1] ,, mRNA sequence.	Homo sapiens	36,066	29-Nov-98
rxa01477	1671	GB_BA2 CGU89648	1105	U89648	Corynebacterium glutamicum unidentified sequence involved in histidine biosynthesis, partial sequence	Corynebacterium glutamicum	49,726	30-MAR-1999
		GB_EST21:AA919685	782	AA919685	vx11g06 r1 Soares 2NbMT Mus musculus cDNA clone IMAGE 1264186 5' similar to gb:M73696 Murine Glvr-1 mRNA, complete cds (MOUSE),, mRNA sequence	Mus musculus	37,762	20-Apr-98
		GB_HTG2.HS1005F21	101795	AL078633	Homo sapiens chromosome 20 clone RP5-1005F21, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	38,371	30-Nov-99
rxa01499	3945	GB_PR4:AC006454	153201	AC006454	Homo sapiens clone DJ0852P06, complete sequence	Homo sapiens	38,033	13-Aug-99
		GB_BA1.LSLYSSYNT	4724	X96558	Lysobacter sp gene encoding synthetase	Lysobacter	42,840	8-Jan-97
		GB_PR4:AC006454	153201	AC006454	Homo sapiens clone DJ0852P06, complete sequence	Homo sapiens	38,823	13-Aug-99
rxa01502	1356	GB_PAT:I92046	2203	I92046	Sequence 13 from patent US 5726299.	Unknown.	39,755	01-DEC-1998
		GB_PAT:I78757	2203	I78757	Sequence 13 from patent US 5693781	Unknown.	39,755	3-Apr-98
		GB_BA1.MTCY359	36021	Z83859	Mycobacterium tuberculosis H37Rv complete genome; segment 84/162	Mycobacterium tuberculosis	36,613	17-Jun-98
rxa01509	597	GB_BA1 SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	60,637	19-MAY-1999
		GB_BA1:MTY15C10	33050	Z95436	Mycobacterium tuberculosis H37Rv complete genome, segment 154/162.	Mycobacterium tuberculosis	59,296	17-Jun-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548	Mycobacterium leprae	59,764	27-Aug-99
rxa01510	1404	GB_GSS9:AQ129927	440	AQ129927	HS_2165_B1_D09_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=2165 Col=17 Row=H, genomic survey sequence.	Homo sapiens	36,136	23-Sep-98
		GB_BA2:AF016585	41097	AF016585	Streptomyces caelestis cytochrome P-450 hydroxylase homolog (nidI) gene, partial cds; polyketide synthase modules 1 through 7 (nidA) genes, complete cds; and N-methyltransferase homolog gene, partial cds.	Streptomyces caelestis	37,464	07-DEC-1997
		GB_HTG4:AC010747	216500	AC010747	Homo sapiens chromosome unknown clone NH0555H09, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,022	29-OCT-1999
rxa01511	1065	GB_BA1:BRLBIOBA	1647	D14084	Brevibacterium flavum gene for biotin synthetase, complete cds	Corynebacterium glutamicum	40,283	3-Feb-99
		GB_GSS3:B45213	358	B45213	HS-1060-B2-D07-MF.ab1 CIT Human Genomic Sperm Library C Homo sapiens genomic clone Plate=CT 782 Col=14 Row=H, genomic survey sequence	Homo sapiens	49,505	21-OCT-1997

TABLE 4: ALIGNMENT RESULTS

		GB_HTG4:AC010747	216500	AC010747	Homo sapiens chromosome unknown clone NH0555H09, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	33,819	29-OCT-1999
rxa01513	2682	GB_BA1:MTCY7H7B	24244	Z95557	Mycobacterium tuberculosis H37Rv complete genome; segment 153/162.	Mycobacterium tuberculosis	40,354	18-Jun-98
		GB_BA2:AF037269	2364	AF037269	Mycobacterium smegmatis cell division protein (FtsH) gene, complete cds.	Mycobacterium smegmatis	60,814	19-Aug-98
		GB_BA1:MLCB2548	38916	AL023093	Mycobacterium leprae cosmid B2548	Mycobacterium leprae	39,992	27-Aug-99
rxa01593	990	GB_BA1:U00012	33312	U00012	Mycobacterium leprae cosmid B1308.	Mycobacterium leprae	39,126	30-Jan-96
		GB_IN1:CELF27E11	25700	AF016413	Caenorhabditis elegans cosmid F27E11.	Caenorhabditis elegans	34,227	2-Aug-97
		GB_OV:DYGAGR	4354	L01423	Discopyge ommata (clone OL4) agrin mRNA, 3' end cds.	Discopyge ommata	38,414	28-Apr-93
rxa01608	1962	GB_BA2:AF119150	18605	AF119150	Vibrio cholerae Rtx toxin gene cluster, complete cds	Vibrio cholerae	36,919	21-MAR-1999
		GB_BA2:AF119150	18605	AF119150	Vibrio cholerae Rtx toxin gene cluster, complete cds.	Vibrio cholerae	38,130	21-MAR-1999
rxa01620								
rxa01640	3441	GB_PR3:HS52D1	148691	Z96811	Human DNA sequence from PAC 52D1 on chromosome Xq21 Contains CA repeats, STS.	Homo sapiens	35,501	23-Nov-99
		GB_BA2 AF079155	686	AF079155	Ralstonia eutropha phasin (phaP) mRNA, complete cds	Ralstonia eutropha	40,497	6-Apr-99
		GB_IN2:AF039570	1866	AF039570	Caenorhabditis elegans aryl hydrocarbon receptor ortholog AHR-1 (ahr-1) mRNA, complete cds	Caenorhabditis elegans	39,699	04-OCT-1999
rxa01653	1584	GB_HTG7:AC010997	187768	AC010997	Homo sapiens clone RP11-399K21, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces	Homo sapiens	34,516	08-DEC-1999
		GB_HTG7:AC010997	187768	AC010997	Homo sapiens clone RP11-399K21, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces	Homo sapiens	36,177	08-DEC-1999
		GB_VI AF030154	34446	AF030154	Bovine adenovirus 3 complete genome	bovine adenovirus type 3	40,345	27-Jan-99
rxa01716	509	GB_BA1:AB010645	16836	AB010645	Acetobacter xylinus genes for endoglucanase, cellulose synthase subunit ABCD and beta-glucosidase, complete cds	Acetobacter xylinus	34,783	13-Feb-99
		GB_BA1:AB010645	16836	AB010645	Acetobacter xylinus genes for endoglucanase, cellulose synthase subunit ABCD and beta-glucosidase, complete cds	Acetobacter xylinus	37,598	13-Feb-99
		GB_BA1 ABCBCSABCD	9540	M37202	A.xylinum bcs A, B, C and D genes, complete cds's	Acetobacter xylinus	39,173	24-Apr-93
rxa01728	1098	GB_BA2:CORCSLYS	2821	M89931	Corynebacterium glutamicum beta C-S lyase (aecD) and branched-chain amino acid uptake carrier (brnQ) genes, complete cds, and hypothetical protein Yhbw (yhbw) gene, partial cds.	Corynebacterium glutamicum	99,636	4-Jun-98
		GB_PL2:HAAP	931	X95952	H annuus mRNA for aquaporin.	Helianthus annuus	39,231	14-Jul-99
		GB_HTG1:CEY32F6	187816	AL008875	Caenorhabditis elegans chromosome V clone Y32F6, *** SEQUENCING IN PROGRESS ***, in unordered pieces	Caenorhabditis elegans	37,431	9-Nov-97
rxa01732	1173	GB_PR4:HUAC004125	194020	AC004125	Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.	Homo sapiens	35,345	23-Nov-99
		GB_PR4:HUAC004125	194020	AC004125	Homo sapiens Chromosome 16 BAC clone CIT987SK-625P11, complete sequence.	Homo sapiens	37,381	23-Nov-99
		GB_IN1:CER11A5	26671	Z83122	Caenorhabditis elegans cosmid R11A5, complete sequence	Caenorhabditis elegans	36,140	2-Sep-99
rxa01810	1200	GB_EST28:AI499508	403	AI499508	to02d01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE.2177857 3' similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 ;, mRNA sequence	Homo sapiens	36,725	11-MAR-1999

TABLE 4: ALIGNMENT RESULTS

		GB_EST28:AI499508	403	AI499508	to02d01.x1 NCI_CGAP_Ut2 Homo sapiens cDNA clone IMAGE.2177857 3' similar to SW:NU4M_PANTR P03906 NADH-UBIQUINONE OXIDOREDUCTASE CHAIN 4 ;, mRNA sequence	Homo sapiens	38,264	11-MAR-1999
rxa01828	1545	GB_BA1:MLCB1770	37821	Z70722	Mycobacterium leprae cosmid B1770.	Mycobacterium leprae	36,411	29-Aug-97
		GB_HTG2:AC008073	173144	AC008073	Homo sapiens clone NH0507M03, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,310	17-Jul-99
		GB_HTG2.AC008073	173144	AC008073	Homo sapiens clone NH0507M03, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	36,310	17-Jul-99
rxa01829	1446	GB_IN1.AB018544	620	AB018544	Hydra magnipapillata mRNA for Hym-176 preprohormone, complete cds.	Hydra magnipapillata	34,855	6-Feb-99
		GB_EST8:AA003136	450	AA003136	mg51e01.r1 Soares mouse embryo NbME13 5 14.5 Mus musculus cDNA clone IMAGE:427320 5' similar to gb X07315 PLACENTAL PROTEIN 15 (HUMAN);, mRNA sequence.	Mus musculus	42,202	19-Jul-96
		GB_IN1.AB018544	620	AB018544	Hydra magnipapillata mRNA for Hym-176 preprohormone, complete cds.	Hydra magnipapillata	35,968	6-Feb-99
rxa01868	2049	GB_BA1.MTV033	21620	AL021928	Mycobacterium tuberculosis H37Rv complete genome; segment 11/162	Mycobacterium tuberculosis	38,679	17-Jun-98
		GB_BA1:MLCL622	42498	Z95398	Mycobacterium leprae cosmid L622.	Mycobacterium leprae	38,911	24-Jun-97
		GB_BA1:MSGB983CS	36788	L78828	Mycobacterium leprae cosmid B983 DNA sequence	Mycobacterium leprae	38,933	15-Jun-96
rxa01934	681	GB_PR4:DJ534K4	216387	AF109907	Homo sapiens S164 gene, partial cds; PS1 and hypothetical protein genes, complete cds, and S171 gene, partial cds.	Homo sapiens	39,189	23-DEC-1998
		GB_HTG2.AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	34,412	11-Jan-99
		GB_HTG2:AC006342	201618	AC006342	Homo sapiens clone DJ0054D12, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces	Homo sapiens	34,412	11-Jan-99
rxa01967	1266	GB_IN2.AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 48C1-48C2, P1 clone DS00568, complete sequence	Drosophila melanogaster	35,252	12-DEC-1998
		GB_BA2:AE001678	13485	AE001678	Chlamydia pneumoniae section 94 of 103 of the complete genome	Chlamydophila pneumoniae	35,203	08-MAR-1999
		GB_IN2:AC005467	62091	AC005467	Drosophila melanogaster, chromosome 2R, region 48C1-48C2, P1 clone DS00568, complete sequence	Drosophila melanogaster	34,699	12-DEC-1998
rxa01993	1166	GB_BA1.PPVANAB	2864	Y14759	Pseudomonas putida vanA and vanB genes	Pseudomonas putida	51,697	09-MAY-1998
		GB_HTG2.AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Caenorhabditis elegans	38,455	23-Feb-99
		GB_HTG2.AC006799	278007	AC006799	Caenorhabditis elegans clone Y51H7, *** SEQUENCING IN PROGRESS ***, 7 unordered pieces.	Caenorhabditis elegans	38,455	23-Feb-99
rxa01994	1098	GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	35,576	29-OCT-1999
		GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces.	Homo sapiens	35,576	29-OCT-1999
		GB_HTG4:AC009961	231522	AC009961	Homo sapiens chromosome unknown clone NH0357L02, WORKING DRAFT SEQUENCE, in unordered pieces	Homo sapiens	35,472	29-OCT-1999
rxa01997	609	GB_BA2:AF112536	1798	AF112536	Corynebacterium glutamicum ribonucleotide reductase beta-chain (nrdF) gene, complete cds.	Corynebacterium glutamicum	37,719	5-Aug-99
		GB_BA1 SCH66	9153	AL049731	Streptomyces coelicolor cosmid H66.	Streptomyces coelicolor	38,655	29-Apr-99
		GB_EST29:AI558691	598	AI558691	fb79c10.y1 Zebrafish WashU MPIMG EST Danio rerio cDNA 5' similar to SW.ATF3_HUMAN P18847 CYCLIC-AMP-DEPENDENT TRANSCRIPTION FACTOR ATF-3 ;, mRNA sequence	Danio rerio	40,232	24-MAR-1999

TABLE 4: ALIGNMENT RESULTS

rxa02052	915	GB_EST3:R64206	453	R64206	yi18d08.r1 Soares placenta Nb2HP Homo sapiens cDNA clone IMAGE:139599 5', mRNA sequence.	Homo sapiens	35,920	26-MAY-1995
		GB_PR2:AC002540	70851	AC002540	Human BAC clone GS025M02 from 7q21-q22, complete sequence.	Homo sapiens	37,099	12-Sep-97
		GB_GSS3:B55001	406	B55001	CIT-HSP-385H2.TRB CIT-HSP Homo sapiens genomic clone 385H2, genomic survey sequence.	Homo sapiens	35,599	20-Jun-98
rxa02064	762	GB_PR4:AF135187	33016	AF135187	Homo sapiens interferon-induced protein p78 (MX1) gene, complete cds.	Homo sapiens	32,935	8-Jul-99
		GB_PR3:AC005612	60904	AC005612	Homo sapiens chromosome 21, P1 clone LBL#8 (LBNL H8), complete sequence.	Homo sapiens	32,935	4-Sep-98
		GB_PR1:HUM8DC11Z	3949	L35666	Homo sapiens (subclone H8 10_f11 from P1 35 H5 C8) DNA sequence.	Homo sapiens	31,995	22-Aug-94
rxa02082	3010	GB_BA1:MSGB32CS	36404	L78818	Mycobacterium leprae cosmid B32 DNA sequence.	Mycobacterium leprae	50,604	15-Jun-96
		GB_BA1:MTCY338	29372	Z74697	Mycobacterium tuberculosis H37Rv complete genome; segment 127/162.	Mycobacterium tuberculosis	38,113	17-Jun-98
		GB_GSS10:AQ242118	766	AQ242118	3I23-4r Ochrobactrum anthropi BAC Library Ochrobactrum anthropi genomic clone 3I23-4r, genomic survey sequence.	Ochrobactrum anthropi	41,876	02-OCT-1998
rxa02083	1533	GB_PR4:AC008055	196899	AC008055	Homo sapiens 12q22-103.4-106.5 BAC RPCI11-718L23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	36,818	09-OCT-1999
		GB_PL2:AC002292	120787	AC002292	Genomic sequence of Arabidopsis BAC F8A5, complete sequence.	Arabidopsis thaliana	37,517	02-OCT-1997
		GB_PR4:AC008055	196899	AC008055	Homo sapiens 12q22-103.4-106.5 BAC RPCI11-718L23 (Roswell Park Cancer Institute Human BAC Library) complete sequence.	Homo sapiens	35,563	09-OCT-1999
rxa02092	1761	GB_BA2:AF031929	2675	AF031929	Lactobacillus helveticus cochaperonin GroES and chaperonin GroEL genes, complete cds; and DNA mismatch repair enzyme (hexA) gene, partial cds.	Lactobacillus helveticus	36,149	8-Aug-98
		GB_HTG1:HSDJ34F7	129811	AL049547	Homo sapiens chromosome 6 clone RP1-34F7, *** SEQUENCING IN PROGRESS ***, in unordered pieces.	Homo sapiens	37,587	23-Nov-99
		GB_PR2:HSU24578	17488	U24578	Human RP1 and complement C4B precursor (C4B) genes, partial cds.	Homo sapiens	36,755	16-MAY-1996
rxa02098	1869	GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	99,766	14-MAY-1999
		GB_BA1:CAJ10319	5368	AJ010319	Corynebacterium glutamicum amtP, glnB, glnD genes and partial ftsY and srp genes.	Corynebacterium glutamicum	36,983	14-MAY-1999
rxa02105	391	GB_EST17:AA660065	352	AA660065	EST00115 watermelon lambda zap express library Citrullus lanatus cDNA clone WMLS233 5' similar to translation initiation factor, mRNA sequence.	Citrullus lanatus	37,231	10-Nov-97
		GB_GSS6:AQ839377	523	AQ839377	HS_4640_B2_F09_T7A CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=4640 Col=18 Row=L, genomic survey sequence.	Homo sapiens	37,500	30-Aug-99
		GB_PL1:SPCC970	31438	AL031530	S.pombe chromosome III cosmid c970.	Schizosaccharomyces pombe	38,268	07-MAY-1999
rxa02111	1407	GB_BA1:SC6G10	36734	AL049497	Streptomyces coelicolor cosmid 6G10.	Streptomyces coelicolor	50,791	24-MAR-1999
		GB_BA1:U00010	41171	U00010	Mycobacterium leprae cosmid B1170.	Mycobacterium leprae	37,563	01-MAR-1994
		GB_BA1:MTCY336	32437	Z95586	Mycobacterium tuberculosis H37Rv complete genome; segment 70/162.	Mycobacterium tuberculosis	39,504	24-Jun-99
rxa02118	465	GB_HTG2:AC007164	158320	AC007164	Homo sapiens clone NH0304A10, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,377	23-Apr-99
		GB_PR3:AC004451	108642	AC004451	Homo sapiens PAC clone DJ0789N01 from 7q21, complete sequence.	Homo sapiens	39,387	20-MAR-1998
		GB_HTG2:AC007164	158320	AC007164	Homo sapiens clone NH0304A10, *** SEQUENCING IN PROGRESS ***, 3 unordered pieces.	Homo sapiens	38,377	23-Apr-99

TABLE 4: ALIGNMENT RESULTS

rxa02120	885	GB_PL2:PUMCDC2A	1288	L34206	Petroselinum crispum protein kinase p34cdc2 (cdc2) mRNA, complete cds.	Petroselinum crispum	37,816	17-Feb-96
		GB_GSS10:AQ214799	431	AQ214799	HS_3010_A2_G12_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3010 Col=24 Row=M, genomic survey sequence.	Homo sapiens	34,591	18-Sep-98
		GB_PL2:PUMCDC2A	1288	L34206	Petroselinum crispum protein kinase p34cdc2 (cdc2) mRNA, complete cds.	Petroselinum crispum	36,541	17-Feb-96
rxa02126	444	GB_GSS4:AQ707596	485	AQ707596	HS_5560_B1_H08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=15 Row=P, genomic survey sequence.	Homo sapiens	38,482	7-Jul-99
		GB_GSS13:AQ494885	411	AQ494885	HS_5195_A1_B11_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=771 Col=21 Row=C, genomic survey sequence.	Homo sapiens	40,897	28-Apr-99
		GB_GSS4:AQ707596	485	AQ707596	HS_5560_B1_H08_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=1136 Col=15 Row=P, genomic survey sequence.	Homo sapiens	43,533	7-Jul-99
rxa02148	1266	GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	36,051	24-Jun-99
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	36,051	24-Jun-99
		GB_HTG2:AC007905	100722	AC007905	Homo sapiens chromosome 16q24.3 clone PAC 754F23, *** SEQUENCING IN PROGRESS ***, 33 unordered pieces.	Homo sapiens	35,402	24-Jun-99
rxa02214	732	GB_GSS13:AQ459868	402	AQ459868	HS_5116_A1_H04_SP6E RPCI-11 Human Male BAC Library Homo sapiens genomic clone Plate=692 Col=7 Row=O, genomic survey sequence.	Homo sapiens	43,035	23-Apr-99
		GB_EST26:AU005050	790	AU005050	AU005050 Bombyx mori p50(Daizo) Bombyx mori cDNA clone ws30188, mRNA sequence.	Bombyx mori	45,902	19-Jan-99
		GB_PL2:F8K7	98581	AC007727	Arabidopsis thaliana chromosome 1 BAC F8K7 sequence, complete sequence.	Arabidopsis thaliana	37,155	29-Jun-99
rxa02316	1137	GB_EST32:AI723424	600	AI723424	hcgls49.T7 Haemonchus contortus Intestinal mRNA Haemonchus contortus cDNA clone hcgls49.T7 T7, mRNA sequence.	Haemonchus contortus	35,953	10-Jun-99
		GB_PR4:AC000134	203300	AC000134	Homo sapiens Chromosome 11q13 BAC Clone 137c7, complete sequence.	Homo sapiens	37,030	06-MAY-1999
		GB_STS:AF021124	575	AF021124	Homo sapiens trinucleotide repeat ctg-68, sequence tagged site.	Homo sapiens	41,913	3-Apr-98
rxa02384	831	GB_PL1:ATA224957	4081	AJ224957	Arabidopsis thaliana RGAL gene.	Arabidopsis thaliana	35,627	19-MAY-1998
		GB_RO:AF022770	577	AF022770	Mus musculus peripherial benzodiazepine receptor associated protein (Pap7) mRNA, partial cds.	Mus musculus	39,652	24-Sep-97
		GB_GSS11:AQ258908	890	AQ258908	nbxb0021F23r CUGI Rice BAC Library Oryza sativa genomic clone nbxb0021F23r, genomic survey sequence.	Oryza sativa	39,515	23-OCT-1998
rxa02411	972	GB_BA1:AB020624	1605	AB020624	Corynebacterium glutamicum murI gene for D-glutamate racemase, complete cds.	Corynebacterium glutamicum	98,868	24-Jul-99
		GB_EST18:AA733776	385	AA733776	vv03f03.r1 Stratagene mouse skin (#937313) Mus musculus cDNA clone IMAGE:1210589 5', mRNA sequence.	Mus musculus	43,864	7-Jan-98
		GB_EST38:AW033449	612	AW033449	EST277020 tomato callus, TAMU Lycopersicon esculentum cDNA clone cLEC28F5, mRNA sequence.	Lycopersicon esculentum	35,620	15-Sep-99

TABLE 4: ALIGNMENT RESULTS

rxa02448	1212	GB_BA1.AB016258	2260	AB016258	Arthrobacter sp gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	60,465	8-Sep-99
		GB_EST37:AW014148	553	AW014148	UI-H-BI0-aaj-c-04-0-UI s1 NCI_CGAP_Sub1 Homo sapiens cDNA clone IMAGE:2709487 3', mRNA sequence	Homo sapiens	44,560	10-Sep-99
		GB_EST14:AA432042	543	AA432042	zw80f01 r1 Soares_testis_NHT Homo sapiens cDNA clone IMAGE.782521 5' similar to WP.T12A7.1 CE06433 ;, mRNA sequence.	Homo sapiens	36,522	22-MAY-1997
rxa02449	1026	GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds.	Arthrobacter sp.	66,244	8-Sep-99
		GB_BA1:CGPUTP	3791	Y09163	C glutamicum putP gene	Corynebacterium glutamicum	39,899	8-Sep-97
		GB_BA1:AB016258	2260	AB016258	Arthrobacter sp. gene for maleylacetate reductase and hydroxyquinol 1,2-dioxygenase, partial and complete cds	Arthrobacter sp	70,410	8-Sep-99
rxa02497	1050	GB_BA2:CGU31224	422	U31224	Corynebacterium glutamicum (ppx) gene, partial cds.	Corynebacterium glutamicum	96,445	2-Aug-96
		GB_BA1:MTCY20G9	37218	Z77162	Mycobacterium tuberculosis H37Rv complete genome; segment 25/162	Mycobacterium tuberculosis	59,429	17-Jun-98
		GB_BA1.SCE7	16911	AL049819	Streptomyces coelicolor cosmid E7.	Streptomyces coelicolor	39,510	10-MAY-1999
rxa02526	1329	GB_GSS10:AQ240233	483	AQ240233	CIT-HSP-2385F9 TR.1 CIT-HSP Homo sapiens genomic clone 2385F9, genomic survey sequence	Homo sapiens	42,475	30-Sep-98
		GB_OV:S48556	195	S48556	{tandem repeat P1 monomer} [Cacatua galerita=sulfur-crested cockatoo, Genomic, 195 nt]	Cacatua galerita	50,515	08-MAY-1993
		GB_PR2:HSM801056	2555	AL117532	Homo sapiens mRNA; cDNA DKFZp434E192 (from clone DKFZp434E192)	Homo sapiens	39,116	15-Sep-99
rxa02530	780	GB_PR3 HSJ753D10	97912	AL049651	Human DNA sequence from clone 753D10 on chromosome 20 Contains genes for SSTR4(somatostatin receptor 4) and THBD(thrombomodulin), ESTs, STSs, GSSs and CpG islands, complete sequence	Homo sapiens	34,248	23-Nov-99
		GB_EST33:AI782764	661	AI782764	EST263643 tomato susceptible, Cornell Lycopersicon esculentum cDNA clone cLES20B10, mRNA sequence	Lycopersicon esculentum	35,385	29-Jun-99
		GB_GSS9:AQ121479	521	AQ121479	HS_3084_A2_B02_MF CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3084 Col=4 Row=C, genomic survey sequence.	Homo sapiens	38,689	22-Sep-98
rxa02535	1278	GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,799	3-Aug-99
		GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces.	Homo sapiens	35,799	3-Aug-99
		GB_HTG3:AC008710	146065	AC008710	Homo sapiens chromosome 5 clone CIT978SKB_7E3, *** SEQUENCING IN PROGRESS ***, 39 unordered pieces	Homo sapiens	34,886	3-Aug-99
rxa02603	1119	GB_BA1:MTV026	23740	AL022076	Mycobacterium tuberculosis H37Rv complete genome; segment 157/162	Mycobacterium tuberculosis	37,975	24-Jun-99
		GB_IN2:AC005714	177740	AC005714	Drosophila melanogaster, chromosome 2R, region 58D4-58E2, BAC clone BACR48M13, complete sequence.	Drosophila melanogaster	41,226	01-MAY-1999
		GB_EST19:AA775050	218	AA775050	ac76e10.s1 Stratagene lung (#937210) Homo sapiens cDNA clone IMAGE 868554 3' similar to gb:Y00371_rna1 HEAT SHOCK COGNATE 71 KD PROTEIN (HUMAN);, mRNA sequence.	Homo sapiens	40,826	5-Feb-98
rxa02641								

TABLE 4: ALIGNMENT RESULTS

rxa02651	1053	GB_BA1:MTCY48	35377	Z74020	Mycobacterium tuberculosis H37Rv complete genome; segment 69/162.	Mycobacterium tuberculosis	62,678	17-Jun-98
		GB_BA1:SC4A10	43147	AL109663	Streptomyces coelicolor cosmid 4A10.	Streptomyces coelicolor A3(2)	39,109	5-Aug-99
		GB_BA1:MLCL458	43839	AL049478	Mycobacterium leprae cosmid L458.	Mycobacterium leprae	62,753	27-Aug-99
rxa02674	1575	GB_BA2:PPU96338	5276	U96338	Pseudomonas putida NCIMB 9866 plasmid pRA4000 p-cresol degradative pathway genes, p-hydroxybenzaldehyde dehydrogenase (pchA), p-cresol methylhydroxylase, cytochrome subunit precursor (pchC), unknown (pchX) and p-cresol methylhydroxylase, flavoprotein subunit (pchF) genes, complete cds.	Pseudomonas putida	58,095	13-MAY-1999
		GB_BA1:SCE9	37730	AL049841	Streptomyces coelicolor cosmid E9.	Streptomyces coelicolor	38,544	19-MAY-1999
		GB_BA2:PPU96339	4464	U96339	Pseudomonas putida NCIMB 9869 plasmid pRA500 p-cresol degradative pathway genes, p-hydroxybenzaldehyde dehydrogenase (pchA) gene, partial cds, and p-cresol methylhydroxylase, cytochrome subunit (pchC), unknown (pchX), p-cresol methylhydroxylase, flavoprotein subunit (pchF), protocatechuate-3,4-dioxygenase, beta subunit (pcaH) and protocatechuate-3,4-dioxygenase, alpha subunit (pcaG) genes, complete cds.	Pseudomonas putida	70,588	13-MAY-1999
rxa02702	1581	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	99,365	6-Feb-99
		GB_BA1:AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds.	Corynebacterium glutamicum	99,317	4-Aug-97
		GB_BA1:BLFTSZ	5546	Y08964	B.lactofermentum murC, ftsQ or divD & ftsZ genes.	Corynebacterium glutamicum	99,296	08-OCT-1998
rxa02703	1212	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	97,468	6-Feb-99
		GB_PL2:VFAMACTRA	1879	Y09591	V.faba mRNA for amino acid transporter.	Vicia faba	38,915	02-DEC-1999
		GB_PAT:E05047	966	E05047	DNA encoding recombinant monoglyceride lipase.	Bacillus sp.	37,158	29-Sep-97
rxa02704	1812	GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	37,946	10-Feb-99
		GB_BA2:AE000961	18765	AE000961	Archaeoglobus fulgidus section 146 of 172 of the complete genome.	Archaeoglobus fulgidus	38,521	15-DEC-1997
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	37,850	10-Feb-99
rxa02705	1539	GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	97,619	07-OCT-1996
		EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	97,619	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:SC4A10	43147	AL109663	Streptomyces coelicolor cosmid 4A10.	Streptomyces coelicolor A3(2)	37,856	5-Aug-99
rxa02706	1221	GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	98,605	07-OCT-1996
		EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	98,605	08-OCT-1997 (Rel. 52, Created)
		GB_BA1:MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome; segment 96/162.	Mycobacterium tuberculosis	34,868	10-Feb-99
rxa02707	1653	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene.	Corynebacterium glutamicum	98,547	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	98,547	07-OCT-1996

TABLE 4: ALIGNMENT RESULTS

		GB_BA1:MLCB268	38859	AL022602	Mycobacterium leprae cosmid B268	Mycobacterium leprae	37,815	27-Aug-99
rxa02710	1686	EM_PAT:E11760	6911	E11760	Base sequence of sucrase gene	Corynebacterium glutamicum	52,124	08-OCT-1997 (Rel. 52, Created)
		GB_PAT:I26124	6911	I26124	Sequence 4 from patent US 5556776.	Unknown.	52,124	07-OCT-1996
		GB_GSS13:AQ484169	515	AQ484169	RPCI-11-264A12 TV RPCI-11 Homo sapiens genomic clone RPCI-11-264A12, genomic survey sequence	Homo sapiens	40,856	24-Apr-99
rxa02711	2235	GB_BA2:XCU45994	1203	U45994	Xanthomonas campestris pv campestris insertion sequence IS1404.	Xanthomonas campestris pv. campestris	39,061	29-Jan-99
		GB_BA2.XCU77781	4160	U77781	Xanthomonas campestris pv. amaranthicola XamI DNA methyltransferase (xamIM) gene, complete cds; insertion sequence IS1389 and unknown genes.	Xanthomonas campestris pv amaranthicola	39,551	9-Feb-99
		GB_BA2:AF108355	1222	AF108355	Xanthomonas campestris pv amaranthicola insertion sequence IS1389-B unknown genes.	Xanthomonas campestris pv. amaranthicola	40,281	09-MAR-1999
rxa02713	1134	GB_BA1.MTCY270	37586	Z95388	Mycobacterium tuberculosis H37Rv complete genome, segment 96/162	Mycobacterium tuberculosis	38,669	10-Feb-99
		GB_PR1:D31907	599	D31907	Homo sapiens gene for zinc regulatory factor, partial cds.	Homo sapiens	36,396	7-Feb-99
		GB_PR1:HSMTFMR	3302	X78710	H sapiens MTF-1 mRNA for metal-regulatory transcription factor.	Homo sapiens	37,243	1-Aug-94
rxa02716	684	GB_PR3 AC002347	134977	AC002347	Homo sapiens chromosome 17, clone 297N7, complete sequence	Homo sapiens	36,282	3-Feb-98
		GB_PR3.HS310J6	87942	AL035593	Human DNA sequence from clone 310J6 on chromosome 6q22 1-22 3 Contains part of a novel gene, ESTs, STSs and GSSs, complete sequence	Homo sapiens	37,291	23-Nov-99
		GB_HTG3:AC011509	111353	AC011509	Homo sapiens chromosome 19 clone CITB-H1_2189E23, *** SEQUENCING IN PROGRESS ***, 35 unordered pieces.	Homo sapiens	37,407	07-OCT-1999
rxa02722	1449	GB_BA1.BLFTSZ	5546	Y08964	B lactofermentum murC, ftsQ or divD & ftsZ genes	Corynebacterium glutamicum	99,652	08-OCT-1998
		GB_BA1.AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds.	Corynebacterium glutamicum	98,535	4-Aug-97
		GB_PAT:E17182	1125	E17182	Brevibacterium flavum ftsQ gene complete cds	Corynebacterium glutamicum	97,235	28-Jul-99
rxa02723	789	GB_BA1:AB015023	2291	AB015023	Corynebacterium glutamicum genes for MurC and FtsQ, complete cds.	Corynebacterium glutamicum	99,113	6-Feb-99
		GB_BA1:BLFTSZ	5546	Y08964	B lactofermentum murC, ftsQ or divD & ftsZ genes	Corynebacterium glutamicum	99,113	08-OCT-1998
		GB_BA1:AB003132	4116	AB003132	Corynebacterium glutamicum gene for MurC, FtsQ, FtsZ, complete cds	Corynebacterium glutamicum	99,113	4-Aug-97
rxa02813	1108	GB_HTG3.AC009658	171795	AC009658	Homo sapiens chromosome 15 clone 344_A_16 map 15, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Homo sapiens	34,622	01-OCT-1999
		GB_HTG3.AC009658	171795	AC009658	Homo sapiens chromosome 15 clone 344_A_16 map 15, *** SEQUENCING IN PROGRESS ***, 29 unordered pieces.	Homo sapiens	34,622	01-OCT-1999
		GB_RO:MMU65079	2300	U65079	Mus musculus actin-binding protein (ENC-1) mRNA, complete cds	Mus musculus	35,013	29-Jul-97
rxa02820	1411	GB_BA1:BFU64514	3837	U64514	Bacillus firmus dppABC operon, dipeptide transporter protein dppA gene, partial cds, and dipeptide transporter proteins dppB and dppC genes, complete cds.	Bacillus firmus	36,859	1-Feb-97
		GB_IN1:CET04C10	20958	Z69885	Caenorhabditis elegans cosmid T04C10, complete sequence.	Caenorhabditis elegans	35,934	2-Sep-99

TABLE 4: ALIGNMENT RESULTS

		GB_EST35:AI823090	720	AI823090	L30-944T3 Ice plant Lambda Uni-Zap XR expression library, 30 hours NaCl treatment Mesembryanthemum crystallinum cDNA clone L30-944 5' similar to 60S ribosomal protein L36 (AC004684)[Arabidopsis thaliana], mRNA sequence.	Mesembryanthemum crystallinum	35,770	21-Jul-99
rxa02828	572	GB_BA1:MTCY10H4	39160	Z80233	Mycobacterium tuberculosis H37Rv complete genome; segment 2/162.	Mycobacterium tuberculosis	39,823	17-Jun-98
		GB_BA1:MTORIREP	8400	X92504	M.tuberculosis origin of replication and genes rnpA, rpmH, dnaA, dnaN, recF.	Mycobacterium tuberculosis	39,823	26-Aug-97
		GB_RO:RATENDOGLY	3906	L37380	Rat apical endosomal glycoprotein mRNA, complete cds.	Rattus norvegicus	38,704	20-Apr-95
rxa02839	470	GB_BA2:ECOUW89	176195	U00006	E. coli chromosomal region from 89.2 to 92.8 minutes.	Escherichia coli	99,362	17-DEC-1993
		GB_BA2:AE000477	11314	AE000477	Escherichia coli K-12 MG1655 section 367 of 400 of the complete genome.	Escherichia coli	99,787	12-Nov-98
		GB_BA1:ECOPLSB	3865	K00127	E.coli plsB and dgk genes coding for sn-glycerol-3-phosphate acyltransferase and diglyceride kinase.	Escherichia coli	33,761	28-Feb-94
rxs03218								

Customer Number: 000959

Attorney's Docket Number BGI-132CP

DECLARATION, PETITION AND POWER OF ATTORNEY FOR PATENT APPLICATION

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name,

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled:

CORYNEBACTERIUM GLUTAMICUM GENES ENCODING PROTEINS INVOLVED IN HOMEOSTASIS AND ADAPTATION

X is attached hereto.

_ was filed on _____ as

Application Serial No. _____

and was amended on _____.
(if applicable)

I do not know and do not believe that the subject matter of this application was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date of this application, or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date of this application on an application filed more than twelve months (six months if this application is for a design) before the filing of this application; and I acknowledge my duty to disclose information of which I am aware which is material to the examination of this application, that no application for patent or inventor's certificate on the subject matter of this application has been filed by me or my representatives or assigns in any country foreign to the United States, except those identified below, and that I have reviewed and understand the contents of the specification, including the claims as amended by any amendment referred to herein.

I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56.

CLAIM OF BENEFIT OF EARLIER FOREIGN APPLICATION(S)

I hereby claim priority benefits under Title 35, United States Code, §119 of any foreign application(s) for patent or inventor's certificate listed below, and have also identified below any foreign application(s) for patent or inventor's certificate filed by me on the same subject matter having a filing date before that of the application(s) from which priority is claimed.

Check one:

_ no such applications have been filed.

X such applications have been filed as follows

EARLIEST FOREIGN APPLICATION(S), IF ANY, FILED WITHIN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Country	Application Number	Date of Filing (month,day,year)	Priority Claimed Under 35 USC 119
DE	19931418.7	07/08/99	X Yes No _
DE	19932124.8	07/09/99	X Yes No _
DE	19932126.4	07/09/99	X Yes No _
DE	19932127.2	07/09/99	X Yes No _
DE	19932133.7	07/09/99	X Yes No _
DE	19932207.4	07/09/99	X Yes No _
DE	19932208.2	07/09/99	X Yes No _
DE	19932225.2	07/09/99	X Yes No _
DE	19932229.5	07/09/99	X Yes No _
DE	19932914.1	07/14/99	X Yes No _
DE	19933006.9	07/14/99	X Yes No _
DE	19940765.7	08/27/99	X Yes No _
DE	19940768.1	08/27/99	X Yes No _
DE	19940831.9	08/27/99	X Yes No _
DE	19940832.7	08/27/99	X Yes No _
DE	19941385.1	08/31/99	X Yes No _
DE	19941396.7	08/31/99	X Yes No _
DE	19942087.4	09/03/99	X Yes No _

ALL FOREIGN APPLICATION(S), IF ANY FILED MORE THAN 12 MONTHS (6 MONTHS FOR DESIGN) PRIOR TO THIS U.S. APPLICATION

Doc Code: AP.PRE.REQ

CLAIM FOR BENEFIT OF U.S. PROVISIONAL APPLICATION(S)

I hereby claim the benefit under 35 U.S.C. §119(e) of any United States provisional application(s) listed below.

60/141,031	June 25, 1999
(Application Serial No.)	(Filing Date)
60/143,694	July 14, 1999
(Application Serial No.)	(Filing Date)
60/151,778	August 31, 1999
(Application Serial No.)	(Filing Date)

Express Mail Label No. EV 325 625 525 US

CLAIM FOR BENEFIT OF EARLIER U.S./PCT APPLICATION(S)

I hereby claim the benefit under Title 35, United States Code, §120 of any earlier United States application(s) or PCT international application(s) designating the United States listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the earlier application(s) in the manner provided by the first paragraph of Title 35, United States Code, §112, I acknowledge the duty to disclose to the Office all information known to me to be material to patentability as defined in Title 37, Code of Federal Regulations, §1.56 which became available between the filing date(s) of the earlier application(s) and the national or PCT international filing date of this application. As to subject matter of this application which is common to my earlier application(s), if any, described below, I do not know and do not believe that the same was known or used by others in the United States or patented or described in a printed publication in any country before my invention thereof, or patented or described in a printed publication in any country or in public use or on sale in the United States more than one year prior to the date(s) of said earlier application(s), or first patented or caused to be patented or made the subject of an inventor's certificate by me or my legal representatives or assigns in a country foreign to the United States prior to the date(s) of said earlier application(s) on an application filed more than twelve months (six months if this application is for a design) before the filing of said earlier application(s); and I acknowledge that no application for patent or inventor's certificate on said subject matter has been filed by me or my representatives or assigns in any country foreign to the United States except those identified herein.

(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)
(Application Serial No.)	(Filing Date)	(Status) (patented,pending,aband.)

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following attorneys and/or agents to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Giulio A. DeConti, Jr., Esq., (617) 227-7400

Wherefore I petition that letters patent be granted to me for the invention or discovery described and claimed in the attached specification and claims, and hereby subscribe my name to said specification and claims and to the foregoing declaration, power of attorney, and this petition.

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

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aactaaaacg accagctcaa cgcaaaggaa tagtttaaag gtg acc act cca cac 115
Val Thr Thr Pro His
1 5

ttg gat tct gca caa gat att gat ctg tcc cgc gtc cac ctc atc ggt 163
Leu Asp Ser Ala Gln Asp Ile Asp Leu Ser Arg Val His Leu Ile Gly
10 15 20

att ggc gga gcc gga atg tct ggc gtt gcc cga atc ctg ctt gcc cgc 211
Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg Ile Leu Leu Ala Arg
25 30 35

ggt aag aca gtc act ggt tcc gat gcc aaa gat tcc cgc acc ttg ctt 259
Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp Ser Arg Thr Leu Leu
40 45 50

cca ctc cgc gcc gtg gga gcc acc atc gca gtg gga cac gct gcg gaa 307
Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val Gly His Ala Ala Glu
55 60 65

aac ctt gag ctt tcc ggc gaa ctt ccc acc gtc gtg gtg acc tct ttt 355
Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val Val Val Thr Ser Phe
70 75 80 85

gcc gcc att ccg caa gac aac ccg gaa ctt gtt cgt gca cgt gaa gaa 403
Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val Arg Ala Arg Glu Glu
90 95 100

ggc att ccg gtt att cgt cgc tcc gat ctg ttg ggc gaa ttg ctg gaa 451
Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu Gly Glu Leu Leu Glu
105 110 115

ggc tcc acc cag gtc ttg atc gcg ggt acc cac ggt aag acc tcc acc 499
Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His Gly Lys Thr Ser Thr

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        120                 125                 130

acc tct atg tct gtg gta gct atg cag gca gcg ggc atg gat cca agc   547
Thr Ser Met Ser Val Val Ala Met Gln Ala Ala Gly Met Asp Pro Ser
    135                 140                 145

ttt gct atc ggc gga cag ctc aac aag gct ggc acc aat gcg cac cat   595
Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly Thr Asn Ala His His
150                 155                 160                 165

gga act ggt gag gtc ttt atc gct gaa gca gat gaa tct gac gca tcg   643
Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp Glu Ser Asp Ala Ser
                170                 175                 180

ctg ctg cgc tac aag cca aat gtt gca gtg gtc acc aat gtg gaa cca   691
Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val Thr Asn Val Glu Pro
            185                 190                 195

gac cac ctg gac ttc ttt aaa acc cct gaa gcc tac ttc caa gtg ttc   739
Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala Tyr Phe Gln Val Phe
        200                 205                 210

gac gat ttc gca gga cgc atc acc ccg aac ggc aag ctg gtt gtg tgc   787
Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly Lys Leu Val Val Cys
    215                 220                 225

ctg aac gat cct cac gca gcg gag ctg ggg gag agg tct gtc cgc aag   835
Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu Arg Ser Val Arg Lys
230                 235                 240                 245

ggt atc aag act gtt ggt tac ggt acc gct gac gcc gta cag gca cac   883
Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp Ala Val Gln Ala His
                250                 255                 260

cct gag gtt cca gcg atg gct acc atc gtg gat tcc caa gtt gtc gca   931
Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp Ser Gln Val Val Ala
            265                 270                 275

gaa ggc acc cgc gcc acc atc aac atc gat gga cag gaa gta tct gtg   979
Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly Gln Glu Val Ser Val
        280                 285                 290

att ctt caa atc cct ggt gat cac atg gta ctc aac ggt gca gcc gcc  1027
Ile Leu Gln Ile Pro Gly Asp His Met Val Leu Asn Gly Ala Ala Ala
    295                 300                 305

ctg ctg gcc gga tac ctg gtg ggt ggg gac gtc gac aag ctt gtt gaa  1075
Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val Asp Lys Leu Val Glu
310                 315                 320                 325

ggc ttg tcg gat ttc tcc ggc gtg cga cgc cgc ttt gag ttc cac ggt  1123
Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg Phe Glu Phe His Gly
                330                 335                 340

gct atc gag ggc ggc aaa ttt aat ggc gct gct att tat gat gat tac  1171
Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala Ile Tyr Asp Asp Tyr
            345                 350                 355

gca cac cac cca acg gaa gta act gca gtg ctc agc gct gcg cgc acc  1219
Ala His His Pro Thr Glu Val Thr Ala Val Leu Ser Ala Ala Arg Thr
        360                 365                 370
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Sequence Page

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cgg gtg aag gcc gct gga aag ggc cgt gtc atc gtc gcg ttc caa cca   1267
Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile Val Ala Phe Gln Pro
    375                 380                 385

cat tta tac tca cgc acc ata gaa ttc caa aag gag ttc gcg ggg gca   1315
His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys Glu Phe Ala Gly Ala
390                 395                 400                 405

ctg tca ctg gca gac gct gcc gtg gtg ctt gag att tac gga gcg cgc   1363
Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu Ile Tyr Gly Ala Arg
                410                 415                 420

gaa caa ccg gtg gat ggc gtg tcc tcg gaa atc atc acc gat gcg atg   1411
Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile Ile Thr Asp Ala Met
            425                 430                 435

acc att cca gtg gtg tac gaa cct aat ttc tct gca gtc cca gaa cgc   1459
Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser Ala Val Pro Glu Arg
        440                 445                 450

att gca gaa atc gca gga cct aat gac atc gtg ctc acc atg ggt gca   1507
Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val Leu Thr Met Gly Ala
    455                 460                 465

ggt tcc gtg acc atg ctt gct cca gaa atc ctg gat cag ctg caa aac   1555
Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu Asp Gln Leu Gln Asn
470                 475                 480                 485

aat taggacgtaa gtgaacaagg cag                                     1581
Asn
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<210> 2
<211> 486
<212> PRT
<213> Corynebacterium glutamicum

<400> 2

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Val His Leu Ile Gly Ile Gly Gly Ala Gly Met Ser Gly Val Ala Arg
             20                  25                  30

Ile Leu Leu Ala Arg Gly Lys Thr Val Thr Gly Ser Asp Ala Lys Asp
         35                  40                  45

Ser Arg Thr Leu Leu Pro Leu Arg Ala Val Gly Ala Thr Ile Ala Val
     50                  55                  60

Gly His Ala Ala Glu Asn Leu Glu Leu Ser Gly Glu Leu Pro Thr Val
 65                  70                  75                  80

Val Val Thr Ser Phe Ala Ala Ile Pro Gln Asp Asn Pro Glu Leu Val
                 85                  90                  95

Arg Ala Arg Glu Glu Gly Ile Pro Val Ile Arg Arg Ser Asp Leu Leu
            100                 105                 110
```

```
Gly Glu Leu Leu Glu Gly Ser Thr Gln Val Leu Ile Ala Gly Thr His
        115                 120                 125

Gly Lys Thr Ser Thr Thr Ser Met Ser Val Val Ala Met Gln Ala Ala
    130                 135                 140

Gly Met Asp Pro Ser Phe Ala Ile Gly Gly Gln Leu Asn Lys Ala Gly
145                 150                 155                 160

Thr Asn Ala His His Gly Thr Gly Glu Val Phe Ile Ala Glu Ala Asp
                165                 170                 175

Glu Ser Asp Ala Ser Leu Leu Arg Tyr Lys Pro Asn Val Ala Val Val
            180                 185                 190

Thr Asn Val Glu Pro Asp His Leu Asp Phe Phe Lys Thr Pro Glu Ala
        195                 200                 205

Tyr Phe Gln Val Phe Asp Asp Phe Ala Gly Arg Ile Thr Pro Asn Gly
    210                 215                 220

Lys Leu Val Val Cys Leu Asn Asp Pro His Ala Ala Glu Leu Gly Glu
225                 230                 235                 240

Arg Ser Val Arg Lys Gly Ile Lys Thr Val Gly Tyr Gly Thr Ala Asp
                245                 250                 255

Ala Val Gln Ala His Pro Glu Val Pro Ala Met Ala Thr Ile Val Asp
            260                 265                 270

Ser Gln Val Val Ala Glu Gly Thr Arg Ala Thr Ile Asn Ile Asp Gly
        275                 280                 285

Gln Glu Val Ser Val Ile Leu Gln Ile Pro Gly Asp His Met Val Leu
    290                 295                 300

Asn Gly Ala Ala Ala Leu Leu Ala Gly Tyr Leu Val Gly Gly Asp Val
305                 310                 315                 320

Asp Lys Leu Val Glu Gly Leu Ser Asp Phe Ser Gly Val Arg Arg Arg
                325                 330                 335

Phe Glu Phe His Gly Ala Ile Glu Gly Gly Lys Phe Asn Gly Ala Ala
            340                 345                 350

Ile Tyr Asp Asp Tyr Ala His His Pro Thr Glu Val Thr Ala Val Leu
        355                 360                 365

Ser Ala Ala Arg Thr Arg Val Lys Ala Ala Gly Lys Gly Arg Val Ile
    370                 375                 380

Val Ala Phe Gln Pro His Leu Tyr Ser Arg Thr Ile Glu Phe Gln Lys
385                 390                 395                 400

Glu Phe Ala Gly Ala Leu Ser Leu Ala Asp Ala Ala Val Val Leu Glu
                405                 410                 415

Ile Tyr Gly Ala Arg Glu Gln Pro Val Asp Gly Val Ser Ser Glu Ile
            420                 425                 430

Ile Thr Asp Ala Met Thr Ile Pro Val Val Tyr Glu Pro Asn Phe Ser
```

Sequence Page

```
        435                 440                 445

Ala Val Pro Glu Arg Ile Ala Glu Ile Ala Gly Pro Asn Asp Ile Val
    450                 455                 460

Leu Thr Met Gly Ala Gly Ser Val Thr Met Leu Ala Pro Glu Ile Leu
465                 470                 475                 480

Asp Gln Leu Gln Asn Asn
                485
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<210> 3
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXA02705

<400> 3

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ttacagcgac tggctccact tagcggaggt ataaataatt atg ggt tct ctg tcc   115
                                              Met Gly Ser Leu Ser
                                                1               5

cat tta cct cag gcg ctg cag ggc cgt att ctt gtg gcc ggc gct ggt   163
His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu Val Ala Gly Ala Gly
                10                  15                  20

gtt tcc ggc ctg tcc att gca aag atg ctc agt gag ttg cat tgc gat   211
Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser Glu Leu His Cys Asp
            25                  30                  35

gtt gtg gtc gcc gac gat aac gaa act gca cgt cac atg ctc att gaa   259
Val Val Val Ala Asp Asp Asn Glu Thr Ala Arg His Met Leu Ile Glu
        40                  45                  50

gta gta gac gtt gca gat atc agc acc gcg cag gct cag gaa cag ctg   307
Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln Ala Gln Glu Gln Leu
    55                  60                  65

gat tct ttc tcc att gtg gtc acc tcc ccg ggc tgg cgc cca aca agc   355
Asp Ser Phe Ser Ile Val Val Thr Ser Pro Gly Trp Arg Pro Thr Ser
70                  75                  80                  85

act ttg ctt gtc gac gcc cac cgc cag ggc ctt gag gtt atc ggt gac   403
Thr Leu Leu Val Asp Ala His Arg Gln Gly Leu Glu Val Ile Gly Asp
                90                  95                  100

gtc gag ctt gct tgg cgc ctg gac cag gca ggt gtt ttc ggc gag cca   451
Val Glu Leu Ala Trp Arg Leu Asp Gln Ala Gly Val Phe Gly Glu Pro
            105                 110                 115

cat acg tgg ctc gca gtc acc ggc acc aac ggt aaa acc acc acc aca   499
His Thr Trp Leu Ala Val Thr Gly Thr Asn Gly Lys Thr Thr Thr Thr
        120                 125                 130
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tca atg ctc gcc gcg atg atg aat gag ggc ggt ttt act gcc aag gca   547
Ser Met Leu Ala Ala Met Met Asn Glu Gly Gly Phe Thr Ala Lys Ala
    135                 140                 145

gtg ggc aat atc ggc atc ccg gtg tct gag gct ttg gta gcg aaa aac   595
Val Gly Asn Ile Gly Ile Pro Val Ser Glu Ala Leu Val Ala Lys Asn
150                 155                 160                 165

cgc att gat gtg tta gtt gca gag ctg tct agt ttc caa ttg cac tgg   643
Arg Ile Asp Val Leu Val Ala Glu Leu Ser Ser Phe Gln Leu His Trp
                170                 175                 180

tct cca acc ttc acc cct gat gct ggc gtg gtg ctc aac ttg gct gag   691
Ser Pro Thr Phe Thr Pro Asp Ala Gly Val Val Leu Asn Leu Ala Glu
            185                 190                 195

gat cac atc gat tgg cac ggt tcc atg cgt gat tat gcg ttg gcc aag   739
Asp His Ile Asp Trp His Gly Ser Met Arg Asp Tyr Ala Leu Ala Lys
        200                 205                 210

atg gaa gtg ctc aag ggc aag gtc gcc atc att ggg gca gac gat cct   787
Met Glu Val Leu Lys Gly Lys Val Ala Ile Ile Gly Ala Asp Asp Pro
    215                 220                 225

tat ttg gtg cag ctg act tct gaa gca gac ttg agt ggt ctc att gga   835
Tyr Leu Val Gln Leu Thr Ser Glu Ala Asp Leu Ser Gly Leu Ile Gly
230                 235                 240                 245

ttt acc gtc aat gag cct gca acc ggc cag ttg ggt gtg aaa gcg ggg   883
Phe Thr Val Asn Glu Pro Ala Thr Gly Gln Leu Gly Val Lys Ala Gly
                250                 255                 260

gag ctc gtc gat aat gcc tac ggc aat aat gtg gtg ctt gca tcc gct   931
Glu Leu Val Asp Asn Ala Tyr Gly Asn Asn Val Val Leu Ala Ser Ala
            265                 270                 275

gac ggc att aat ccc gcc ggc cct gcc ggt gtt ttg gac gct ttg gct   979
Asp Gly Ile Asn Pro Ala Gly Pro Ala Gly Val Leu Asp Ala Leu Ala
        280                 285                 290

gca gct gcg gtg gcg cgc tcg cag ggc gtg gca cct gag gcg atc gcg   1027
Ala Ala Ala Val Ala Arg Ser Gln Gly Val Ala Pro Glu Ala Ile Ala
    295                 300                 305

cgt gcg ttg gat tct ttt gag gtg gca ggc cac cgt ggc cag gtc gtc   1075
Arg Ala Leu Asp Ser Phe Glu Val Ala Gly His Arg Gly Gln Val Val
310                 315                 320                 325

gcc gag cat gac ggt gtt cat ttc att gac aac tcc aag gcg acc aac   1123
Ala Glu His Asp Gly Val His Phe Ile Asp Asn Ser Lys Ala Thr Asn
                330                 335                 340

ccc cac gct gct gat tct gcg cta gct ggg cat gat tca gtc att tgg   1171
Pro His Ala Ala Asp Ser Ala Leu Ala Gly His Asp Ser Val Ile Trp
            345                 350                 355

gtt gtc ggc gga cag ctc aaa ggc gcg gac att gcg cca ctg gtg aaa   1219
Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile Ala Pro Leu Val Lys
        360                 365                 370

aag cac gaa cag cgc atc aag gca gca ttg gtg ttg ggc gca gat cgt   1267
```

Applicant's Copy

```
Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val Leu Gly Ala Asp Arg
    375                 380                 385

gct gaa atc gtg gca gcg ttg aag gaa cac gcg tcg cag gcc tct gta   1315
Ala Glu Ile Val Ala Ala Leu Lys Glu His Ala Ser Gln Ala Ser Val
390                 395                 400                 405

ttt gtc act gac aag acg gag cca ttt gag gca atg gaa gaa atc gtc   1363
Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala Met Glu Glu Ile Val
                410                 415                 420

act gag gca ttt agc atc agc gaa ccc ggc gat acc gtg ttg ctt gcc   1411
Thr Glu Ala Phe Ser Ile Ser Glu Pro Gly Asp Thr Val Leu Leu Ala
            425                 430                 435

cct gcc gct gcg tct ttg gac atg ttc aaa ggc atg ggc cag cgt ggc   1459
Pro Ala Ala Ala Ser Leu Asp Met Phe Lys Gly Met Gly Gln Arg Gly
        440                 445                 450

gac ctc ttt gca cac aac atc att ggc aca atc aaa gga tta acg gaa   1507
Asp Leu Phe Ala His Asn Ile Ile Gly Thr Ile Lys Gly Leu Thr Glu
    455                 460                 465

gag aaa ggc tgatcatgac caccggagcc tca                            1539
Glu Lys Gly
470
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<210> 4
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 4

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Met Gly Ser Leu Ser His Leu Pro Gln Ala Leu Gln Gly Arg Ile Leu
  1               5                  10                  15

Val Ala Gly Ala Gly Val Ser Gly Leu Ser Ile Ala Lys Met Leu Ser
             20                  25                  30

Glu Leu His Cys Asp Val Val Val Ala Asp Asp Asn Glu Thr Ala Arg
         35                  40                  45

His Met Leu Ile Glu Val Val Asp Val Ala Asp Ile Ser Thr Ala Gln
     50                  55                  60

Ala Gln Glu Gln Leu Asp Ser Phe Ser Ile Val Val Thr Ser Pro Gly
 65                  70                  75                  80

Trp Arg Pro Thr Ser Thr Leu Leu Val Asp Ala His Arg Gln Gly Leu
                 85                  90                  95

Glu Val Ile Gly Asp Val Glu Leu Ala Trp Arg Leu Asp Gln Ala Gly
            100                 105                 110

Val Phe Gly Glu Pro His Thr Trp Leu Ala Val Thr Gly Thr Asn Gly
        115                 120                 125

Lys Thr Thr Thr Thr Ser Met Leu Ala Ala Met Met Asn Glu Gly Gly
    130                 135                 140
```

```
Phe Thr Ala Lys Ala Val Gly Asn Ile Gly Ile Pro Val Ser Glu Ala
145                 150                 155                 160

Leu Val Ala Lys Asn Arg Ile Asp Val Leu Val Ala Glu Leu Ser Ser
                165                 170                 175

Phe Gln Leu His Trp Ser Pro Thr Phe Thr Pro Asp Ala Gly Val Val
            180                 185                 190

Leu Asn Leu Ala Glu Asp His Ile Asp Trp His Gly Ser Met Arg Asp
        195                 200                 205

Tyr Ala Leu Ala Lys Met Glu Val Leu Lys Gly Lys Val Ala Ile Ile
    210                 215                 220

Gly Ala Asp Asp Pro Tyr Leu Val Gln Leu Thr Ser Glu Ala Asp Leu
225                 230                 235                 240

Ser Gly Leu Ile Gly Phe Thr Val Asn Glu Pro Ala Thr Gly Gln Leu
                245                 250                 255

Gly Val Lys Ala Gly Glu Leu Val Asp Asn Ala Tyr Gly Asn Asn Val
            260                 265                 270

Val Leu Ala Ser Ala Asp Gly Ile Asn Pro Ala Gly Pro Ala Gly Val
        275                 280                 285

Leu Asp Ala Leu Ala Ala Ala Ala Val Ala Arg Ser Gln Gly Val Ala
    290                 295                 300

Pro Glu Ala Ile Ala Arg Ala Leu Asp Ser Phe Glu Val Ala Gly His
305                 310                 315                 320

Arg Gly Gln Val Val Ala Glu His Asp Gly Val His Phe Ile Asp Asn
                325                 330                 335

Ser Lys Ala Thr Asn Pro His Ala Ala Asp Ser Ala Leu Ala Gly His
            340                 345                 350

Asp Ser Val Ile Trp Val Val Gly Gly Gln Leu Lys Gly Ala Asp Ile
        355                 360                 365

Ala Pro Leu Val Lys Lys His Glu Gln Arg Ile Lys Ala Ala Leu Val
    370                 375                 380

Leu Gly Ala Asp Arg Ala Glu Ile Val Ala Ala Leu Lys Glu His Ala
385                 390                 395                 400

Ser Gln Ala Ser Val Phe Val Thr Asp Lys Thr Glu Pro Phe Glu Ala
                405                 410                 415

Met Glu Glu Ile Val Thr Glu Ala Phe Ser Ile Ser Glu Pro Gly Asp
            420                 425                 430

Thr Val Leu Leu Ala Pro Ala Ala Ala Ser Leu Asp Met Phe Lys Gly
        435                 440                 445

Met Gly Gln Arg Gly Asp Leu Phe Ala His Asn Ile Ile Gly Thr Ile
    450                 455                 460

Lys Gly Leu Thr Glu Glu Lys Gly
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Sequence Listing

465 470

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<211> 1392
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1369)
<223> RXA01254

<400> 5
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aaaagcgcta gtgccacttg cttaactaga ctcgtttttc atg aag ctt tca ctg 115
Met Lys Leu Ser Leu
1 5

cct gca ccc cta cgc cgt tta cgc agc gct gcc gcc atc atc tca gca 163
Pro Ala Pro Leu Arg Arg Leu Arg Ser Ala Ala Ala Ile Ile Ser Ala
10 15 20

aaa gtt gcg aca tcc gcg tcc aaa gcc aca ggt cgc gga tcc ggt ggc 211
Lys Val Ala Thr Ser Ala Ser Lys Ala Thr Gly Arg Gly Ser Gly Gly
25 30 35

atg atc ggc gga ctg gtg gcc agc aag gta gac ccg gac atc atg tcc 259
Met Ile Gly Gly Leu Val Ala Ser Lys Val Asp Pro Asp Ile Met Ser
40 45 50

aac ctc atc aac aac cgc cca aca gtg ctg gtc acg ggc aca aat ggc 307
Asn Leu Ile Asn Asn Arg Pro Thr Val Leu Val Thr Gly Thr Asn Gly
55 60 65

aag tcc acc acc acc cgc atg ctg gcc gcc gcg atg cgc agc act tac 355
Lys Ser Thr Thr Thr Arg Met Leu Ala Ala Ala Met Arg Ser Thr Tyr
70 75 80 85

acc gtc gcc acc aat gaa ggc ggc gac aac atg gac gcc ggc atc att 403
Thr Val Ala Thr Asn Glu Gly Gly Asp Asn Met Asp Ala Gly Ile Ile
90 95 100

tct gcg ctg ctc gct ggc cga aac gcc tca cac gtg gtc ttg gaa gtc 451
Ser Ala Leu Leu Ala Gly Arg Asn Ala Ser His Val Val Leu Glu Val
105 110 115

gat gag ctg cac gta ccc gcc gcc atc gaa cgc ctc aag ccc gac gcc 499
Asp Glu Leu His Val Pro Ala Ala Ile Glu Arg Leu Lys Pro Asp Ala
120 125 130

ctc gtg ctg ctc aac ctt tcc cgc gac cag ctc gac cgc gtt ggc gaa 547
Leu Val Leu Leu Asn Leu Ser Arg Asp Gln Leu Asp Arg Val Gly Glu
135 140 145

att aac aaa atc gaa cgt gtc ctg cgc gat gcc gtg cgc tct cga cct 595
Ile Asn Lys Ile Glu Arg Val Leu Arg Asp Ala Val Arg Ser Arg Pro
150 155 160 165

gag atg acc gtc atc gcc aac tgc gac gac gtc ctc gtt acc tcc gtg 643

```
Glu Met Thr Val Ile Ala Asn Cys Asp Asp Val Leu Val Thr Ser Val
                170                 175                 180

gct ttc gac gcc gaa aac gtc atc tgg gtc ggc gcc ggc acc ggc tgg   691
Ala Phe Asp Ala Glu Asn Val Ile Trp Val Gly Ala Gly Thr Gly Trp
            185                 190                 195

caa ggt gaa tcc gcc acc tgc cca cgc acc gaa tcc cgc atc ctc cac   739
Gln Gly Glu Ser Ala Thr Cys Pro Arg Thr Glu Ser Arg Ile Leu His
        200                 205                 210

gac gga cgc cac tgg agc gcc gaa aag acg ctt ctc gac ggc cgc acc   787
Asp Gly Arg His Trp Ser Ala Glu Lys Thr Leu Leu Asp Gly Arg Thr
    215                 220                 225

ttc gca cgc ccc acc ccc tca tgg gag gtt gac ggt gat acc atc cat   835
Phe Ala Arg Pro Thr Pro Ser Trp Glu Val Asp Gly Asp Thr Ile His
230                 235                 240                 245

tca cca tcc ggc gat ctc acc ttg gat ctc aac ctc cca ggt cag gcc   883
Ser Pro Ser Gly Asp Leu Thr Leu Asp Leu Asn Leu Pro Gly Gln Ala
                250                 255                 260

aac cgt ggc aac gcg gca caa gca atc gca gcc tcc acc gta ttt aat   931
Asn Arg Gly Asn Ala Ala Gln Ala Ile Ala Ala Ser Thr Val Phe Asn
            265                 270                 275

gtg ccc gtt tcc tcc gca ctg ccc gca gtc aac tcc gtc aac aac gtt   979
Val Pro Val Ser Ser Ala Leu Pro Ala Val Asn Ser Val Asn Asn Val
        280                 285                 290

gct gga cgc tat tcc acc atc act gtc ggt gaa cac aag gtc cac ctc   1027
Ala Gly Arg Tyr Ser Thr Ile Thr Val Gly Glu His Lys Val His Leu
    295                 300                 305

ctg ctc gcc aaa aac cca gca ggc tgg caa gaa gcc ctc tcc atg gtt   1075
Leu Leu Ala Lys Asn Pro Ala Gly Trp Gln Glu Ala Leu Ser Met Val
310                 315                 320                 325

gat cgc aca gct gat ggc tta gtc atc gtc gtc aat ggc cag gtt gcc   1123
Asp Arg Thr Ala Asp Gly Leu Val Ile Val Val Asn Gly Gln Val Ala
                330                 335                 340

gac ggc gaa gac ctc tcc tgg ctt tgg gac gtc cgc ttc gaa gac ttc   1171
Asp Gly Glu Asp Leu Ser Trp Leu Trp Asp Val Arg Phe Glu Asp Phe
            345                 350                 355

gaa aac ctc tcc gtc aaa gcc tcc ggc gag cgc ggc acc gac ctg gca   1219
Glu Asn Leu Ser Val Lys Ala Ser Gly Glu Arg Gly Thr Asp Leu Ala
        360                 365                 370

gtc cgc ctc acc tac gcc gaa atc gac cac gaa ctc atc tcc aac ccc   1267
Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu Leu Ile Ser Asn Pro
    375                 380                 385

gtc gac gcc atc gca gcc tgc cct cct ggc cgc atc gaa gtc ctc gcc   1315
Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg Ile Glu Val Leu Ala
390                 395                 400                 405

aac tac acc gca ttc cga gac ctc aaa aag gct ctg gag aaa ggg acc   1363
Asn Tyr Thr Ala Phe Arg Asp Leu Lys Lys Ala Leu Glu Lys Gly Thr
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410 415 420

gaa caa taatgaccac cctcaacatc ggc 1392
Glu Gln

<210> 6
<211> 423
<212> PRT
<213> Corynebacterium glutamicum

<400> 6

Met	Lys	Leu	Ser	Leu	Pro	Ala	Pro	Leu	Arg	Arg	Leu	Arg	Ser	Ala	Ala
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Ala	Ile	Ile	Ser	Ala	Lys	Val	Ala	Thr	Ser	Ala	Ser	Lys	Ala	Thr	Gly
		20					25					30			
Arg	Gly	Ser	Gly	Gly	Met	Ile	Gly	Gly	Leu	Val	Ala	Ser	Lys	Val	Asp
	35					40					45				
Pro	Asp	Ile	Met	Ser	Asn	Leu	Ile	Asn	Asn	Arg	Pro	Thr	Val	Leu	Val
50					55					60					
Thr	Gly	Thr	Asn	Gly	Lys	Ser	Thr	Thr	Thr	Arg	Met	Leu	Ala	Ala	Ala
65				70					75						80
Met	Arg	Ser	Thr	Tyr	Thr	Val	Ala	Thr	Asn	Glu	Gly	Gly	Asp	Asn	Met
			85					90					95		
Asp	Ala	Gly	Ile	Ile	Ser	Ala	Leu	Leu	Ala	Gly	Arg	Asn	Ala	Ser	His
		100					105					110			
Val	Val	Leu	Glu	Val	Asp	Glu	Leu	His	Val	Pro	Ala	Ala	Ile	Glu	Arg
	115					120					125				
Leu	Lys	Pro	Asp	Ala	Leu	Val	Leu	Leu	Asn	Leu	Ser	Arg	Asp	Gln	Leu
130					135					140					
Asp	Arg	Val	Gly	Glu	Ile	Asn	Lys	Ile	Glu	Arg	Val	Leu	Arg	Asp	Ala
145				150					155						160
Val	Arg	Ser	Arg	Pro	Glu	Met	Thr	Val	Ile	Ala	Asn	Cys	Asp	Asp	Val
			165					170					175		
Leu	Val	Thr	Ser	Val	Ala	Phe	Asp	Ala	Glu	Asn	Val	Ile	Trp	Val	Gly
		180					185					190			
Ala	Gly	Thr	Gly	Trp	Gln	Gly	Glu	Ser	Ala	Thr	Cys	Pro	Arg	Thr	Glu
	195					200					205				
Ser	Arg	Ile	Leu	His	Asp	Gly	Arg	His	Trp	Ser	Ala	Glu	Lys	Thr	Leu
210					215					220					
Leu	Asp	Gly	Arg	Thr	Phe	Ala	Arg	Pro	Thr	Pro	Ser	Trp	Glu	Val	Asp
225				230					235						240
Gly	Asp	Thr	Ile	His	Ser	Pro	Ser	Gly	Asp	Leu	Thr	Leu	Asp	Leu	Asn
			245					250					255		

```
Leu Pro Gly Gln Ala Asn Arg Gly Asn Ala Ala Gln Ala Ile Ala Ala
            260                 265                 270

Ser Thr Val Phe Asn Val Pro Val Ser Ser Ala Leu Pro Ala Val Asn
        275                 280                 285

Ser Val Asn Asn Val Ala Gly Arg Tyr Ser Thr Ile Thr Val Gly Glu
    290                 295                 300

His Lys Val His Leu Leu Leu Ala Lys Asn Pro Ala Gly Trp Gln Glu
305                 310                 315                 320

Ala Leu Ser Met Val Asp Arg Thr Ala Asp Gly Leu Val Ile Val Val
                325                 330                 335

Asn Gly Gln Val Ala Asp Gly Glu Asp Leu Ser Trp Leu Trp Asp Val
            340                 345                 350

Arg Phe Glu Asp Phe Glu Asn Leu Ser Val Lys Ala Ser Gly Glu Arg
        355                 360                 365

Gly Thr Asp Leu Ala Val Arg Leu Thr Tyr Ala Glu Ile Asp His Glu
    370                 375                 380

Leu Ile Ser Asn Pro Val Asp Ala Ile Ala Ala Cys Pro Pro Gly Arg
385                 390                 395                 400

Ile Glu Val Leu Ala Asn Tyr Thr Ala Phe Arg Asp Leu Lys Lys Ala
                405                 410                 415

Leu Glu Lys Gly Thr Glu Gln
            420
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Sequence Listing

<210> 7
<211> 1653
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1630)
<223> RXN02707

<400> 7

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ccttactacg gaagaaggat aggccacagt catgatcaca atg acc ctt ggg gaa   115
                                          Met Thr Leu Gly Glu
                                            1               5

atc gct gac atc gtt gga ggc agg ctt act ggc ggt gct caa gaa gat   163
Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly Gly Ala Gln Glu Asp
                10                  15                  20

acg ctt gtg agc tcc agc gtg gag ttt gat tct cga tcc ctc aca ccg   211
Thr Leu Val Ser Ser Ser Val Glu Phe Asp Ser Arg Ser Leu Thr Pro
            25                  30                  35

ggt ggc ttg ttt tta gca ctt ccg ggt gct cgt gta gac ggc cat gat   259
Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg Val Asp Gly His Asp
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```
         40                  45                  50

ttt gct gca act gca att gag aaa ggt gcg gtt gca gta ttg gca gcc   307
Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val Ala Val Leu Ala Ala
     55                  60                  65

cgt gag gtt gac gta cct gcg atc gtc gtg cct cca gta aaa atc cag   355
Arg Glu Val Asp Val Pro Ala Ile Val Val Pro Pro Val Lys Ile Gln
 70                  75                  80                  85

gaa tcc aat gct gac att tat gct cat gat cca gat ggg cat ggc gcg   403
Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro Asp Gly His Gly Ala
                 90                  95                 100

gcg gta gtg gag gcg ttg tct cgg ttg gct cgc cac gtg gtg gat atc   451
Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg His Val Val Asp Ile
            105                 110                 115

tgc gtg gct ggc cat caa ttg aac gtt gtg gct att act ggt tct gcg   499
Cys Val Ala Gly His Gln Leu Asn Val Val Ala Ile Thr Gly Ser Ala
        120                 125                 130

gga aag act tct acg aag gat ttc atc gcg acg gtt ctt gac caa gat   547
Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr Val Leu Asp Gln Asp
    135                 140                 145

ggg cca act gtg gct cct ccg ggc tcg ttt aac aat gag ctt ggt ttg   595
Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn Asn Glu Leu Gly Leu
150                 155                 160                 165

cca cac acc gcg ctc cgc tgc aca acc gat act aag tat ttg gtg gct   643
Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr Lys Tyr Leu Val Ala
                170                 175                 180

gag atg tcc gcg cgt ggc att gga cat att aag cac ctg aca gag att   691
Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys His Leu Thr Glu Ile
            185                 190                 195

gct ccg cca cgg att gca gct gtg ctc aac gtc ggc cat gcg cac ctg   739
Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val Gly His Ala His Leu
        200                 205                 210

ggt gaa ttt gga tcc cgc gag aat atc gcg cag gca aaa ggc gag atc   787
Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln Ala Lys Gly Glu Ile
    215                 220                 225

att gaa gcg ctg ccc tcg aag aaa acg agc tcg gta cca gtc ctg aat   835
Ile Glu Ala Leu Pro Ser Lys Lys Thr Ser Ser Val Pro Val Leu Asn
230                 235                 240                 245

act gat cct ttt gtc gcc cgg atg gct cca cgc act aag gcg cgc gtg   883
Thr Asp Pro Phe Val Ala Arg Met Ala Pro Arg Thr Lys Ala Arg Val
                250                 255                 260

gtg tgg ttt acc acc gat gca ggc caa gca aaa aag tct gat tat tgg   931
Val Trp Phe Thr Thr Asp Ala Gly Gln Ala Lys Lys Ser Asp Tyr Trp
            265                 270                 275

gca acg agt att tca ctg gac gct gtt gcg cgg gca agc ttt acg ctg   979
Ala Thr Ser Ile Ser Leu Asp Ala Val Ala Arg Ala Ser Phe Thr Leu
        280                 285                 290
```

```
aac acg aag gac ggc tct tgg ccg gtc acc ctg cag gtt ttt ggt gag   1027
Asn Thr Lys Asp Gly Ser Trp Pro Val Thr Leu Gln Val Phe Gly Glu
    295                 300                 305

cac cag gtt gct aat gca ctt gct gct gct gcc att gcc atg gaa gct   1075
His Gln Val Ala Asn Ala Leu Ala Ala Ala Ala Ile Ala Met Glu Ala
310                 315                 320                 325

ggc gtc gcc cca gaa ttg gtg gtt gct gga ttg gaa gca cat tca gct   1123
Gly Val Ala Pro Glu Leu Val Val Ala Gly Leu Glu Ala His Ser Ala
                330                 335                 340

gct tcc gcg cac cgc atg gat gta aag acc cgt gcc gac ggc gtg acc   1171
Ala Ser Ala His Arg Met Asp Val Lys Thr Arg Ala Asp Gly Val Thr
            345                 350                 355

atc atc aac gat tct tac aac gcg aat cct gat tct atg cgt gca ggt   1219
Ile Ile Asn Asp Ser Tyr Asn Ala Asn Pro Asp Ser Met Arg Ala Gly
        360                 365                 370

atc gcg gct ctt gcg tac aca gct agt ggt cgt tct gaa gca aca agc   1267
Ile Ala Ala Leu Ala Tyr Thr Ala Ser Gly Arg Ser Glu Ala Thr Ser
    375                 380                 385

tgg gca gtg ctt ggc caa atg ggt gag ctt ggc gat gac gcc tcg gaa   1315
Trp Ala Val Leu Gly Gln Met Gly Glu Leu Gly Asp Asp Ala Ser Glu
390                 395                 400                 405

gcc cat gcc gaa ctt ggt gct gag ctg gct aaa tac aat gtt caa gaa   1363
Ala His Ala Glu Leu Gly Ala Glu Leu Ala Lys Tyr Asn Val Gln Glu
                410                 415                 420

ctt gtc gca gtg ggg gag aac cct aac tgt gca gca ctt gca gag tcc   1411
Leu Val Ala Val Gly Glu Asn Pro Asn Cys Ala Ala Leu Ala Glu Ser
            425                 430                 435

gca gcg agc ctg ggt gtg agt act cac gta gtt tca gac gtt gat gca   1459
Ala Ala Ser Leu Gly Val Ser Thr His Val Val Ser Asp Val Asp Ala
        440                 445                 450

gcg ctc gag ttg ctc gca ggc cat att aag cgg gat gat gta gtg ctg   1507
Ala Leu Glu Leu Leu Ala Gly His Ile Lys Arg Asp Asp Val Val Leu
    455                 460                 465

gtt aag gct tca aat gct gat cgc ctg tgg agg gtc gca gaa gca cta   1555
Val Lys Ala Ser Asn Ala Asp Arg Leu Trp Arg Val Ala Glu Ala Leu
470                 475                 480                 485

cat ggc atg gtg ccg ggc ctc aaa aac aca ggt ggc tcg gtc aac gac   1603
His Gly Met Val Pro Gly Leu Lys Asn Thr Gly Gly Ser Val Asn Asp
                490                 495                 500

gat tct cgt cgg aac gtg gaa gga cag tagaaaacaa tgcaacagat         1650
Asp Ser Arg Arg Asn Val Glu Gly Gln
            505                 510

tat                                                              1653
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<210> 8

<211> 510
<212> PRT
<213> Corynebacterium glutamicum

<400> 8

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Met Thr Leu Gly Glu Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly
  1               5                  10                  15

Gly Ala Gln Glu Asp Thr Leu Val Ser Ser Ser Val Glu Phe Asp Ser
             20                  25                  30

Arg Ser Leu Thr Pro Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg
         35                  40                  45

Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
     50                  55                  60

Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
 65                  70                  75                  80

Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
                 85                  90                  95

Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
            100                 105                 110

His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
        115                 120                 125

Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
    130                 135                 140

Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
145                 150                 155                 160

Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
                165                 170                 175

Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
            180                 185                 190

His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
        195                 200                 205

Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
    210                 215                 220

Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ser Ser
225                 230                 235                 240

Val Pro Val Leu Asn Thr Asp Pro Phe Val Ala Arg Met Ala Pro Arg
                245                 250                 255

Thr Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala Gly Gln Ala Lys
            260                 265                 270

Lys Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp Ala Val Ala Arg
        275                 280                 285

Ala Ser Phe Thr Leu Asn Thr Lys Asp Gly Ser Trp Pro Val Thr Leu
    290                 295                 300
```

```
Gln Val Phe Gly Glu His Gln Val Ala Asn Ala Leu Ala Ala Ala Ala
305                 310                 315                 320

Ile Ala Met Glu Ala Gly Val Ala Pro Glu Leu Val Val Ala Gly Leu
                325                 330                 335

Glu Ala His Ser Ala Ala Ser Ala His Arg Met Asp Val Lys Thr Arg
            340                 345                 350

Ala Asp Gly Val Thr Ile Ile Asn Asp Ser Tyr Asn Ala Asn Pro Asp
        355                 360                 365

Ser Met Arg Ala Gly Ile Ala Ala Leu Ala Tyr Thr Ala Ser Gly Arg
    370                 375                 380

Ser Glu Ala Thr Ser Trp Ala Val Leu Gly Gln Met Gly Glu Leu Gly
385                 390                 395                 400

Asp Asp Ala Ser Glu Ala His Ala Glu Leu Gly Ala Glu Leu Ala Lys
                405                 410                 415

Tyr Asn Val Gln Glu Leu Val Ala Val Gly Glu Asn Pro Asn Cys Ala
            420                 425                 430

Ala Leu Ala Glu Ser Ala Ala Ser Leu Gly Val Ser Thr His Val Val
        435                 440                 445

Ser Asp Val Asp Ala Ala Leu Glu Leu Leu Ala Gly His Ile Lys Arg
    450                 455                 460

Asp Asp Val Val Leu Val Lys Ala Ser Asn Ala Asp Arg Leu Trp Arg
465                 470                 475                 480

Val Ala Glu Ala Leu His Gly Met Val Pro Gly Leu Lys Asn Thr Gly
                485                 490                 495

Gly Ser Val Asn Asp Asp Ser Arg Arg Asn Val Glu Gly Gln
            500                 505                 510
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<210> 9
<211> 468
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(445)
<223> FRXA02707

<400> 9

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tacaacgcga atcctgattc tatgcgtgca ggtatcgcgg ctcttgcgta cacagctagt 60

ggtcgttctg aagcaacaaa gctgggcagt gcttggccaa atg ggt gag ctt ggc   115
                                              Met Gly Glu Leu Gly
                                                1               5

gat gac gcc tcg gaa gcc cat gcc gaa ctt ggt gct gag ctg gct aaa   163
Asp Asp Ala Ser Glu Ala His Ala Glu Leu Gly Ala Glu Leu Ala Lys
                  10                  15                  20
```

US-10-605-145A-9

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tac aat gtt caa gaa ctt gtc gca gtg ggg gag aac cct aac tgt gca   211
Tyr Asn Val Gln Glu Leu Val Ala Val Gly Glu Asn Pro Asn Cys Ala
             25                  30                  35

gca ctt gca gag tcc gca gcg agc ctg ggt gtg agt act cac gta gtt   259
Ala Leu Ala Glu Ser Ala Ala Ser Leu Gly Val Ser Thr His Val Val
         40                  45                  50

tca gac gtt gat gca gcg ctc gag ttg ctc gca ggc cat att aag cgg   307
Ser Asp Val Asp Ala Ala Leu Glu Leu Leu Ala Gly His Ile Lys Arg
     55                  60                  65

gat gat gta gtg ctg gtt aag gct tca aat gct gat cgc ctg tgg agg   355
Asp Asp Val Val Leu Val Lys Ala Ser Asn Ala Asp Arg Leu Trp Arg
 70                  75                  80                  85

gtc gca gaa gca cta cat ggc atg gtg ccg ggc ctc aaa aac aca ggt   403
Val Ala Glu Ala Leu His Gly Met Val Pro Gly Leu Lys Asn Thr Gly
                 90                  95                 100

ggc tcg gtc aac gac gat tct cgt cgg aac gtg gaa gga cag           445
Gly Ser Val Asn Asp Asp Ser Arg Arg Asn Val Glu Gly Gln
            105                 110                 115

tagaaaacaa tgcaacagat tat                                        468
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<210> 10
<211> 115
<212> PRT
<213> Corynebacterium glutamicum

<400> 10

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Met Gly Glu Leu Gly Asp Asp Ala Ser Glu Ala His Ala Glu Leu Gly
  1               5                  10                  15

Ala Glu Leu Ala Lys Tyr Asn Val Gln Glu Leu Val Ala Val Gly Glu
             20                  25                  30

Asn Pro Asn Cys Ala Ala Leu Ala Glu Ser Ala Ala Ser Leu Gly Val
         35                  40                  45

Ser Thr His Val Val Ser Asp Val Asp Ala Ala Leu Glu Leu Leu Ala
     50                  55                  60

Gly His Ile Lys Arg Asp Asp Val Val Leu Val Lys Ala Ser Asn Ala
 65                  70                  75                  80

Asp Arg Leu Trp Arg Val Ala Glu Ala Leu His Gly Met Val Pro Gly
                 85                  90                  95

Leu Lys Asn Thr Gly Gly Ser Val Asn Asp Asp Ser Arg Arg Asn Val
            100                 105                 110

Glu Gly Gln
        115
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<210> 11
<211> 558

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(535)
<223> FRXA02708

<400> 11
gagaatatcg cgcaggcaaa aggcgagatc attgaagcgc tgccctcgaa gaaaacggct 60

cggtaccagt cctgaatact aggatccttt tgtcgcccgg atg gct cca cgc act 115
Met Ala Pro Arg Thr
1 5

aag gcg cgc gtg gtg tgg ttt acc acc gat gca ggc caa gca aaa aag 163
Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala Gly Gln Ala Lys Lys
10 15 20

tct gat tat tgg gca acg agt att tca ctg gac gct gtt gcg cgg gca 211
Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp Ala Val Ala Arg Ala
25 30 35

agc ttt acg ctg aac acg aag gac ggc tct tgg ccg gtc acc ctg cag 259
Ser Phe Thr Leu Asn Thr Lys Asp Gly Ser Trp Pro Val Thr Leu Gln
40 45 50

gtt ttt ggt gag cac cag gtt gct aat gca ctt gct gct gct gcc att 307
Val Phe Gly Glu His Gln Val Ala Asn Ala Leu Ala Ala Ala Ala Ile
55 60 65

gcc atg gaa gct ggc gtc gcc cca gaa ttg gtg gtt gct gga ttg gaa 355
Ala Met Glu Ala Gly Val Ala Pro Glu Leu Val Val Ala Gly Leu Glu
70 75 80 85

gca cat tca gct gct tcc gcg cac cgc atg gat gta aag acc cgt gcc 403
Ala His Ser Ala Ala Ser Ala His Arg Met Asp Val Lys Thr Arg Ala
90 95 100

gac ggc gtg acc atc atc aac gat tct tac aac gcg aat cct gat tct 451
Asp Gly Val Thr Ile Ile Asn Asp Ser Tyr Asn Ala Asn Pro Asp Ser
105 110 115

atg cgt gca ggt atc gcg gct ctt gcg tac aca gct agt ggt cgt tct 499
Met Arg Ala Gly Ile Ala Ala Leu Ala Tyr Thr Ala Ser Gly Arg Ser
120 125 130

gaa gca aca aag ctg ggc agt gct tgg cca aat ggg tgagcttggc 545
Glu Ala Thr Lys Leu Gly Ser Ala Trp Pro Asn Gly
135 140 145

gatgacgcct cgg 558

<210> 12
<211> 145
<212> PRT
<213> Corynebacterium glutamicum

<400> 12
Met Ala Pro Arg Thr Lys Ala Arg Val Val Trp Phe Thr Thr Asp Ala

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  1               5                  10                  15

Gly Gln Ala Lys Lys Ser Asp Tyr Trp Ala Thr Ser Ile Ser Leu Asp
            20                  25                  30

Ala Val Ala Arg Ala Ser Phe Thr Leu Asn Thr Lys Asp Gly Ser Trp
        35                  40                  45

Pro Val Thr Leu Gln Val Phe Gly Glu His Gln Val Ala Asn Ala Leu
    50                  55                  60

Ala Ala Ala Ala Ile Ala Met Glu Ala Gly Val Ala Pro Glu Leu Val
65                  70                  75                  80

Val Ala Gly Leu Glu Ala His Ser Ala Ala Ser Ala His Arg Met Asp
                85                  90                  95

Val Lys Thr Arg Ala Asp Gly Val Thr Ile Ile Asn Asp Ser Tyr Asn
            100                 105                 110

Ala Asn Pro Asp Ser Met Arg Ala Gly Ile Ala Ala Leu Ala Tyr Thr
        115                 120                 125

Ala Ser Gly Arg Ser Glu Ala Thr Lys Leu Gly Ser Ala Trp Pro Asn
    130                 135                 140

Gly
145
```

Pgp9pkt_95pct

<210> 13
<211> 852
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(829)
<223> FRXA02709

<400> 13

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ccttactacg gaagaaggat aggccacagt catgatcaca atg acc ctt ggg gaa   115
                                              Met Thr Leu Gly Glu
                                                1               5

atc gct gac atc gtt gga ggc agg ctt act ggc ggt gct caa gaa gat   163
Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly Gly Ala Gln Glu Asp
                10                  15                  20

acg ctt gtg agc tcc agc gtg gag ttt gat tct cga tcc ctc aca ccg   211
Thr Leu Val Ser Ser Ser Val Glu Phe Asp Ser Arg Ser Leu Thr Pro
            25                  30                  35

ggt ggc ttg ttt tta gca ctt ccg ggt gct cgt gta gac ggc cat gat   259
Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg Val Asp Gly His Asp
        40                  45                  50

ttt gct gca act gca att gag aaa ggt gcg gtt gca gta ttg gca gcc   307
Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val Ala Val Leu Ala Ala
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55 60 65

cgt gag gtt gac gta cct gcg atc gtc gtg cct cca gta aaa atc cag 355
Arg Glu Val Asp Val Pro Ala Ile Val Val Pro Pro Val Lys Ile Gln
70 75 80 85

gaa tcc aat gct gac att tat gct cat gat cca gat ggg cat ggc gcg 403
Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro Asp Gly His Gly Ala
90 95 100

gcg gta gtg gag gcg ttg tct cgg ttg gct cgc cac gtg gtg gat atc 451
Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg His Val Val Asp Ile
105 110 115

tgc gtg gct ggc cat caa ttg aac gtt gtg gct att act ggt tct gcg 499
Cys Val Ala Gly His Gln Leu Asn Val Val Ala Ile Thr Gly Ser Ala
120 125 130

gga aag act tct acg aag gat ttc atc gcg acg gtt ctt gac caa gat 547
Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr Val Leu Asp Gln Asp
135 140 145

ggg cca act gtg gct cct ccg ggc tcg ttt aac aat gag ctt ggt ttg 595
Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn Asn Glu Leu Gly Leu
150 155 160 165

cca cac acc gcg ctc cgc tgc aca acc gat act aag tat ttg gtg gct 643
Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr Lys Tyr Leu Val Ala
170 175 180

gag atg tcc gcg cgt ggc att gga cat att aag cac ctg aca gag att 691
Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys His Leu Thr Glu Ile
185 190 195

gct ccg cca cgg att gca gct gtg ctc aac gtc ggc cat gcg cac ctg 739
Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val Gly His Ala His Leu
200 205 210

ggt gaa ttt gga tcc cgc gag aat atc gcg cag gca aaa ggc gag atc 787
Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln Ala Lys Gly Glu Ile
215 220 225

att gaa gcg ctg ccc tcg aag aaa acg gct cgg tac cag tcc 829
Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg Tyr Gln Ser
230 235 240

tgaatactag gatccttttg tcg 852

<210> 14
<211> 243
<212> PRT
<213> Corynebacterium glutamicum

<400> 14
Met Thr Leu Gly Glu Ile Ala Asp Ile Val Gly Gly Arg Leu Thr Gly
1 5 10 15

Gly Ala Gln Glu Asp Thr Leu Val Ser Ser Ser Val Glu Phe Asp Ser
20 25 30

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Arg Ser Leu Thr Pro Gly Gly Leu Phe Leu Ala Leu Pro Gly Ala Arg
         35                  40                  45

Val Asp Gly His Asp Phe Ala Ala Thr Ala Ile Glu Lys Gly Ala Val
     50                  55                  60

Ala Val Leu Ala Ala Arg Glu Val Asp Val Pro Ala Ile Val Val Pro
 65                  70                  75                  80

Pro Val Lys Ile Gln Glu Ser Asn Ala Asp Ile Tyr Ala His Asp Pro
                 85                  90                  95

Asp Gly His Gly Ala Ala Val Val Glu Ala Leu Ser Arg Leu Ala Arg
            100                 105                 110

His Val Val Asp Ile Cys Val Ala Gly His Gln Leu Asn Val Val Ala
        115                 120                 125

Ile Thr Gly Ser Ala Gly Lys Thr Ser Thr Lys Asp Phe Ile Ala Thr
    130                 135                 140

Val Leu Asp Gln Asp Gly Pro Thr Val Ala Pro Pro Gly Ser Phe Asn
145                 150                 155                 160

Asn Glu Leu Gly Leu Pro His Thr Ala Leu Arg Cys Thr Thr Asp Thr
                165                 170                 175

Lys Tyr Leu Val Ala Glu Met Ser Ala Arg Gly Ile Gly His Ile Lys
            180                 185                 190

His Leu Thr Glu Ile Ala Pro Pro Arg Ile Ala Ala Val Leu Asn Val
        195                 200                 205

Gly His Ala His Leu Gly Glu Phe Gly Ser Arg Glu Asn Ile Ala Gln
    210                 215                 220

Ala Lys Gly Glu Ile Ile Glu Ala Leu Pro Ser Lys Lys Thr Ala Arg
225                 230                 235                 240

Tyr Gln Ser
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Copied from PCT

<210> 15
<211> 1686
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1663)
<223> RXA02710

<400> 15
gaatttcata atctgaactt ttgtttgaac tcttttcggc atcacccacg tgccgcgtcc 60

gaattattaa cacctagaaa cctgtggagg agagaaaacc atg gca acc acg ttg 115
                                                Met Ala Thr Thr Leu
                                                  1   5

ctg gac ctc acc aaa ctt atc gat ggc atc ctc aag ggc tct gcc cag 163

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Leu Asp Leu Thr Lys Leu Ile Asp Gly Ile Leu Lys Gly Ser Ala Gln
                10                  15                  20

ggc gtt ccc gct cac gca gta ggg gaa caa gca atc gcg gct att ggt   211
Gly Val Pro Ala His Ala Val Gly Glu Gln Ala Ile Ala Ala Ile Gly
            25                  30                  35

ctt gac tcc tcc agc tta cct acc tcg gac gct att ttt gct gca gtt   259
Leu Asp Ser Ser Ser Leu Pro Thr Ser Asp Ala Ile Phe Ala Ala Val
        40                  45                  50

cca gga acc cgc act cac ggc gca cag ttt gca ggt acg gat aac gct   307
Pro Gly Thr Arg Thr His Gly Ala Gln Phe Ala Gly Thr Asp Asn Ala
    55                  60                  65

gcg aaa gct gtg gcc att ttg act gac gca gct gga ctt gag gtg ctc   355
Ala Lys Ala Val Ala Ile Leu Thr Asp Ala Ala Gly Leu Glu Val Leu
70                  75                  80                  85

aac gaa gca gga gag acc cgc cca gtc atc gtt gtt gat gat gtc cgc   403
Asn Glu Ala Gly Glu Thr Arg Pro Val Ile Val Val Asp Asp Val Arg
                90                  95                  100

gca gta ctt ggc gca gca tca tca agc att tat ggc gat cct tca aaa   451
Ala Val Leu Gly Ala Ala Ser Ser Ser Ile Tyr Gly Asp Pro Ser Lys
            105                 110                 115

gat ttc acg ctc att gga gtc act gga acc tca ggt aaa acc acc acc   499
Asp Phe Thr Leu Ile Gly Val Thr Gly Thr Ser Gly Lys Thr Thr Thr
        120                 125                 130

agc tac ctc ttg gaa aaa gga ctc atg gag gca ggc cac aaa gtt ggt   547
Ser Tyr Leu Leu Glu Lys Gly Leu Met Glu Ala Gly His Lys Val Gly
    135                 140                 145

ttg atc ggc acc aca ggt aca cgt att gac ggg gaa gaa gta ccc aca   595
Leu Ile Gly Thr Thr Gly Thr Arg Ile Asp Gly Glu Glu Val Pro Thr
150                 155                 160                 165

aag ctc acc act cca gaa gcg ccg act ctg cag gca ttg ttt gct cga   643
Lys Leu Thr Thr Pro Glu Ala Pro Thr Leu Gln Ala Leu Phe Ala Arg
                170                 175                 180

atg cgc gat cac ggt gtc acc cac gtg gtg atg gaa gta tcc agc cat   691
Met Arg Asp His Gly Val Thr His Val Val Met Glu Val Ser Ser His
            185                 190                 195

gca ttg tca ttg ggc aga gtt gcg ggt tcc cac ttt gat gta gct gcg   739
Ala Leu Ser Leu Gly Arg Val Ala Gly Ser His Phe Asp Val Ala Ala
        200                 205                 210

ttt acc aac ctg tcg cag gat cac ctt gat ttc cac ccc acc atg gat   787
Phe Thr Asn Leu Ser Gln Asp His Leu Asp Phe His Pro Thr Met Asp
    215                 220                 225

gat tac ttt gac gcg aag gca ttg ttc ttc cgc gca gat tct cca ctt   835
Asp Tyr Phe Asp Ala Lys Ala Leu Phe Phe Arg Ala Asp Ser Pro Leu
230                 235                 240                 245

gtg gct gac aaa cag gtc gtg tgc gtg gat gat tct tgg ggt cag cgc   883
Val Ala Asp Lys Gln Val Val Cys Val Asp Asp Ser Trp Gly Gln Arg
```

```
                    250                 255                 260

atg gcc agc gtg gca gcg gat gtg caa aca gta tcc acc ctt ggg caa   931
Met Ala Ser Val Ala Ala Asp Val Gln Thr Val Ser Thr Leu Gly Gln
            265                 270                 275

gaa gca gac ttc agc gct aca gac atc aat gtc agc gac tct ggc gcc   979
Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val Ser Asp Ser Gly Ala
        280                 285                 290

cag agt ttt aag atc aac gcc ccc tca aac cag tcc tac cag gtc gag   1027
Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln Ser Tyr Gln Val Glu
    295                 300                 305

cta gct ctt cca ggt gcg ttc aac gtt gct aac gcc acg ttg gca ttt   1075
Leu Ala Leu Pro Gly Ala Phe Asn Val Ala Asn Ala Thr Leu Ala Phe
310                 315                 320                 325

gcc gct gcg gca cgc gtg ggt gtt gat ggc gaa gcg ttt gct cga ggc   1123
Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu Ala Phe Ala Arg Gly
                330                 335                 340

atg tcc aag gtc gcg gtt cca ggc cgt atg gaa cgc att gat gag gga   1171
Met Ser Lys Val Ala Val Pro Gly Arg Met Glu Arg Ile Asp Glu Gly
            345                 350                 355

caa gac ttc ctt gca gtg gtg gat tat gcc cac aag cct gct gca gtg   1219
Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His Lys Pro Ala Ala Val
        360                 365                 370

gct gct gtg ttg gat acg ttg agg acc cag att gac ggg cgc ctc gga   1267
Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile Asp Gly Arg Leu Gly
    375                 380                 385

gtg gtt atc ggt gct ggt gga gac cgc gat tcc acc aag cgt ggc ccc   1315
Val Val Ile Gly Ala Gly Gly Asp Arg Asp Ser Thr Lys Arg Gly Pro
390                 395                 400                 405

atg ggg cag ttg tcc gca cag cgt gct gat cta gtt att gtc act gat   1363
Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu Val Ile Val Thr Asp
                410                 415                 420

gac aac cct cgt tca gag gtg cct gcc acg att cgc gca gca gtc act   1411
Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile Arg Ala Ala Val Thr
            425                 430                 435

gca gga gca cag cag ggt gct tca gag tcc gaa cga ccg gtg gaa gtc   1459
Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu Arg Pro Val Glu Val
        440                 445                 450

cta gaa att ggt gac cgt gca gaa gca att cgc gtt ttg gtc gag tgg   1507
Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg Val Leu Val Glu Trp
    455                 460                 465

gca cag cct gga gat ggc att gta gta gct gga aaa ggc cat gaa gtt   1555
Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly Lys Gly His Glu Val
470                 475                 480                 485

gga caa cta gtt gct ggt gtc acc cac cat ttt gat gac cgc gaa gaa   1603
Gly Gln Leu Val Ala Gly Val Thr His His Phe Asp Asp Arg Glu Glu
                490                 495                 500
```

```
gtt cgc gct gct ttg aca gaa aag ctc aac aat aaa ctt ccc ctt act   1651
Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn Lys Leu Pro Leu Thr
            505                 510                 515

acg gaa gaa gga taggccacag tcatgatcac aat                        1686
Thr Glu Glu Gly
        520
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<210> 16
<211> 521
<212> PRT
<213> Corynebacterium glutamicum

<400> 16

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Met Ala Thr Thr Leu Leu Asp Leu Thr Lys Leu Ile Asp Gly Ile Leu
  1               5                  10                  15

Lys Gly Ser Ala Gln Gly Val Pro Ala His Ala Val Gly Glu Gln Ala
             20                  25                  30

Ile Ala Ala Ile Gly Leu Asp Ser Ser Ser Leu Pro Thr Ser Asp Ala
         35                  40                  45

Ile Phe Ala Ala Val Pro Gly Thr Arg Thr His Gly Ala Gln Phe Ala
     50                  55                  60

Gly Thr Asp Asn Ala Ala Lys Ala Val Ala Ile Leu Thr Asp Ala Ala
 65                  70                  75                  80

Gly Leu Glu Val Leu Asn Glu Ala Gly Glu Thr Arg Pro Val Ile Val
                 85                  90                  95

Val Asp Asp Val Arg Ala Val Leu Gly Ala Ala Ser Ser Ser Ile Tyr
            100                 105                 110

Gly Asp Pro Ser Lys Asp Phe Thr Leu Ile Gly Val Thr Gly Thr Ser
        115                 120                 125

Gly Lys Thr Thr Thr Ser Tyr Leu Leu Glu Lys Gly Leu Met Glu Ala
    130                 135                 140

Gly His Lys Val Gly Leu Ile Gly Thr Thr Gly Thr Arg Ile Asp Gly
145                 150                 155                 160

Glu Glu Val Pro Thr Lys Leu Thr Thr Pro Glu Ala Pro Thr Leu Gln
                165                 170                 175

Ala Leu Phe Ala Arg Met Arg Asp His Gly Val Thr His Val Val Met
            180                 185                 190

Glu Val Ser Ser His Ala Leu Ser Leu Gly Arg Val Ala Gly Ser His
        195                 200                 205

Phe Asp Val Ala Ala Phe Thr Asn Leu Ser Gln Asp His Leu Asp Phe
    210                 215                 220

His Pro Thr Met Asp Asp Tyr Phe Asp Ala Lys Ala Leu Phe Phe Arg
225                 230                 235                 240
```

```
Ala Asp Ser Pro Leu Val Ala Asp Lys Gln Val Val Cys Val Asp Asp
                245                 250                 255

Ser Trp Gly Gln Arg Met Ala Ser Val Ala Ala Asp Val Gln Thr Val
            260                 265                 270

Ser Thr Leu Gly Gln Glu Ala Asp Phe Ser Ala Thr Asp Ile Asn Val
        275                 280                 285

Ser Asp Ser Gly Ala Gln Ser Phe Lys Ile Asn Ala Pro Ser Asn Gln
    290                 295                 300

Ser Tyr Gln Val Glu Leu Ala Leu Pro Gly Ala Phe Asn Val Ala Asn
305                 310                 315                 320

Ala Thr Leu Ala Phe Ala Ala Ala Ala Arg Val Gly Val Asp Gly Glu
                325                 330                 335

Ala Phe Ala Arg Gly Met Ser Lys Val Ala Val Pro Gly Arg Met Glu
            340                 345                 350

Arg Ile Asp Glu Gly Gln Asp Phe Leu Ala Val Val Asp Tyr Ala His
        355                 360                 365

Lys Pro Ala Ala Val Ala Ala Val Leu Asp Thr Leu Arg Thr Gln Ile
    370                 375                 380

Asp Gly Arg Leu Gly Val Val Ile Gly Ala Gly Gly Asp Arg Asp Ser
385                 390                 395                 400

Thr Lys Arg Gly Pro Met Gly Gln Leu Ser Ala Gln Arg Ala Asp Leu
                405                 410                 415

Val Ile Val Thr Asp Asp Asn Pro Arg Ser Glu Val Pro Ala Thr Ile
            420                 425                 430

Arg Ala Ala Val Thr Ala Gly Ala Gln Gln Gly Ala Ser Glu Ser Glu
        435                 440                 445

Arg Pro Val Glu Val Leu Glu Ile Gly Asp Arg Ala Glu Ala Ile Arg
    450                 455                 460

Val Leu Val Glu Trp Ala Gln Pro Gly Asp Gly Ile Val Val Ala Gly
465                 470                 475                 480

Lys Gly His Glu Val Gly Gln Leu Val Ala Gly Val Thr His His Phe
                485                 490                 495

Asp Asp Arg Glu Glu Val Arg Ala Ala Leu Thr Glu Lys Leu Asn Asn
            500                 505                 510

Lys Leu Pro Leu Thr Thr Glu Glu Gly
        515                 520
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<210> 17
<211> 618
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(595)
<223> RXN00531

<400> 17
gcctgcggga atcggcactt tcaggatagg acaacctaat ataaataagc ttaggctaag 60

ggccggtgac aatttatcaa gcagtgctat aataggggtc atg gca aac tac aca 115
Met Ala Asn Tyr Thr
1 5

gtc cct gga atc aac gag aat gac gca aag cag ctt att gat gga ctg 163
Val Pro Gly Ile Asn Glu Asn Asp Ala Lys Gln Leu Ile Asp Gly Leu
10 15 20

cag gag cgt ctc acc gac tac aac gat ctt cac ctc atc ttg aag cac 211
Gln Glu Arg Leu Thr Asp Tyr Asn Asp Leu His Leu Ile Leu Lys His
25 30 35

gtg cac tgg aac gtc act ggc ccc aac ttc att gct gtt cac gaa atg 259
Val His Trp Asn Val Thr Gly Pro Asn Phe Ile Ala Val His Glu Met
40 45 50

ctc gac cca cag gtt gac ctt gtt cgt ggc tat gct gac gaa gtt gca 307
Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr Ala Asp Glu Val Ala
55 60 65

gag cgc att ttc acc ctc gga ggc gca cca gtt gga acc cca gaa ggc 355
Glu Arg Ile Phe Thr Leu Gly Gly Ala Pro Val Gly Thr Pro Glu Gly
70 75 80 85

cac gtt gct gac cgc acc cca ctg caa tat gag cgc aat gcc gga aat 403
His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu Arg Asn Ala Gly Asn
90 95 100

gtc caa gca cac ctc act gac ctc aat cgc gtg tac acc caa gtg ctg 451
Val Gln Ala His Leu Thr Asp Leu Asn Arg Val Tyr Thr Gln Val Leu
105 110 115

acc gga gtt cgc gag tcc atg gca tca gcc ggc cca gtg gat cca gta 499
Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly Pro Val Asp Pro Val
120 125 130

act gaa gac atc tac atc agc cag gcc gcg gag ctg gag aaa ttc cag 547
Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu Leu Glu Lys Phe Gln
135 140 145

tgg ttc atc cgc gca cac att gtt gat gta gac gga aac atc caa gag 595
Trp Phe Ile Arg Ala His Ile Val Asp Val Asp Gly Asn Ile Gln Glu
150 155 160 165

taaaacgtcg aaaagcgtta agg 618

<210> 18
<211> 165
<212> PRT
<213> Corynebacterium glutamicum

<400> 18
Met Ala Asn Tyr Thr Val Pro Gly Ile Asn Glu Asn Asp Ala Lys Gln

```
  1               5                  10                  15

Leu Ile Asp Gly Leu Gln Glu Arg Leu Thr Asp Tyr Asn Asp Leu His
             20                  25                  30

Leu Ile Leu Lys His Val His Trp Asn Val Thr Gly Pro Asn Phe Ile
         35                  40                  45

Ala Val His Glu Met Leu Asp Pro Gln Val Asp Leu Val Arg Gly Tyr
     50                  55                  60

Ala Asp Glu Val Ala Glu Arg Ile Phe Thr Leu Gly Gly Ala Pro Val
 65                  70                  75                  80

Gly Thr Pro Glu Gly His Val Ala Asp Arg Thr Pro Leu Gln Tyr Glu
                 85                  90                  95

Arg Asn Ala Gly Asn Val Gln Ala His Leu Thr Asp Leu Asn Arg Val
            100                 105                 110

Tyr Thr Gln Val Leu Thr Gly Val Arg Glu Ser Met Ala Ser Ala Gly
        115                 120                 125

Pro Val Asp Pro Val Thr Glu Asp Ile Tyr Ile Ser Gln Ala Ala Glu
    130                 135                 140

Leu Glu Lys Phe Gln Trp Phe Ile Arg Ala His Ile Val Asp Val Asp
145                 150                 155                 160

Gly Asn Ile Gln Glu
                165
```

Copyright

<210> 19
<211> 1095
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1072)
<223> RXA00944

<400> 19
aaatagtggg attaacccat taattttatc gctctattta gtttcgtcac tgtgtcgtta 60

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atcaattgac ttcctgcgtg gttgaatcag cgcaaggatt gtg gat ttt tgg act   115
                                              Val Asp Phe Trp Thr
                                                1               5

att ctc gac acc atg act tcc ctc ctt act ccc att gca atc cgt gga   163
Ile Leu Asp Thr Met Thr Ser Leu Leu Thr Pro Ile Ala Ile Arg Gly
                10                  15                  20

tta gaa att ccc aat agg atg tgg ctc gcg ccc atg tgc cag tac caa   211
Leu Glu Ile Pro Asn Arg Met Trp Leu Ala Pro Met Cys Gln Tyr Gln
            25                  30                  35

gcc aat aac ctc gat ggg gtt cca ctt gat tgg cac ctc gtg cat tac   259
Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp His Leu Val His Tyr
        40                  45                  50
```

```
gga gcc cga gct gtt ggc ggc ttc gga ctc ctc atc gcg gaa tcc acc   307
Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu Ile Ala Glu Ser Thr
     55                  60                  65

ggc att agt cca gag gga aga atc tca tcg cgt tgc act ggc cta tgg   355
Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg Cys Thr Gly Leu Trp
 70                  75                  80                  85

aat gag gcc caa gtt gag gca tgg gag aga att aca aat ttt gtc cac   403
Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile Thr Asn Phe Val His
                 90                  95                 100

gct caa ggt gga ctg atc ggt gtg caa ctt aac cat gca ggc cgc aaa   451
Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn His Ala Gly Arg Lys
            105                 110                 115

gcg agc aca tat ccg gcc ctt cct aac ttc cct act ggt act caa tca   499
Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro Thr Gly Thr Gln Ser
        120                 125                 130

gtt gac gag ggt gga tgg gaa acc ttt ggg cct agt gct gtc gct cag   547
Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro Ser Ala Val Ala Gln
    135                 140                 145

ccg ggg ctt gca gat ccg acc gaa ttg acc cgc gaa ggt att gaa aag   595
Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg Glu Gly Ile Glu Lys
150                 155                 160                 165

gtt att cag gat ttc gct gct gct gca gag cgc gcg gtg cgt gca ggg   643
Val Ile Gln Asp Phe Ala Ala Ala Ala Glu Arg Ala Val Arg Ala Gly
                170                 175                 180

ttt gat gct gtg gag gtc cat ggt gcc cac ggt tac ctg ttg cat cag   691
Phe Asp Ala Val Glu Val His Gly Ala His Gly Tyr Leu Leu His Gln
            185                 190                 195

ttc ctc act ccc ctc gca aat aaa cgt act gat att tat gga ggt tcg   739
Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp Ile Tyr Gly Gly Ser
        200                 205                 210

ttt gag aat cgc aca cga cta ttt agg gaa gta gcc cag gcg atc cgt   787
Phe Glu Asn Arg Thr Arg Leu Phe Arg Glu Val Ala Gln Ala Ile Arg
    215                 220                 225

gca gtg att ccg ggc tcg atg cca ctg att gcc cgg atc tct gcc acg   835
Ala Val Ile Pro Gly Ser Met Pro Leu Ile Ala Arg Ile Ser Ala Thr
230                 235                 240                 245

gac tgg att gat gat gaa cct tcg tgg gat gac gat caa acc gtc tcg   883
Asp Trp Ile Asp Asp Glu Pro Ser Trp Asp Asp Asp Gln Thr Val Ser
                250                 255                 260

ctt gtg tca gga tct gaa aaa gct ggg tgt gga tgc agt cga tat ttc   931
Leu Val Ser Gly Ser Glu Lys Ala Gly Cys Gly Cys Ser Arg Tyr Phe
            265                 270                 275

cac cgg agg tgc agt acc cgc gac aat ccc tgt gga gcc gag cta tca   979
His Arg Arg Cys Ser Thr Arg Asp Asn Pro Cys Gly Ala Glu Leu Ser
        280                 285                 290
```

```
agt gaa att tgc tcg tcg tgt gaa gca aga ggt ggg tat ccc tac ctc   1027
Ser Glu Ile Cys Ser Ser Cys Glu Ala Arg Gly Gly Tyr Pro Tyr Leu
    295                 300                 305

cgc ggt tgg att aat tac tca tgt ggg tca ggc gca ggg gca tct       1072
Arg Gly Trp Ile Asn Tyr Ser Cys Gly Ser Gly Ala Gly Ala Ser
310                 315                 320

tgatcgtgga gatgcggaca tta                                        1095
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<210> 20
<211> 324
<212> PRT
<213> Corynebacterium glutamicum

<400> 20

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Val Asp Phe Trp Thr Ile Leu Asp Thr Met Thr Ser Leu Leu Thr Pro
  1               5                  10                  15

Ile Ala Ile Arg Gly Leu Glu Ile Pro Asn Arg Met Trp Leu Ala Pro
            20                  25                  30

Met Cys Gln Tyr Gln Ala Asn Asn Leu Asp Gly Val Pro Leu Asp Trp
        35                  40                  45

His Leu Val His Tyr Gly Ala Arg Ala Val Gly Gly Phe Gly Leu Leu
    50                  55                  60

Ile Ala Glu Ser Thr Gly Ile Ser Pro Glu Gly Arg Ile Ser Ser Arg
65                  70                  75                  80

Cys Thr Gly Leu Trp Asn Glu Ala Gln Val Glu Ala Trp Glu Arg Ile
                85                  90                  95

Thr Asn Phe Val His Ala Gln Gly Gly Leu Ile Gly Val Gln Leu Asn
            100                 105                 110

His Ala Gly Arg Lys Ala Ser Thr Tyr Pro Ala Leu Pro Asn Phe Pro
        115                 120                 125

Thr Gly Thr Gln Ser Val Asp Glu Gly Gly Trp Glu Thr Phe Gly Pro
    130                 135                 140

Ser Ala Val Ala Gln Pro Gly Leu Ala Asp Pro Thr Glu Leu Thr Arg
145                 150                 155                 160

Glu Gly Ile Glu Lys Val Ile Gln Asp Phe Ala Ala Ala Ala Glu Arg
                165                 170                 175

Ala Val Arg Ala Gly Phe Asp Ala Val Glu Val His Gly Ala His Gly
            180                 185                 190

Tyr Leu Leu His Gln Phe Leu Thr Pro Leu Ala Asn Lys Arg Thr Asp
        195                 200                 205

Ile Tyr Gly Gly Ser Phe Glu Asn Arg Tnr Arg Leu Phe Arg Glu Val
    210                 215                 220

Ala Gln Ala Ile Arg Ala Val Ile Pro Gly Ser Met Pro Leu Ile Ala
225                 230                 235                 240
```

```
Arg Ile Ser Ala Thr Asp Trp Ile Asp Asp Glu Pro Ser Trp Asp Asp
                245                 250                 255

Asp Gln Thr Val Ser Leu Val Ser Gly Ser Glu Lys Ala Gly Cys Gly
            260                 265                 270

Cys Ser Arg Tyr Phe His Arg Arg Cys Ser Thr Arg Asp Asn Pro Cys
        275                 280                 285

Gly Ala Glu Leu Ser Ser Glu Ile Cys Ser Ser Cys Glu Ala Arg Gly
    290                 295                 300

Gly Tyr Pro Tyr Leu Arg Gly Trp Ile Asn Tyr Ser Cys Gly Ser Gly
305                 310                 315                 320

Ala Gly Ala Ser
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<210> 21
<211> 990
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(967)
<223> RXS02560

<400> 21

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ttggggcaag ccagctaacg catttcttgt ggaaaccgca gacattgagg ccgcccacgc 60

ggaacttcta agagcagtgg aatgaaataa tccggtgctg atg cag ggc aac tcg   115
                                        Met Gln Gly Asn Ser
                                          1               5

ctt aat ctg gca gac aac agc gag aga aag aag ccc atg ccg tca cca   163
Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys Pro Met Pro Ser Pro
                 10                  15                  20

gga gaa ctt tta gcc gcc cgc tac gga caa cct gca acc tgg acg cca   211
Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro Ala Thr Trp Thr Pro
             25                  30                  35

ccg cag tgg aat gag acg ctt gat gtc att cac cag cat cga tca gtt   259
Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His Gln His Arg Ser Val
         40                  45                  50

cgc agg tgg ttg gat aaa ccg gtt gat gat gac acc atc cgc acc att   307
Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp Thr Ile Arg Thr Ile
     55                  60                  65

att tcc gcc gca caa tcg gct gga acc tct tcc aat aag cag gtc att   355
Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser Asn Lys Gln Val Ile
 70                  75                  80                  85

tct gtc atc gtg gtt aaa gat cct gag ctg agg aaa ggc ctc gcg ggg   403
Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg Lys Gly Leu Ala Gly
                 90                  95                 100
```

```
atc act cgc cag atg ttt ccg cac ctt gag cag gtt ccc gcg gtg ctg   451
Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln Val Pro Ala Val Leu
            105                 110                 115

att tgg ttg att gat tat tcc cga atc agt gcg gtg gca gcc aga gaa   499
Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala Val Ala Ala Arg Glu
        120                 125                 130

gat ctc cca aca ggg gct ctt gat tat ctc gat gag gcc gcg tgg ggg   547
Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp Glu Ala Ala Trp Gly
    135                 140                 145

ttc ctc gac gcc gga atc gca gct caa aac gct gca att gct gcg gag   595
Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala Ala Ile Ala Ala Glu
150                 155                 160                 165

tca ctt gga ttg gga acg ctc tat ttg ggt tcg gtg cgc aac gat gcg   643
Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser Val Arg Asn Asp Ala
                170                 175                 180

gaa gcc gtg cac aaa ttg ctt ggc ctt cca cct gag atc gtg cct gtc   691
Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro Glu Ile Val Pro Val
            185                 190                 195

gtg ggc ttg gaa atg ggg cat gcg gat ccg cct gaa cct gcc gga att   739
Val Gly Leu Glu Met Gly His Ala Asp Pro Pro Glu Pro Ala Gly Ile
        200                 205                 210

aaa cct ccc ctg cca caa gaa gcc att gtt cac tgg gat acc tac acc   787
Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His Trp Asp Thr Tyr Thr
    215                 220                 225

gag aaa aac ctc gaa ctt atc gat tcc tac gac cgc gcc ctc gac act   835
Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp Arg Ala Leu Asp Thr
230                 235                 240                 245

tac tat tct cgc tac ggc cag cac cag ctc tgg tcg aag cag acg gcg   883
Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp Ser Lys Gln Thr Ala
                250                 255                 260

cat agg gcg gcg tcg aaa agc ttt tca aaa acc aac agg cag ttc ctt   931
His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr Asn Arg Gln Phe Leu
            265                 270                 275

agg ggc gtg ttt gag cgc gcc ggg ttt ggg ctg aga taaaagcatg       977
Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu Arg
        280                 285

attatggacg cct                                                   990
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Sequence Listing

<210> 22
<211> 289
<212> PRT
<213> Corynebacterium glutamicum

<400> 22

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Met Gln Gly Asn Ser Leu Asn Leu Ala Asp Asn Ser Glu Arg Lys Lys
  1               5                  10                  15

Pro Met Pro Ser Pro Gly Glu Leu Leu Ala Ala Arg Tyr Gly Gln Pro
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```
            20                  25                  30

Ala Thr Trp Thr Pro Pro Gln Trp Asn Glu Thr Leu Asp Val Ile His
         35                  40                  45

Gln His Arg Ser Val Arg Arg Trp Leu Asp Lys Pro Val Asp Asp Asp
     50                  55                  60

Thr Ile Arg Thr Ile Ile Ser Ala Ala Gln Ser Ala Gly Thr Ser Ser
 65                  70                  75                  80

Asn Lys Gln Val Ile Ser Val Ile Val Val Lys Asp Pro Glu Leu Arg
                 85                  90                  95

Lys Gly Leu Ala Gly Ile Thr Arg Gln Met Phe Pro His Leu Glu Gln
            100                 105                 110

Val Pro Ala Val Leu Ile Trp Leu Ile Asp Tyr Ser Arg Ile Ser Ala
        115                 120                 125

Val Ala Ala Arg Glu Asp Leu Pro Thr Gly Ala Leu Asp Tyr Leu Asp
    130                 135                 140

Glu Ala Ala Trp Gly Phe Leu Asp Ala Gly Ile Ala Ala Gln Asn Ala
145                 150                 155                 160

Ala Ile Ala Ala Glu Ser Leu Gly Leu Gly Thr Leu Tyr Leu Gly Ser
                165                 170                 175

Val Arg Asn Asp Ala Glu Ala Val His Lys Leu Leu Gly Leu Pro Pro
            180                 185                 190

Glu Ile Val Pro Val Val Gly Leu Glu Met Gly His Ala Asp Pro Pro
        195                 200                 205

Glu Pro Ala Gly Ile Lys Pro Pro Leu Pro Gln Glu Ala Ile Val His
    210                 215                 220

Trp Asp Thr Tyr Thr Glu Lys Asn Leu Glu Leu Ile Asp Ser Tyr Asp
225                 230                 235                 240

Arg Ala Leu Asp Thr Tyr Tyr Ser Arg Tyr Gly Gln His Gln Leu Trp
                245                 250                 255

Ser Lys Gln Thr Ala His Arg Ala Ala Ser Lys Ser Phe Ser Lys Thr
            260                 265                 270

Asn Arg Gln Phe Leu Arg Gly Val Phe Glu Arg Ala Gly Phe Gly Leu
        275                 280                 285

Arg
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<210> 23
<211> 255
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(232)
<223> RXS03119

<400> 23
tgggaggtgt cgcaccaagt acttttgcga agcgccatct gacggatttt caaaagatgt 60

atatgctcgg tgcggaaacc tacgaaagga ttttttaccc atg gct gta tac gaa 115
Met Ala Val Tyr Glu
1 5

ctc cca gaa ctc gac tac gca tac gac gct ctc gag cca cac atc gtc 163
Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu Glu Pro His Ile Val
10 15 20

gct gaa atc atg gag ctt gac cag tcc aag gac cac gca acc tac gtt 211
Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp His Ala Thr Tyr Val
25 30 35

gcg ggc gca aat gca gca ctc taggcactag agaaggcacg cga 255
Ala Gly Ala Asn Ala Ala Leu
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<210> 24
<211> 44
<212> PRT
<213> Corynebacterium glutamicum

<400> 24
Met Ala Val Tyr Glu Leu Pro Glu Leu Asp Tyr Ala Tyr Asp Ala Leu
1 5 10 15

Glu Pro His Ile Val Ala Glu Ile Met Glu Leu Asp Gln Ser Lys Asp
20 25 30

His Ala Thr Tyr Val Ala Gly Ala Asn Ala Ala Leu
35 40

<210> 25
<211> 249
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(226)
<223> RXS03120

<400> 25
ctgggcagtt cttgggtacg accacatatc cggtcgcctg gttatcgagc agctcaccga 60

ccaggagggc aacatctcct tcgacatcac cccagttctg atg ctc gat atg tgg 115
Met Leu Asp Met Trp
1 5

gag cac gct ttc tac ctg cag tac atg aac gtt aag gca gat tac gtc 163
Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val Lys Ala Asp Tyr Val
10 15 20

aag gct gtt tgg aac gtc ttc aac tgg gac gac gca aga gca cgc ttc 211

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Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp Ala Arg Ala Arg Phe
            25                  30                  35

gca gca gct tcc aag taagcatttt tagtccgtgc aat                    249
Ala Ala Ala Ser Lys
         40


<210> 26
<211> 42
<212> PRT
<213> Corynebacterium glutamicum

<400> 26
Met Leu Asp Met Trp Glu His Ala Phe Tyr Leu Gln Tyr Met Asn Val
  1               5                  10                  15

Lys Ala Asp Tyr Val Lys Ala Val Trp Asn Val Phe Asn Trp Asp Asp
            20                  25                  30

Ala Arg Ala Arg Phe Ala Ala Ala Ser Lys
         35                  40


<210> 27
<211> 1311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1288)
<223> RXA01430

<400> 27
gaaaaactag agaagcacct ctagctggta ttcttactgc agtcacgtgg atgaactata 60

tccattgata attttgaaca tgaatgatgg aaggagcagg gtg tct aaa gtc ctg   115
                                            Val Ser Lys Val Leu
                                              1               5

aga gtt ggc gat cgc agc ccg cgc gtg gca gaa gtg cgc act acg ctc   163
Arg Val Gly Asp Arg Ser Pro Arg Val Ala Glu Val Arg Thr Thr Leu
                10                  15                  20

gct cgc ctc ggt gtg att gaa ggc tat tcc agg gag atg tct gca aag   211
Ala Arg Leu Gly Val Ile Glu Gly Tyr Ser Arg Glu Met Ser Ala Lys
            25                  30                  35

aca gaa tcc cag aag ttc cac gaa gaa gag acg ctt ttc gac gaa gaa   259
Thr Glu Ser Gln Lys Phe His Glu Glu Glu Thr Leu Phe Asp Glu Glu
         40                  45                  50

ctc agc ctc agc atc aag tca ttc cag caa gct cga gga gtc gtt ccc   307
Leu Ser Leu Ser Ile Lys Ser Phe Gln Gln Ala Arg Gly Val Val Pro
     55                  60                  65

tcc ggg ctt att gac gac ccc acc ctg cgc gca atc cgc gaa gcc tcc   355
Ser Gly Leu Ile Asp Asp Pro Thr Leu Arg Ala Ile Arg Glu Ala Ser
 70                  75                  80                  85
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tac acc ctg gga acc cgc gtg ctg gcc tac cag ccc ggc aac cag ctt   403
Tyr Thr Leu Gly Thr Arg Val Leu Ala Tyr Gln Pro Gly Asn Gln Leu
                 90                  95                 100

gtt ggt gac gac gtt gta gaa atc caa tcc cat ctc caa gag ctc ggc   451
Val Gly Asp Asp Val Val Glu Ile Gln Ser His Leu Gln Glu Leu Gly
            105                 110                 115

ttc tac gcc gac cgt gtg gat gga cat ttt ggc gag ctc aca cac aaa   499
Phe Tyr Ala Asp Arg Val Asp Gly His Phe Gly Glu Leu Thr His Lys
        120                 125                 130

gct gtg atg aac tac caa ctc aac tac ggc atg cag gta gac ggc atc   547
Ala Val Met Asn Tyr Gln Leu Asn Tyr Gly Met Gln Val Asp Gly Ile
    135                 140                 145

tgt ggc cct gac acc atc cgt gcg ctg tcc cga ctt ggt ctg cgc atc   595
Cys Gly Pro Asp Thr Ile Arg Ala Leu Ser Arg Leu Gly Leu Arg Ile
150                 155                 160                 165

aag ggt ggc tct gct caa gct atc cgt gaa cgc gaa cgc atg cgc aat   643
Lys Gly Gly Ser Ala Gln Ala Ile Arg Glu Arg Glu Arg Met Arg Asn
                170                 175                 180

gca ggc cca cgt ctt gct ggc aag cgt gtg gtc att gat cct gcg ctt   691
Ala Gly Pro Arg Leu Ala Gly Lys Arg Val Val Ile Asp Pro Ala Leu
            185                 190                 195

ggg ggc tcc aac aag ggt cag atc gtg aaa ggc ccc tac ggt gag atc   739
Gly Gly Ser Asn Lys Gly Gln Ile Val Lys Gly Pro Tyr Gly Glu Ile
        200                 205                 210

tct gag gaa gaa atc ctc tgg gat ttg gcc acc cgc ctg gaa ggt cgc   787
Ser Glu Glu Glu Ile Leu Trp Asp Leu Ala Thr Arg Leu Glu Gly Arg
    215                 220                 225

atg atc gca aca ggc atg gaa acc att ctg tcg cgc ccg cac atg gat   835
Met Ile Ala Thr Gly Met Glu Thr Ile Leu Ser Arg Pro His Met Asp
230                 235                 240                 245

gat ccc agc agc cgt gat cgc gcg tcg atc gcg aat gct ttc ggc gct   883
Asp Pro Ser Ser Arg Asp Arg Ala Ser Ile Ala Asn Ala Phe Gly Ala
                250                 255                 260

gac ctc atg ctg agc ctg cac tgc gat tcc tac ccg aat gaa aaa gct   931
Asp Leu Met Leu Ser Leu His Cys Asp Ser Tyr Pro Asn Glu Lys Ala
            265                 270                 275

aac ggc gtg gcc agc ttc tac ttc ggt tcg gaa aac ggc acc aac tcc   979
Asn Gly Val Ala Ser Phe Tyr Phe Gly Ser Glu Asn Gly Thr Asn Ser
        280                 285                 290

ttg acc ggt gaa acg ctc tcc gcg tac atc caa aaa gag atc gtt gcc   1027
Leu Thr Gly Glu Thr Leu Ser Ala Tyr Ile Gln Lys Glu Ile Val Ala
    295                 300                 305

cgc acc cca ctg aac aac tgt ggc agc cat gcc cgt acc tgg gat ctg   1075
Arg Thr Pro Leu Asn Asn Cys Gly Ser His Ala Arg Thr Trp Asp Leu
310                 315                 320                 325

ctg cgc ctc acg cgc atg ccc atg gtg gaa gtt gtc acc ggt tac ctc   1123
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Sequence Page

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Leu Arg Leu Thr Arg Met Pro Met Val Glu Val Val Thr Gly Tyr Leu
                330                 335                 340

acc aac ccc gat gac ctg gca gtt ctg act gat cca caa atg cgt gat   1171
Thr Asn Pro Asp Asp Leu Ala Val Leu Thr Asp Pro Gln Met Arg Asp
            345                 350                 355

cac att gcc gaa gcc atc gtt gtc gcc gtc aag cgc ctg tac ctc ctt   1219
His Ile Ala Glu Ala Ile Val Val Ala Val Lys Arg Leu Tyr Leu Leu
        360                 365                 370

gat gag gaa gca cag ccc aag acc gga acc ttc aag ttc tct gag ctg   1267
Asp Glu Glu Ala Gln Pro Lys Thr Gly Thr Phe Lys Phe Ser Glu Leu
    375                 380                 385

ttg caa tca gag cag gct ggc taaatcgcgc ccatctcttg aag             1311
Leu Gln Ser Glu Gln Ala Gly
390                 395


<210> 28
<211> 396
<212> PRT
<213> Corynebacterium glutamicum

<400> 28
Val Ser Lys Val Leu Arg Val Gly Asp Arg Ser Pro Arg Val Ala Glu
  1               5                  10                  15

Val Arg Thr Thr Leu Ala Arg Leu Gly Val Ile Glu Gly Tyr Ser Arg
             20                  25                  30

Glu Met Ser Ala Lys Thr Glu Ser Gln Lys Phe His Glu Glu Glu Thr
         35                  40                  45

Leu Phe Asp Glu Glu Leu Ser Leu Ser Ile Lys Ser Phe Gln Gln Ala
     50                  55                  60

Arg Gly Val Val Pro Ser Gly Leu Ile Asp Asp Pro Thr Leu Arg Ala
 65                  70                  75                  80

Ile Arg Glu Ala Ser Tyr Thr Leu Gly Thr Arg Val Leu Ala Tyr Gln
                 85                  90                  95

Pro Gly Asn Gln Leu Val Gly Asp Asp Val Val Glu Ile Gln Ser His
            100                 105                 110

Leu Gln Glu Leu Gly Phe Tyr Ala Asp Arg Val Asp Gly His Phe Gly
        115                 120                 125

Glu Leu Thr His Lys Ala Val Met Asn Tyr Gln Leu Asn Tyr Gly Met
    130                 135                 140

Gln Val Asp Gly Ile Cys Gly Pro Asp Thr Ile Arg Ala Leu Ser Arg
145                 150                 155                 160

Leu Gly Leu Arg Ile Lys Gly Gly Ser Ala Gln Ala Ile Arg Glu Arg
                165                 170                 175

Glu Arg Met Arg Asn Ala Gly Pro Arg Leu Ala Gly Lys Arg Val Val
            180                 185                 190
```

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Ile Asp Pro Ala Leu Gly Gly Ser Asn Lys Gly Gln Ile Val Lys Gly
        195                 200                 205

Pro Tyr Gly Glu Ile Ser Glu Glu Glu Ile Leu Trp Asp Leu Ala Thr
    210                 215                 220

Arg Leu Glu Gly Arg Met Ile Ala Thr Gly Met Glu Thr Ile Leu Ser
225                 230                 235                 240

Arg Pro His Met Asp Asp Pro Ser Ser Arg Asp Arg Ala Ser Ile Ala
                245                 250                 255

Asn Ala Phe Gly Ala Asp Leu Met Leu Ser Leu His Cys Asp Ser Tyr
            260                 265                 270

Pro Asn Glu Lys Ala Asn Gly Val Ala Ser Phe Tyr Phe Gly Ser Glu
        275                 280                 285

Asn Gly Thr Asn Ser Leu Thr Gly Glu Thr Leu Ser Ala Tyr Ile Gln
    290                 295                 300

Lys Glu Ile Val Ala Arg Thr Pro Leu Asn Asn Cys Gly Ser His Ala
305                 310                 315                 320

Arg Thr Trp Asp Leu Leu Arg Leu Thr Arg Met Pro Met Val Glu Val
                325                 330                 335

Val Thr Gly Tyr Leu Thr Asn Pro Asp Asp Leu Ala Val Leu Thr Asp
            340                 345                 350

Pro Gln Met Arg Asp His Ile Ala Glu Ala Ile Val Val Ala Val Lys
        355                 360                 365

Arg Leu Tyr Leu Leu Asp Glu Glu Ala Gln Pro Lys Thr Gly Thr Phe
    370                 375                 380

Lys Phe Ser Glu Leu Leu Gln Ser Glu Gln Ala Gly
385                 390                 395
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Sequence Listing

<210> 29
<211> 2199
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2176)
<223> RXA02641

<400> 29

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aggcttctca gttgtttcat atagtctcag ccgcaccaat atcatcaggg agaacatcgt 60

gcagcaacga cgccgcatca gcgagactcg gaaaaaaccg atg ctc gct att att   115
                                            Met Leu Ala Ile Ile
                                              1               5

ttg acc gcc gta ttg ggc gca tct ggc ctt gca gcc gct ggc act cag   163
Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala Ala Ala Gly Thr Gln
                10                  15                  20
```

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tac ctc aat act cag ggc gaa ggc atc ggt ccg gtc gcc gtc caa aac   211
Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro Val Ala Val Gln Asn
             25                  30                  35

gac agt gaa tcg ttt aat tcc ggc acc aac gtg gtt gtt gaa gac gca   259
Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val Val Val Glu Asp Ala
         40                  45                  50

gca gtc acc gcc cag ggt gaa ggc gga ggc gct cgc acc gtc aag gaa   307
Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala Arg Thr Val Lys Glu
     55                  60                  65

ttc cag cgt gac cag caa ttc tct agt ttt gct ctt acc tgg acc ggt   355
Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala Leu Thr Trp Thr Gly
 70                  75                  80                  85

aaa aaa gac atc act gct ttt gtt cgc gca gaa cag gaa gac ggc acc   403
Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu Gln Glu Asp Gly Thr
                 90                  95                 100

tgg tca cag tgg tac gac ttg gag cca atg gtc aat gaa gat caa ggc   451
Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val Asn Glu Asp Gln Gly
            105                 110                 115

acc aac gga act gag ctg atc tgg cac ggc cct acc aac aag atc cag   499
Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro Thr Asn Lys Ile Gln
        120                 125                 130

gtt tcc acc ctc aac gtg gat ctc ttt gga gca gat gct gca gcc gct   547
Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala Asp Ala Ala Ala Ala
    135                 140                 145

gat gaa aac ggt caa gac att cca gca gta gat gca gcc gag gca gcg   595
Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp Ala Ala Glu Ala Ala
150                 155                 160                 165

cca gca gca gaa cct gca cca gct gaa gca cca gtc gag gaa gct cct   643
Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro Val Glu Glu Ala Pro
                170                 175                 180

gca cct gtc gca gaa cca gca cca gct gct gaa cct atc gct gag cca   691
Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu Pro Ile Ala Glu Pro
            185                 190                 195

gtc gct gat tac tca gca aat gac ggc ctc gct ccc ctg cca tcc aac   739
Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala Pro Leu Pro Ser Asn
        200                 205                 210

tat ggc gac atc cag cct gtt gcc gat gtt gat gac ggc cta aac gca   787
Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp Asp Gly Leu Asn Ala
    215                 220                 225

gta ttt atc gat ggc aac gct gat gca ggc gtg ggt atc gct aac gtt   835
Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val Gly Ile Ala Asn Val
230                 235                 240                 245

gct gac acc gat ggc atg cca aag gtg att tct cgt gct ggt tgg ggt   883
Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser Arg Ala Gly Trp Gly
                250                 255                 260
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gcg gac gaa agt ctg cgc tgc tca aac cca act att gat gat ggc gtt   931
Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr Ile Asp Asp Gly Val
            265                 270                 275

tct gcg atc acc att cac cac act gcg ggt tcc aac aac tac acc gag   979
Ser Ala Ile Thr Ile His His Thr Ala Gly Ser Asn Asn Tyr Thr Glu
        280                 285                 290

gcg cag gct gca gcc cag gtt cgt agt gct tac agc tac cac gcc aag   1027
Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr Ser Tyr His Ala Lys
    295                 300                 305

aac ctc ggc tgg tgc gat atc gga tac cag tca ttg gtt gat aag tac   1075
Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser Leu Val Asp Lys Tyr
310                 315                 320                 325

ggc aac atc tac gaa ggc cgt gcc ggc ggc atg acc aat gct gtt cag   1123
Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met Thr Asn Ala Val Gln
                330                 335                 340

ggt gct cac gct ggc ggc ttc aac cag aat act tgg gca atc tcc atg   1171
Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr Trp Ala Ile Ser Met
            345                 350                 355

att ggc gac tat tcc tac aac gct ccc cct cag gaa acc atc aat gct   1219
Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln Glu Thr Ile Asn Ala
        360                 365                 370

gtc ggt gag ctt gct ggt tgg cgt gca aag gtt gcc ggt ttc gac cca   1267
Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val Ala Gly Phe Asp Pro
    375                 380                 385

act ggg act gat act cac tac tcg gag ggt act tct tac gcg aag tac   1315
Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr Ser Tyr Ala Lys Tyr
390                 395                 400                 405

tcc tat ggc acc cga gtg tca ctt cct aat atc ttg gct cac cgc aat   1363
Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile Leu Ala His Arg Asn
                410                 415                 420

gtc ggc ctg acc gca tgt cct ggc gat gct ggc tat gcg caa atg gag   1411
Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly Tyr Ala Gln Met Glu
            425                 430                 435

aat atc cgc cag atc gtt aag gca aag tac acc agc ttg cag aat ggc   1459
Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr Ser Leu Gln Asn Gly
        440                 445                 450

aac aca ggt ggc acg act acc acc ccg gcg aca acg ccg aag gag acg   1507
Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr Thr Pro Lys Glu Thr
    455                 460                 465

tcg aca agc aat gct cct tcg acg acc act gcc cag ctt gta act ccc   1555
Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala Gln Leu Val Thr Pro
470                 475                 480                 485

gct gaa cct cag cag tac agc gaa tcc gat gcc ctg gca gct ctg ctg   1603
Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala Leu Ala Ala Leu Leu
                490                 495                 500

aca ggt ggc tct tcc ggc ggc acc gac ctg ctc aat ggc gca aac tct   1651
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Sequence Listing

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Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu Asn Gly Ala Asn Ser
            505                 510                 515

gag cag ctc ctg act ggc ctg ggt tcc att gcg gct gtg ctg att gct   1699
Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala Ala Val Leu Ile Ala
        520                 525                 530

gcg tct ttg gct gat ggt ggc ctg aat ggt ctg atc agc aat gtt ggt   1747
Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu Ile Ser Asn Val Gly
    535                 540                 545

agc aac aac ggc gtc cca gtg ctt ggc gat atc aag atc act gac gtc   1795
Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile Lys Ile Thr Asp Val
550                 555                 560                 565

atc cca atc gtt gat acc gcg atc aac cta acc gga gac aat aag tac   1843
Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr Gly Asp Asn Lys Tyr
                570                 575                 580

tct cgc ggt tgg aac gac ctg aac aac acg ctt gga cca gtg ctt ggc   1891
Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu Gly Pro Val Leu Gly
            585                 590                 595

gct gcc act ggt ggc gaa acc acc gtg aag tac acc agc gac cag aac   1939
Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr Thr Ser Asp Gln Asn
        600                 605                 610

tct gag gtt act ttc gtg ccg ttt gaa aat ggc atc atg gtg tct tcc   1987
Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly Ile Met Val Ser Ser
    615                 620                 625

cct gag gct gga act cac ggc ctg tgg ggc gca atc ggt gac gcg tgg   2035
Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala Ile Gly Asp Ala Trp
630                 635                 640                 645

gct cag cag ggc gct gac ctt ggc cct ctg gga ctt cca acc agt aat   2083
Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly Leu Pro Thr Ser Asn
                650                 655                 660

gaa tac acc gtt ggc gaa cag ctt cgt gtt gat ttc cag aat ggt tac   2131
Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp Phe Gln Asn Gly Tyr
            665                 670                 675

atc act tac gat tct gcg act ggc cag gca agc att cag ctg aac       2176
Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser Ile Gln Leu Asn
        680                 685                 690

tagtctcaat tagagccgaa aac                                        2199


<210> 30
<211> 692
<212> PRT
<213> Corynebacterium glutamicum

<400> 30
Met Leu Ala Ile Ile Leu Thr Ala Val Leu Gly Ala Ser Gly Leu Ala
  1               5                  10                  15

Ala Ala Gly Thr Gln Tyr Leu Asn Thr Gln Gly Glu Gly Ile Gly Pro
             20                  25                  30
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```
Val Ala Val Gln Asn Asp Ser Glu Ser Phe Asn Ser Gly Thr Asn Val
         35                  40                  45

Val Val Glu Asp Ala Ala Val Thr Ala Gln Gly Glu Gly Gly Gly Ala
     50                  55                  60

Arg Thr Val Lys Glu Phe Gln Arg Asp Gln Gln Phe Ser Ser Phe Ala
 65                  70                  75                  80

Leu Thr Trp Thr Gly Lys Lys Asp Ile Thr Ala Phe Val Arg Ala Glu
                 85                  90                  95

Gln Glu Asp Gly Thr Trp Ser Gln Trp Tyr Asp Leu Glu Pro Met Val
            100                 105                 110

Asn Glu Asp Gln Gly Thr Asn Gly Thr Glu Leu Ile Trp His Gly Pro
        115                 120                 125

Thr Asn Lys Ile Gln Val Ser Thr Leu Asn Val Asp Leu Phe Gly Ala
    130                 135                 140

Asp Ala Ala Ala Ala Asp Glu Asn Gly Gln Asp Ile Pro Ala Val Asp
145                 150                 155                 160

Ala Ala Glu Ala Ala Pro Ala Ala Glu Pro Ala Pro Ala Glu Ala Pro
                165                 170                 175

Val Glu Glu Ala Pro Ala Pro Val Ala Glu Pro Ala Pro Ala Ala Glu
            180                 185                 190

Pro Ile Ala Glu Pro Val Ala Asp Tyr Ser Ala Asn Asp Gly Leu Ala
        195                 200                 205

Pro Leu Pro Ser Asn Tyr Gly Asp Ile Gln Pro Val Ala Asp Val Asp
    210                 215                 220

Asp Gly Leu Asn Ala Val Phe Ile Asp Gly Asn Ala Asp Ala Gly Val
225                 230                 235                 240

Gly Ile Ala Asn Val Ala Asp Thr Asp Gly Met Pro Lys Val Ile Ser
                245                 250                 255

Arg Ala Gly Trp Gly Ala Asp Glu Ser Leu Arg Cys Ser Asn Pro Thr
            260                 265                 270

Ile Asp Asp Gly Val Ser Ala Ile Thr Ile His His Thr Ala Gly Ser
        275                 280                 285

Asn Asn Tyr Thr Glu Ala Gln Ala Ala Ala Gln Val Arg Ser Ala Tyr
    290                 295                 300

Ser Tyr His Ala Lys Asn Leu Gly Trp Cys Asp Ile Gly Tyr Gln Ser
305                 310                 315                 320

Leu Val Asp Lys Tyr Gly Asn Ile Tyr Glu Gly Arg Ala Gly Gly Met
                325                 330                 335

Thr Asn Ala Val Gln Gly Ala His Ala Gly Gly Phe Asn Gln Asn Thr
            340                 345                 350
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Trp Ala Ile Ser Met Ile Gly Asp Tyr Ser Tyr Asn Ala Pro Pro Gln
        355                 360                 365

Glu Thr Ile Asn Ala Val Gly Glu Leu Ala Gly Trp Arg Ala Lys Val
    370                 375                 380

Ala Gly Phe Asp Pro Thr Gly Thr Asp Thr His Tyr Ser Glu Gly Thr
385                 390                 395                 400

Ser Tyr Ala Lys Tyr Ser Tyr Gly Thr Arg Val Ser Leu Pro Asn Ile
                405                 410                 415

Leu Ala His Arg Asn Val Gly Leu Thr Ala Cys Pro Gly Asp Ala Gly
            420                 425                 430

Tyr Ala Gln Met Glu Asn Ile Arg Gln Ile Val Lys Ala Lys Tyr Thr
        435                 440                 445

Ser Leu Gln Asn Gly Asn Thr Gly Gly Thr Thr Thr Thr Pro Ala Thr
    450                 455                 460

Thr Pro Lys Glu Thr Ser Thr Ser Asn Ala Pro Ser Thr Thr Thr Ala
465                 470                 475                 480

Gln Leu Val Thr Pro Ala Glu Pro Gln Gln Tyr Ser Glu Ser Asp Ala
                485                 490                 495

Leu Ala Ala Leu Leu Thr Gly Gly Ser Ser Gly Gly Thr Asp Leu Leu
            500                 505                 510

Asn Gly Ala Asn Ser Glu Gln Leu Leu Thr Gly Leu Gly Ser Ile Ala
        515                 520                 525

Ala Val Leu Ile Ala Ala Ser Leu Ala Asp Gly Gly Leu Asn Gly Leu
    530                 535                 540

Ile Ser Asn Val Gly Ser Asn Asn Gly Val Pro Val Leu Gly Asp Ile
545                 550                 555                 560

Lys Ile Thr Asp Val Ile Pro Ile Val Asp Thr Ala Ile Asn Leu Thr
                565                 570                 575

Gly Asp Asn Lys Tyr Ser Arg Gly Trp Asn Asp Leu Asn Asn Thr Leu
            580                 585                 590

Gly Pro Val Leu Gly Ala Ala Thr Gly Gly Glu Thr Thr Val Lys Tyr
        595                 600                 605

Thr Ser Asp Gln Asn Ser Glu Val Thr Phe Val Pro Phe Glu Asn Gly
    610                 615                 620

Ile Met Val Ser Ser Pro Glu Ala Gly Thr His Gly Leu Trp Gly Ala
625                 630                 635                 640

Ile Gly Asp Ala Trp Ala Gln Gln Gly Ala Asp Leu Gly Pro Leu Gly
                645                 650                 655

Leu Pro Thr Ser Asn Glu Tyr Thr Val Gly Glu Gln Leu Arg Val Asp
            660                 665                 670

Phe Gln Asn Gly Tyr Ile Thr Tyr Asp Ser Ala Thr Gly Gln Ala Ser
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675 680 685

Ile Gln Leu Asn
690

<210> 31
<211> 1377
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1354)
<223> RXA00135

<400> 31
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gttacgcaca ggggtgggga acacggataa ggtggggcac gtg aaa gac aag ttt 115
Val Lys Asp Lys Phe
1 5

tta gtc act ggt gga gca cag ctg cag ggc gct gta aaa gtt tac ggc 163
Leu Val Thr Gly Gly Ala Gln Leu Gln Gly Ala Val Lys Val Tyr Gly
10 15 20

gca aaa aac agc gtt ttg aag ctc atg gca gca gca ctt ctc gct gaa 211
Ala Lys Asn Ser Val Leu Lys Leu Met Ala Ala Ala Leu Leu Ala Glu
25 30 35

ggc aca aca act cta acc aat tgc ccc gaa atc ctc gac gtc ccc ctg 259
Gly Thr Thr Thr Leu Thr Asn Cys Pro Glu Ile Leu Asp Val Pro Leu
40 45 50

atg cgc gac gtc ctc gtt ggt ctt ggc tgc gat gtc acc atc gac ggc 307
Met Arg Asp Val Leu Val Gly Leu Gly Cys Asp Val Thr Ile Asp Gly
55 60 65

tca acc gta acc att act acc cct gca gaa ctc agc tcc aat gct gac 355
Ser Thr Val Thr Ile Thr Thr Pro Ala Glu Leu Ser Ser Asn Ala Asp
70 75 80 85

ttc cca gca gtc acc caa ttc cgt gca tcc gta tgt gtg ctt ggt cca 403
Phe Pro Ala Val Thr Gln Phe Arg Ala Ser Val Cys Val Leu Gly Pro
90 95 100

ttg aca gca cgt tgt ggt cgc gca gtt gta tcc ctt ccc ggc ggt gac 451
Leu Thr Ala Arg Cys Gly Arg Ala Val Val Ser Leu Pro Gly Gly Asp
105 110 115

gcc att gga tcc cgt cca ctc gac atg cat caa agc ggc ctg gaa aag 499
Ala Ile Gly Ser Arg Pro Leu Asp Met His Gln Ser Gly Leu Glu Lys
120 125 130

ctt ggt gcc acc acc cgc att tcc cac ggt gca gta gtt gca gaa gct 547
Leu Gly Ala Thr Thr Arg Ile Ser His Gly Ala Val Val Ala Glu Ala
135 140 145

gaa aag ctc gtc ggt gcc aac atc acc ctg gat ttc ccg tcc gtc ggc 595
Glu Lys Leu Val Gly Ala Asn Ile Thr Leu Asp Phe Pro Ser Val Gly

```
150                 155                 160                 165

gcc acc gaa aac atc ctc act gca tcc gtc atg gca gaa gga cgc aca   643
Ala Thr Glu Asn Ile Leu Thr Ala Ser Val Met Ala Glu Gly Arg Thr
                170                 175                 180

gta tta gat aac gca gcg cgc gaa cca gaa att gtt gat ctc tgc cgt   691
Val Leu Asp Asn Ala Ala Arg Glu Pro Glu Ile Val Asp Leu Cys Arg
            185                 190                 195

atg ctt cga tcc atg ggc gcc aac att gaa ggt gaa gga agc cca ccc   739
Met Leu Arg Ser Met Gly Ala Asn Ile Glu Gly Glu Gly Ser Pro Pro
        200                 205                 210

atc acc atc gaa ggc gta gag aaa ctc acc cca act cag cac gaa gta   787
Ile Thr Ile Glu Gly Val Glu Lys Leu Thr Pro Thr Gln His Glu Val
    215                 220                 225

atc ggc gac cgc atc gtt gcc gga acg tgg gca tac gcc gct gcg atg   835
Ile Gly Asp Arg Ile Val Ala Gly Thr Trp Ala Tyr Ala Ala Ala Met
230                 235                 240                 245

act cgt ggc gat att aca gtt ggc gga atc gca cca agg tat ctg cac   883
Thr Arg Gly Asp Ile Thr Val Gly Gly Ile Ala Pro Arg Tyr Leu His
                250                 255                 260

ctt cca ttg gaa aag ctc aag atc gcc ggc gcc aag gtg gaa acc tac   931
Leu Pro Leu Glu Lys Leu Lys Ile Ala Gly Ala Lys Val Glu Thr Tyr
            265                 270                 275

gaa aac ggc ttc cgc gtc caa atg gat aag cag cct gag gca acc gac   979
Glu Asn Gly Phe Arg Val Gln Met Asp Lys Gln Pro Glu Ala Thr Asp
        280                 285                 290

tac caa acc ctc ccg ttc cca ggg ttc cct aca gat ctg caa ccc atg  1027
Tyr Gln Thr Leu Pro Phe Pro Gly Phe Pro Thr Asp Leu Gln Pro Met
    295                 300                 305

gca att gga atc aac gca gta tct aat gga act tca gta att aca gag  1075
Ala Ile Gly Ile Asn Ala Val Ser Asn Gly Thr Ser Val Ile Thr Glu
310                 315                 320                 325

aat gtc ttt gaa tca cga ttc cgc ttc gtc gat gaa atg ctt cgc ctg  1123
Asn Val Phe Glu Ser Arg Phe Arg Phe Val Asp Glu Met Leu Arg Leu
                330                 335                 340

ggc gct gac gcg aat gtc gat ggg cac cac gta gta atc cga gga att  1171
Gly Ala Asp Ala Asn Val Asp Gly His His Val Val Ile Arg Gly Ile
            345                 350                 355

gaa cag ctt tcc tct act tcc gtg tgg tct tca gat atc cgt gca gga  1219
Glu Gln Leu Ser Ser Thr Ser Val Trp Ser Ser Asp Ile Arg Ala Gly
        360                 365                 370

gca gga ctg gtt ctt gcc gcc ctt tgc gca gac gga gtg acc gaa gtt  1267
Ala Gly Leu Val Leu Ala Ala Leu Cys Ala Asp Gly Val Thr Glu Val
    375                 380                 385

cac gat gtt ttc cac atc gac cgc gga tac ccc aac ttc gtg gaa aat  1315
His Asp Val Phe His Ile Asp Arg Gly Tyr Pro Asn Phe Val Glu Asn
390                 395                 400                 405
```

Sequence Listing

```
ctg cag aaa ctc gga gcg acc atc gaa agg gtt tct tcc taacgaagcc    1364
Leu Gln Lys Leu Gly Ala Thr Ile Glu Arg Val Ser Ser
                410                 415

ttcccatcaa gca                                                   1377
```

<210> 32
<211> 418
<212> PRT
<213> Corynebacterium glutamicum

<400> 32

```
Val Lys Asp Lys Phe Leu Val Thr Gly Gly Ala Gln Leu Gln Gly Ala
  1               5                  10                  15

Val Lys Val Tyr Gly Ala Lys Asn Ser Val Leu Lys Leu Met Ala Ala
             20                  25                  30

Ala Leu Leu Ala Glu Gly Thr Thr Thr Leu Thr Asn Cys Pro Glu Ile
         35                  40                  45

Leu Asp Val Pro Leu Met Arg Asp Val Leu Val Gly Leu Gly Cys Asp
     50                  55                  60

Val Thr Ile Asp Gly Ser Thr Val Thr Ile Thr Thr Pro Ala Glu Leu
 65                  70                  75                  80

Ser Ser Asn Ala Asp Phe Pro Ala Val Thr Gln Phe Arg Ala Ser Val
                 85                  90                  95

Cys Val Leu Gly Pro Leu Thr Ala Arg Cys Gly Arg Ala Val Val Ser
            100                 105                 110

Leu Pro Gly Gly Asp Ala Ile Gly Ser Arg Pro Leu Asp Met His Gln
        115                 120                 125

Ser Gly Leu Glu Lys Leu Gly Ala Thr Thr Arg Ile Ser His Gly Ala
    130                 135                 140

Val Val Ala Glu Ala Glu Lys Leu Val Gly Ala Asn Ile Thr Leu Asp
145                 150                 155                 160

Phe Pro Ser Val Gly Ala Thr Glu Asn Ile Leu Thr Ala Ser Val Met
                165                 170                 175

Ala Glu Gly Arg Thr Val Leu Asp Asn Ala Ala Arg Glu Pro Glu Ile
            180                 185                 190

Val Asp Leu Cys Arg Met Leu Arg Ser Met Gly Ala Asn Ile Glu Gly
        195                 200                 205

Glu Gly Ser Pro Pro Ile Thr Ile Glu Gly Val Glu Lys Leu Thr Pro
    210                 215                 220

Thr Gln His Glu Val Ile Gly Asp Arg Ile Val Ala Gly Thr Trp Ala
225                 230                 235                 240

Tyr Ala Ala Ala Met Thr Arg Gly Asp Ile Thr Val Gly Gly Ile Ala
                245                 250                 255
```

```
Pro Arg Tyr Leu His Leu Pro Leu Glu Lys Leu Lys Ile Ala Gly Ala
            260                 265                 270

Lys Val Glu Thr Tyr Glu Asn Gly Phe Arg Val Gln Met Asp Lys Gln
        275                 280                 285

Pro Glu Ala Thr Asp Tyr Gln Thr Leu Pro Phe Pro Gly Phe Pro Thr
    290                 295                 300

Asp Leu Gln Pro Met Ala Ile Gly Ile Asn Ala Val Ser Asn Gly Thr
305                 310                 315                 320

Ser Val Ile Thr Glu Asn Val Phe Glu Ser Arg Phe Arg Phe Val Asp
                325                 330                 335

Glu Met Leu Arg Leu Gly Ala Asp Ala Asn Val Asp Gly His His Val
            340                 345                 350

Val Ile Arg Gly Ile Glu Gln Leu Ser Ser Thr Ser Val Trp Ser Ser
        355                 360                 365

Asp Ile Arg Ala Gly Ala Gly Leu Val Leu Ala Ala Leu Cys Ala Asp
    370                 375                 380

Gly Val Thr Glu Val His Asp Val Phe His Ile Asp Arg Gly Tyr Pro
385                 390                 395                 400

Asn Phe Val Glu Asn Leu Gln Lys Leu Gly Ala Thr Ile Glu Arg Val
                405                 410                 415

Ser Ser
```

<210> 33
<211> 1221
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1198)
<223> RXA02706

<400> 33

```
ggtcgcagaa gcactacatg gcatggtgcc gggcctcaaa aacacaggtg gctcggtcaa 60

cgacgattct cgtcggaacg tggaaggaca gtagaaaaca atg caa cag att atg   115
                                              Met Gln Gln Ile Met
                                                1               5

gtc agt gga acg gtt gcg ttc ctc gtc tca atc ttt ctc acc ccg gtg   163
Val Ser Gly Thr Val Ala Phe Leu Val Ser Ile Phe Leu Thr Pro Val
                10                  15                  20

ttg atc cgt tat ttc act aac cgc cag ttg ggc cag gaa atc cgt gaa   211
Leu Ile Arg Tyr Phe Thr Asn Arg Gln Leu Gly Gln Glu Ile Arg Glu
            25                  30                  35

gaa ggc ctg cag tct cac ttg cgt aag cgt ggc act cca acc atg ggt   259
```

```
Glu Gly Leu Gln Ser His Leu Arg Lys Arg Gly Thr Pro Thr Met Gly
         40                  45                  50

ggc att gcg att atc gcg ggc att gtt gtg gcc tat gtg ttt acc aat   307
Gly Ile Ala Ile Ile Ala Gly Ile Val Val Ala Tyr Val Phe Thr Asn
     55                  60                  65

atc ttg gcc atg atc caa ggc gtt ggt gga ttc aca gtc tcc ggc ttg   355
Ile Leu Ala Met Ile Gln Gly Val Gly Gly Phe Thr Val Ser Gly Leu
 70                  75                  80                  85

ctc gtg ttg ggt ctg acc ttg ggc ctt ggt gcc act ggt ttc gcc gat   403
Leu Val Leu Gly Leu Thr Leu Gly Leu Gly Ala Thr Gly Phe Ala Asp
                 90                  95                 100

gac ttc atc aag ctg tac atg aac cga aac ctt ggt ttg aac aag acc   451
Asp Phe Ile Lys Leu Tyr Met Asn Arg Asn Leu Gly Leu Asn Lys Thr
            105                 110                 115

gct aag ctg gtg tct cag ctg gcc att gcg ttg atc ttt ggt ttt ttg   499
Ala Lys Leu Val Ser Gln Leu Ala Ile Ala Leu Ile Phe Gly Phe Leu
        120                 125                 130

gta ctg cag ttt ccc gat gaa aac ggt ctg acc cca gca tca acc cac   547
Val Leu Gln Phe Pro Asp Glu Asn Gly Leu Thr Pro Ala Ser Thr His
    135                 140                 145

ctg tca ttc att cgc gat atc gac acc att gac ctt ggc ttc ggg ggc   595
Leu Ser Phe Ile Arg Asp Ile Asp Thr Ile Asp Leu Gly Phe Gly Gly
150                 155                 160                 165

agc gtt ttt ggc atc atc gtg ttc ctc atc ttt atc tac gtt gtg gtc   643
Ser Val Phe Gly Ile Ile Val Phe Leu Ile Phe Ile Tyr Val Val Val
                170                 175                 180

agc gcg tgg tcg aat gcc gtg aac atc act gac ggt ttg gat ggt ttg   691
Ser Ala Trp Ser Asn Ala Val Asn Ile Thr Asp Gly Leu Asp Gly Leu
            185                 190                 195

gcc gca ggt acc aca gca ttt gtc atg ggt gct tac acc ttg atc acg   739
Ala Ala Gly Thr Thr Ala Phe Val Met Gly Ala Tyr Thr Leu Ile Thr
        200                 205                 210

ttc tgg cag ttc cga aac tcc tgc gat act gca gtg gaa gcg ggt tgc   787
Phe Trp Gln Phe Arg Asn Ser Cys Asp Thr Ala Val Glu Ala Gly Cys
    215                 220                 225

tat acg gtg cgt gat cca ctg gat ttg tcc gtg ttg tgt gct gct ggt   835
Tyr Thr Val Arg Asp Pro Leu Asp Leu Ser Val Leu Cys Ala Ala Gly
230                 235                 240                 245

ctg ggc gcc acc ttg ggc ttt ctg tgg tgg aat gcg gcg ccg gca aag   883
Leu Gly Ala Thr Leu Gly Phe Leu Trp Trp Asn Ala Ala Pro Ala Lys
                250                 255                 260

atc ttc atg ggc gat act ggt tct ttg gca ctg ggc ggt ttg gtt gca   931
Ile Phe Met Gly Asp Thr Gly Ser Leu Ala Leu Gly Gly Leu Val Ala
            265                 270                 275

ggt att tct gtg gtt agt cgc acc gag ctg ctc atg gtt atc atc ggc   979
Gly Ile Ser Val Val Ser Arg Thr Glu Leu Leu Met Val Ile Ile Gly
```

```
        280                 285                 290

gcg ctg ttt gtc att gag atc gct tct gtt gcg atc cag atc ggc gtg   1027
Ala Leu Phe Val Ile Glu Ile Ala Ser Val Ala Ile Gln Ile Gly Val
    295                 300                 305

ttt aag acc cgc ggt aag cgt gtg ttc aaa atg gct ccg atc cac cac   1075
Phe Lys Thr Arg Gly Lys Arg Val Phe Lys Met Ala Pro Ile His His
310                 315                 320                 325

cac ttc gag gcc ctt ggg tgg gct gaa act acc gtg acc atc cgt ttc   1123
His Phe Glu Ala Leu Gly Trp Ala Glu Thr Thr Val Thr Ile Arg Phe
                330                 335                 340

tgg ctg atc gcg atc atg gct gtg ttg gcg ggt gtc ggt gtg ttt tac   1171
Trp Leu Ile Ala Ile Met Ala Val Leu Ala Gly Val Gly Val Phe Tyr
            345                 350                 355

agc gac tgg ctc cac tta gcg gag gta taaataatta tgggttctct         1218
Ser Asp Trp Leu His Leu Ala Glu Val
        360                 365

gtc                                                               1221
```

Sequence Listing

<210> 34
<211> 366
<212> PRT
<213> Corynebacterium glutamicum

<400> 34

```
Met Gln Gln Ile Met Val Ser Gly Thr Val Ala Phe Leu Val Ser Ile
  1               5                  10                  15

Phe Leu Thr Pro Val Leu Ile Arg Tyr Phe Thr Asn Arg Gln Leu Gly
             20                  25                  30

Gln Glu Ile Arg Glu Glu Gly Leu Gln Ser His Leu Arg Lys Arg Gly
         35                  40                  45

Thr Pro Thr Met Gly Gly Ile Ala Ile Ile Ala Gly Ile Val Val Ala
     50                  55                  60

Tyr Val Phe Thr Asn Ile Leu Ala Met Ile Gln Gly Val Gly Gly Phe
 65                  70                  75                  80

Thr Val Ser Gly Leu Leu Val Leu Gly Leu Thr Leu Gly Leu Gly Ala
                 85                  90                  95

Thr Gly Phe Ala Asp Asp Phe Ile Lys Leu Tyr Met Asn Arg Asn Leu
            100                 105                 110

Gly Leu Asn Lys Thr Ala Lys Leu Val Ser Gln Leu Ala Ile Ala Leu
        115                 120                 125

Ile Phe Gly Phe Leu Val Leu Gln Phe Pro Asp Glu Asn Gly Leu Thr
    130                 135                 140

Pro Ala Ser Thr His Leu Ser Phe Ile Arg Asp Ile Asp Thr Ile Asp
145                 150                 155                 160
```

```
Leu Gly Phe Gly Gly Ser Val Phe Gly Ile Ile Val Phe Leu Ile Phe
                165                 170                 175

Ile Tyr Val Val Val Ser Ala Trp Ser Asn Ala Val Asn Ile Thr Asp
            180                 185                 190

Gly Leu Asp Gly Leu Ala Ala Gly Thr Thr Ala Phe Val Met Gly Ala
        195                 200                 205

Tyr Thr Leu Ile Thr Phe Trp Gln Phe Arg Asn Ser Cys Asp Thr Ala
    210                 215                 220

Val Glu Ala Gly Cys Tyr Thr Val Arg Asp Pro Leu Asp Leu Ser Val
225                 230                 235                 240

Leu Cys Ala Ala Gly Leu Gly Ala Thr Leu Gly Phe Leu Trp Trp Asn
                245                 250                 255

Ala Ala Pro Ala Lys Ile Phe Met Gly Asp Thr Gly Ser Leu Ala Leu
            260                 265                 270

Gly Gly Leu Val Ala Gly Ile Ser Val Val Ser Arg Thr Glu Leu Leu
        275                 280                 285

Met Val Ile Ile Gly Ala Leu Phe Val Ile Glu Ile Ala Ser Val Ala
    290                 295                 300

Ile Gln Ile Gly Val Phe Lys Thr Arg Gly Lys Arg Val Phe Lys Met
305                 310                 315                 320

Ala Pro Ile His His His Phe Glu Ala Leu Gly Trp Ala Glu Thr Thr
                325                 330                 335

Val Thr Ile Arg Phe Trp Leu Ile Ala Ile Met Ala Val Leu Ala Gly
            340                 345                 350

Val Gly Val Phe Tyr Ser Asp Trp Leu His Leu Ala Glu Val
        355                 360                 365
```

Sequence Listing

<210> 35
<211> 972
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(949)
<223> RXA02411

<400> 35
gcagcgaatc gtctggtttc ttgatcgggt gaatcagcca ttgccatatt gtgacacatc 60

ttggacggat aaaaagggaa gcaacgcgag gtggcttatg atg gca acc gtg act 115
                                    Met Ala Thr Val Thr
                                      1   5

gat ttc agt gga tct atg att gaa cgc ccc gtg cca ggt gct gat gcg 163
Asp Phe Ser Gly Ser Met Ile Glu Arg Pro Val Pro Gly Ala Asp Ala
                10   15   20

```
ccg att gga att ttt gat tct gga gtt ggc gga tta acc gta gct cgc   211
Pro Ile Gly Ile Phe Asp Ser Gly Val Gly Gly Leu Thr Val Ala Arg
             25                  30                  35

aca atc atc gat caa ttg cca cat gaa tca gtt att tat atc ggt gat   259
Thr Ile Ile Asp Gln Leu Pro His Glu Ser Val Ile Tyr Ile Gly Asp
         40                  45                  50

act gcc aat ggc cct tat ggt ccg ttg cct atc gct aag gtc cgt gag   307
Thr Ala Asn Gly Pro Tyr Gly Pro Leu Pro Ile Ala Lys Val Arg Glu
     55                  60                  65

cac gcc atc cgc att gcc gat gag ttg gtg gaa cgc gga tgc aag atg   355
His Ala Ile Arg Ile Ala Asp Glu Leu Val Glu Arg Gly Cys Lys Met
 70                  75                  80                  85

att gtc att gcc tgc aac act gcg tcc gct gcg ttt ctc cga gat gcc   403
Ile Val Ile Ala Cys Asn Thr Ala Ser Ala Ala Phe Leu Arg Asp Ala
                 90                  95                 100

cgt gaa cga tac agt gtg cca gtc gtg gaa gtt att ctt ccc gca gta   451
Arg Glu Arg Tyr Ser Val Pro Val Val Glu Val Ile Leu Pro Ala Val
            105                 110                 115

agg cgt gcg gtg gca tcc acc cgc aat ggc aaa gtg ggc gtg atc ggc   499
Arg Arg Ala Val Ala Ser Thr Arg Asn Gly Lys Val Gly Val Ile Gly
        120                 125                 130

aca gtg gga acc att aac tcc ggt gcg tac cag gat ctt ttc tct gca   547
Thr Val Gly Thr Ile Asn Ser Gly Ala Tyr Gln Asp Leu Phe Ser Ala
    135                 140                 145

agc ccc tcc att gtg gtc aac gca gtg gca tgc cca cgg ttt gtg gat   595
Ser Pro Ser Ile Val Val Asn Ala Val Ala Cys Pro Arg Phe Val Asp
150                 155                 160                 165

ttc gtg gaa cgc gga att acc agc ggc agg cag atc ctc aac att gcg   643
Phe Val Glu Arg Gly Ile Thr Ser Gly Arg Gln Ile Leu Asn Ile Ala
                170                 175                 180

cag gat tat tta gag cct ttg caa gca gaa ggg gtg gac acc ctc gtg   691
Gln Asp Tyr Leu Glu Pro Leu Gln Ala Glu Gly Val Asp Thr Leu Val
            185                 190                 195

ctt gga tgc acc cac tat cca ctg ctt tcc ggt gtc att cag ttg gca   739
Leu Gly Cys Thr His Tyr Pro Leu Leu Ser Gly Val Ile Gln Leu Ala
        200                 205                 210

atg ggg gac cac gta agt ttg gtc tct agc gcg gaa gaa act gcg aaa   787
Met Gly Asp His Val Ser Leu Val Ser Ser Ala Glu Glu Thr Ala Lys
    215                 220                 225

gac gtg ctg aga att ttg agc cag caa gat ctt tta gcc gat ccg gac   835
Asp Val Leu Arg Ile Leu Ser Gln Gln Asp Leu Leu Ala Asp Pro Asp
230                 235                 240                 245

atg cat cct gag cca agt tat agc ttt gaa tca aca ggc gat ccg gaa   883
Met His Pro Glu Pro Ser Tyr Ser Phe Glu Ser Thr Gly Asp Pro Glu
                250                 255                 260

atc ttt gcg caa tta agc cgc cga ttc ctt gga cca att gtt tcc caa   931
```

Replacement Sheet

```
Ile Phe Ala Gln Leu Ser Arg Arg Phe Leu Gly Pro Ile Val Ser Gln
            265                 270                 275

gtg aga caa aac gag gga taaccccagg tgtgtgttct acc                  972
Val Arg Gln Asn Glu Gly
        280
```

<210> 36
<211> 283
<212> PRT
<213> Corynebacterium glutamicum

<400> 36

```
Met Ala Thr Val Thr Asp Phe Ser Gly Ser Met Ile Glu Arg Pro Val
  1               5                  10                  15

Pro Gly Ala Asp Ala Pro Ile Gly Ile Phe Asp Ser Gly Val Gly Gly
             20                  25                  30

Leu Thr Val Ala Arg Thr Ile Ile Asp Gln Leu Pro His Glu Ser Val
         35                  40                  45

Ile Tyr Ile Gly Asp Thr Ala Asn Gly Pro Tyr Gly Pro Leu Pro Ile
     50                  55                  60

Ala Lys Val Arg Glu His Ala Ile Arg Ile Ala Asp Glu Leu Val Glu
 65                  70                  75                  80

Arg Gly Cys Lys Met Ile Val Ile Ala Cys Asn Thr Ala Ser Ala Ala
                 85                  90                  95

Phe Leu Arg Asp Ala Arg Glu Arg Tyr Ser Val Pro Val Val Glu Val
            100                 105                 110

Ile Leu Pro Ala Val Arg Arg Ala Val Ala Ser Thr Arg Asn Gly Lys
        115                 120                 125

Val Gly Val Ile Gly Thr Val Gly Thr Ile Asn Ser Gly Ala Tyr Gln
    130                 135                 140

Asp Leu Phe Ser Ala Ser Pro Ser Ile Val Val Asn Ala Val Ala Cys
145                 150                 155                 160

Pro Arg Phe Val Asp Phe Val Glu Arg Gly Ile Thr Ser Gly Arg Gln
                165                 170                 175

Ile Leu Asn Ile Ala Gln Asp Tyr Leu Glu Pro Leu Gln Ala Glu Gly
            180                 185                 190

Val Asp Thr Leu Val Leu Gly Cys Thr His Tyr Pro Leu Leu Ser Gly
        195                 200                 205

Val Ile Gln Leu Ala Met Gly Asp His Val Ser Leu Val Ser Ser Ala
    210                 215                 220

Glu Glu Thr Ala Lys Asp Val Leu Arg Ile Leu Ser Gln Gln Asp Leu
225                 230                 235                 240

Leu Ala Asp Pro Asp Met His Pro Glu Pro Ser Tyr Ser Phe Glu Ser
                245                 250                 255
```

```
Thr Gly Asp Pro Glu Ile Phe Ala Gln Leu Ser Arg Arg Phe Leu Gly
            260                 265                 270

Pro Ile Val Ser Gln Val Arg Gln Asn Glu Gly
        275                 280


<210> 37
<211> 1203
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1180)
<223> RXN01022

<400> 37
cggtgtgtgc caccgagata tgaaagtaac tgacatgatt gtggctctca tgggcaggtc 60

taagaaggct gagtagtctt aggttgtaag cttcaatgct gtg agc aac tct aat   115
                                          Val Ser Asn Ser Asn
                                            1               5

tct gga aaa gtc cgc gtc gca gtc gtt tat ggt ggt cgc agt tct gag   163
Ser Gly Lys Val Arg Val Ala Val Val Tyr Gly Gly Arg Ser Ser Glu
                  10                  15                  20

cac tcc gtc tcc tgc gtc tcc gct ggt gct atc atg gcc cat ctc gat   211
His Ser Val Ser Cys Val Ser Ala Gly Ala Ile Met Ala His Leu Asp
              25                  30                  35

cct gag aag tac gat gtg att ccc gtc ggc att act gtc gac ggc gcg   259
Pro Glu Lys Tyr Asp Val Ile Pro Val Gly Ile Thr Val Asp Gly Ala
          40                  45                  50

tgg gtt gtt ggt gaa acc gat cca cag aag cta act ctc atc gat cgc   307
Trp Val Val Gly Glu Thr Asp Pro Gln Lys Leu Thr Leu Ile Asp Arg
      55                  60                  65

acc atg cct gag gtg gag cat cat gaa gag gtt cgc cca agc ctg gat   355
Thr Met Pro Glu Val Glu His His Glu Glu Val Arg Pro Ser Leu Asp
  70                  75                  80                  85

ccc gca cac cgt gga gag ttc cac ttt tcc gat ggc agc ttg tat gcc   403
Pro Ala His Arg Gly Glu Phe His Phe Ser Asp Gly Ser Leu Tyr Ala
                  90                  95                 100

acc gct gat gtg att ttc cct gtg ctg cat ggt cgt ttt ggt gaa gac   451
Thr Ala Asp Val Ile Phe Pro Val Leu His Gly Arg Phe Gly Glu Asp
              105                 110                 115

ggc act gtg cag ggt ctg ttt gca ctg tct gat att ccg gtc gtt ggc   499
Gly Thr Val Gln Gly Leu Phe Ala Leu Ser Asp Ile Pro Val Val Gly
          120                 125                 130

cca ggt gtg ctg gcc tct gct gcg gga atg gac aag gaa tac act aag   547
Pro Gly Val Leu Ala Ser Ala Ala Gly Met Asp Lys Glu Tyr Thr Lys
      135                 140                 145
```

```
aag ctc atg gca gcg gaa ggg ctg ccc gtt ggc cgt gag gtg att cta   595
Lys Leu Met Ala Ala Glu Gly Leu Pro Val Gly Arg Glu Val Ile Leu
150                 155                 160                 165

cgt gat cgt acc gag ctg acc gag gca gaa aag aac ctg ctg ggc ctg   643
Arg Asp Arg Thr Glu Leu Thr Glu Ala Glu Lys Asn Leu Leu Gly Leu
                170                 175                 180

cct gta ttt gtg aag cct gcg cgt ggt ggc tca tcg att ggt atc tct   691
Pro Val Phe Val Lys Pro Ala Arg Gly Gly Ser Ser Ile Gly Ile Ser
            185                 190                 195

cgt gtt act gcg tgg gag gat ttt aat aag gct gtg ggg ctt gct cgt   739
Arg Val Thr Ala Trp Glu Asp Phe Asn Lys Ala Val Gly Leu Ala Arg
        200                 205                 210

gcc cat gat gag aag gtc att gtg gaa tca gag atc gtt ggc tct gag   787
Ala His Asp Glu Lys Val Ile Val Glu Ser Glu Ile Val Gly Ser Glu
    215                 220                 225

gtg gag tgt ggc gtg ctg cag tat cca gac ggt cgt atc gtg gcg tct   835
Val Glu Cys Gly Val Leu Gln Tyr Pro Asp Gly Arg Ile Val Ala Ser
230                 235                 240                 245

gtt cct gcg ttg ctg tct ggc acc gaa tca ggc gct ggt gga ttc tat   883
Val Pro Ala Leu Leu Ser Gly Thr Glu Ser Gly Ala Gly Gly Phe Tyr
                250                 255                 260

gac ttt gat acc aag tac ttg gac aac gtt gtt act gca gag atc cca   931
Asp Phe Asp Thr Lys Tyr Leu Asp Asn Val Val Thr Ala Glu Ile Pro
            265                 270                 275

gca ccg ctt gat gag aag acc acg gaa ctg atc cag tct ttg gct gtg   979
Ala Pro Leu Asp Glu Lys Thr Thr Glu Leu Ile Gln Ser Leu Ala Val
        280                 285                 290

gaa tct ttc cag gct ctt gcg tgt gaa ggc ctt gct cgc gtg gac ttc   1027
Glu Ser Phe Gln Ala Leu Ala Cys Glu Gly Leu Ala Arg Val Asp Phe
    295                 300                 305

ttt gtt acc gcc aat ggt cct gtg ctc aat gag atc aac acc atg cca   1075
Phe Val Thr Ala Asn Gly Pro Val Leu Asn Glu Ile Asn Thr Met Pro
310                 315                 320                 325

gga ttt acc ccc att tcc atg tac cca cag atg ttc act gca tca ggc   1123
Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met Phe Thr Ala Ser Gly
                330                 335                 340

gtg gct tat gag gaa ttg ttg gat gtg ttg gtg cag cag gca ttg cac   1171
Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val Gln Gln Ala Leu His
            345                 350                 355

cgc gac aac tagcatcaaa taaaaacagc ccc                            1203
Arg Asp Asn
        360
```

<210> 38
<211> 360
<212> PRT
<213> Corynebacterium glutamicum

<400> 38

```
Val Ser Asn Ser Asn Ser Gly Lys Val Arg Val Ala Val Val Tyr Gly
  1               5                  10                  15

Gly Arg Ser Ser Glu His Ser Val Ser Cys Val Ser Ala Gly Ala Ile
             20                  25                  30

Met Ala His Leu Asp Pro Glu Lys Tyr Asp Val Ile Pro Val Gly Ile
         35                  40                  45

Thr Val Asp Gly Ala Trp Val Val Gly Glu Thr Asp Pro Gln Lys Leu
     50                  55                  60

Thr Leu Ile Asp Arg Thr Met Pro Glu Val Glu His His Glu Glu Val
 65                  70                  75                  80

Arg Pro Ser Leu Asp Pro Ala His Arg Gly Glu Phe His Phe Ser Asp
                 85                  90                  95

Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro Val Leu His Gly
            100                 105                 110

Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe Ala Leu Ser Asp
        115                 120                 125

Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala Ala Gly Met Asp
    130                 135                 140

Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly Leu Pro Val Gly
145                 150                 155                 160

Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr Glu Ala Glu Lys
                165                 170                 175

Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala Arg Gly Gly Ser
            180                 185                 190

Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp Phe Asn Lys Ala
        195                 200                 205

Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile Val Glu Ser Glu
    210                 215                 220

Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln Tyr Pro Asp Gly
225                 230                 235                 240

Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly Thr Glu Ser Gly
                245                 250                 255

Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu Asp Asn Val Val
            260                 265                 270

Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr Thr Glu Leu Ile
        275                 280                 285

Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala Cys Glu Gly Leu
    290                 295                 300

Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro Val Leu Asn Glu
305                 310                 315                 320
```

Replacement Sheet

```
Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met Tyr Pro Gln Met
                325                 330                 335

Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu Asp Val Leu Val
            340                 345                 350

Gln Gln Ala Leu His Arg Asp Asn
        355                 360
```

<210> 39
<211> 827
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(804)
<223> FRXA01022

<400> 39

```
cac ttt tcc gat ggc agc ttg tat gcc acc gct gat gtg att ttc cct   48
His Phe Ser Asp Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro
  1               5                  10                  15

gtg ctg cat ggt cgt ttt ggt gaa gac ggc act gtg cag ggt ctg ttt   96
Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe
             20                  25                  30

gca ctg tct gat att ccg gtc gtt ggc cca ggt gtg ctg gcc tct gct  144
Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala
          35                  40                  45

gcg gga atg gac aag gaa tac act aag aag ctc atg gca gcg gaa ggg  192
Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly
      50                  55                  60

ctg ccc gtt ggc cgt gag gtg att cta cgt gat cgt acc gag ctg acc  240
Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr
 65                  70                  75                  80

gag gca gaa aag aac ctg ctg ggc ctg cct gta ttt gtg aag cct gcg  288
Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala
                 85                  90                  95

cgt ggt ggc tca tcg att ggt atc tct cgt gtt act gcg tgg gag gat  336
Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp
            100                 105                 110

ttt aat aag gct gtg ggg ctt gct cgt gcc cat gat gag aag gtc att  384
Phe Asn Lys Ala Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile
        115                 120                 125

gtg gaa tca gag atc gtt ggc tct gag gtg gag tgt ggc gtg ctg cag  432
Val Glu Ser Glu Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln
    130                 135                 140

tat cca gac ggt cgt atc gtg gcg tct gtt cct gcg ttg ctg tct ggc  480
Tyr Pro Asp Gly Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly
145                 150                 155                 160
```

```
acc gaa tca ggc gct ggt gga ttc tat gac ttt gat acc aag tac ttg   528
Thr Glu Ser Gly Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu
                165                 170                 175

gac aac gtt gtt act gca gag atc cca gca ccg ctt gat gag aag acc   576
Asp Asn Val Val Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr
            180                 185                 190

acg gaa ctg atc cag tct ttg gct gtg gaa tct ttc cag gct ctt gcg   624
Thr Glu Leu Ile Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala
        195                 200                 205

tgt gaa ggc ctt gct cgc gtg gac ttc ttt gtt acc gcc aat ggt cct   672
Cys Glu Gly Leu Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro
    210                 215                 220

gtg ctc aat gag atc aac acc atg cca gga ttt acc ccc att tcc atg   720
Val Leu Asn Glu Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met
225                 230                 235                 240

tac cca cag atg ttc act gca tca ggc gtg gct tat gag gaa ttg ttg   768
Tyr Pro Gln Met Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu
                245                 250                 255

gat gtg ttg gtg cag cag gca ttg cac cgc gac aac tagcatcaaa        814
Asp Val Leu Val Gln Gln Ala Leu His Arg Asp Asn
            260                 265

taaaaacagc ccc                                                   827
```

Sequence Listing

<210> 40
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 40

```
His Phe Ser Asp Gly Ser Leu Tyr Ala Thr Ala Asp Val Ile Phe Pro
  1               5                  10                  15

Val Leu His Gly Arg Phe Gly Glu Asp Gly Thr Val Gln Gly Leu Phe
             20                  25                  30

Ala Leu Ser Asp Ile Pro Val Val Gly Pro Gly Val Leu Ala Ser Ala
         35                  40                  45

Ala Gly Met Asp Lys Glu Tyr Thr Lys Lys Leu Met Ala Ala Glu Gly
     50                  55                  60

Leu Pro Val Gly Arg Glu Val Ile Leu Arg Asp Arg Thr Glu Leu Thr
 65                  70                  75                  80

Glu Ala Glu Lys Asn Leu Leu Gly Leu Pro Val Phe Val Lys Pro Ala
                 85                  90                  95

Arg Gly Gly Ser Ser Ile Gly Ile Ser Arg Val Thr Ala Trp Glu Asp
            100                 105                 110

Phe Asn Lys Ala Val Gly Leu Ala Arg Ala His Asp Glu Lys Val Ile
        115                 120                 125
```

```
Val Glu Ser Glu Ile Val Gly Ser Glu Val Glu Cys Gly Val Leu Gln
    130                 135                 140

Tyr Pro Asp Gly Arg Ile Val Ala Ser Val Pro Ala Leu Leu Ser Gly
145                 150                 155                 160

Thr Glu Ser Gly Ala Gly Gly Phe Tyr Asp Phe Asp Thr Lys Tyr Leu
                165                 170                 175

Asp Asn Val Val Thr Ala Glu Ile Pro Ala Pro Leu Asp Glu Lys Thr
            180                 185                 190

Thr Glu Leu Ile Gln Ser Leu Ala Val Glu Ser Phe Gln Ala Leu Ala
        195                 200                 205

Cys Glu Gly Leu Ala Arg Val Asp Phe Phe Val Thr Ala Asn Gly Pro
    210                 215                 220

Val Leu Asn Glu Ile Asn Thr Met Pro Gly Phe Thr Pro Ile Ser Met
225                 230                 235                 240

Tyr Pro Gln Met Phe Thr Ala Ser Gly Val Ala Tyr Glu Glu Leu Leu
                245                 250                 255

Asp Val Leu Val Gln Gln Ala Leu His Arg Asp Asn
            260                 265


<210> 41
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXA02703

<400> 41
caaagcaggc ctaccgagcg ccgttccgag agtcgcgcga tgattggcgt gacaaccgca 60

accgcagata aatgtgaaat caggagaact acgaataaag atg gct aac tcc cca   115
                                                Met Ala Asn Ser Pro
                                                  1               5

aaa ccc atg cgg gtt gtc gtt gct ggt ggc ggt acc gca gga cat att   163
Lys Pro Met Arg Val Val Val Ala Gly Gly Gly Thr Ala Gly His Ile
                 10                  15                  20

gag cct gcg ttg gca gtg gct gaa gcg ctg cgc gat aag cac ggt gca   211
Glu Pro Ala Leu Ala Val Ala Glu Ala Leu Arg Asp Lys His Gly Ala
             25                  30                  35

aca gtt tcg gct tta ggt act gct cgt ggt ttg gaa aca acc ctg gtg   259
Thr Val Ser Ala Leu Gly Thr Ala Arg Gly Leu Glu Thr Thr Leu Val
         40                  45                  50

cct gat cgt ggg ttt gag ctt cat ctc atc gag ccg gtt cca gtc cca   307
Pro Asp Arg Gly Phe Glu Leu His Leu Ile Glu Pro Val Pro Val Pro
     55                  60                  65
```

```
cgc aag ccc aat atg gat ttg ttg aag ctc cca ttc cgg gta gct aag   355
Arg Lys Pro Asn Met Asp Leu Leu Lys Leu Pro Phe Arg Val Ala Lys
 70                  75                  80                  85

gca tta ggc caa gca cgc aag gca ctg aag gac aca gac gct caa gcg   403
Ala Leu Gly Gln Ala Arg Lys Ala Leu Lys Asp Thr Asp Ala Gln Ala
                 90                  95                 100

gtc atc ggc ttt ggc ggt tat gta tct gct ccg gct tat atg gcg gcg   451
Val Ile Gly Phe Gly Gly Tyr Val Ser Ala Pro Ala Tyr Met Ala Ala
            105                 110                 115

aag tct ttg ggc ttg cca ttt ttt gtc cac gaa gcc aac gcc cgt gca   499
Lys Ser Leu Gly Leu Pro Phe Phe Val His Glu Ala Asn Ala Arg Ala
        120                 125                 130

ggc atg gcc aac aaa ttg ggc gtc aag ctc ggt ggc gtt ggc ctt aat   547
Gly Met Ala Asn Lys Leu Gly Val Lys Leu Gly Gly Val Gly Leu Asn
    135                 140                 145

gct gtt gct ggt tcc ggc atg gac ggc gac gtg gtg ggc att ccg att   595
Ala Val Ala Gly Ser Gly Met Asp Gly Asp Val Val Gly Ile Pro Ile
150                 155                 160                 165

cgt gct gtt tta agt ggc gcg cgg gat gag tcc gca gct gac cga gcc   643
Arg Ala Val Leu Ser Gly Ala Arg Asp Glu Ser Ala Ala Asp Arg Ala
                170                 175                 180

agg gac act tgg ggt ttg gac aag gac cgc caa acc att ttt gtc acc   691
Arg Asp Thr Trp Gly Leu Asp Lys Asp Arg Gln Thr Ile Phe Val Thr
            185                 190                 195

ggt ggt tcg cag ggc tct gtg agt atc aac aag gcc gtc gag caa gct   739
Gly Gly Ser Gln Gly Ser Val Ser Ile Asn Lys Ala Val Glu Gln Ala
        200                 205                 210

gta gat cag ctg gtg gag gca ggt ttc cag gtg ctc cac gcc gtg ggt   787
Val Asp Gln Leu Val Glu Ala Gly Phe Gln Val Leu His Ala Val Gly
    215                 220                 225

aag aaa aac gag ttg cct gca gcg aaa ccc ggc tac cat ccc gtt ccg   835
Lys Lys Asn Glu Leu Pro Ala Ala Lys Pro Gly Tyr His Pro Val Pro
230                 235                 240                 245

ttt atc gac gat atg cag gct gcc tac acc gtt gct gat ctt atc gtg   883
Phe Ile Asp Asp Met Gln Ala Ala Tyr Thr Val Ala Asp Leu Ile Val
                250                 255                 260

tgc cgc tcc ggc gcg atg acg gtt gca gag gtc acc gcc gcc ggc gtc   931
Cys Arg Ser Gly Ala Met Thr Val Ala Glu Val Thr Ala Ala Gly Val
            265                 270                 275

ccc gcg att tat gtc ccg ctg cct cac ggc aac ggt gag cag gct ctc   979
Pro Ala Ile Tyr Val Pro Leu Pro His Gly Asn Gly Glu Gln Ala Leu
        280                 285                 290

aac gcc cag gct gtc att aaa gct ggt gcc gca cgc cag atc gac gac  1027
Asn Ala Gln Ala Val Ile Lys Ala Gly Ala Ala Arg Gln Ile Asp Asp
    295                 300                 305
```

Sequence Listing

```
gcg gac ttc acc gcc cag acg ctt atc gac gcc acc ctt gac att ctc   1075
Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala Thr Leu Asp Ile Leu
310                 315                 320                 325

ctt cat ccc tcc aca cac caa tcg atg tcg gac gca gct aaa acc tcc   1123
Leu His Pro Ser Thr His Gln Ser Met Ser Asp Ala Ala Lys Thr Ser
                330                 335                 340

acc gca ggt aac gcc tcc acg gtg att gca gac atg att gct gca act   1171
Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp Met Ile Ala Ala Thr
            345                 350                 355

atc aat agc caa cac aac taaaacgacc agctcaacgc aaa                1212
Ile Asn Ser Gln His Asn
        360
```

<210> 42
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 42

```
Met Ala Asn Ser Pro Lys Pro Met Arg Val Val Val Ala Gly Gly Gly
  1               5                  10                  15

Thr Ala Gly His Ile Glu Pro Ala Leu Ala Val Ala Glu Ala Leu Arg
             20                  25                  30

Asp Lys His Gly Ala Thr Val Ser Ala Leu Gly Thr Ala Arg Gly Leu
         35                  40                  45

Glu Thr Thr Leu Val Pro Asp Arg Gly Phe Glu Leu His Leu Ile Glu
     50                  55                  60

Pro Val Pro Val Pro Arg Lys Pro Asn Met Asp Leu Leu Lys Leu Pro
 65                  70                  75                  80

Phe Arg Val Ala Lys Ala Leu Gly Gln Ala Arg Lys Ala Leu Lys Asp
                 85                  90                  95

Thr Asp Ala Gln Ala Val Ile Gly Phe Gly Gly Tyr Val Ser Ala Pro
            100                 105                 110

Ala Tyr Met Ala Ala Lys Ser Leu Gly Leu Pro Phe Phe Val His Glu
        115                 120                 125

Ala Asn Ala Arg Ala Gly Met Ala Asn Lys Leu Gly Val Lys Leu Gly
    130                 135                 140

Gly Val Gly Leu Asn Ala Val Ala Gly Ser Gly Met Asp Gly Asp Val
145                 150                 155                 160

Val Gly Ile Pro Ile Arg Ala Val Leu Ser Gly Ala Arg Asp Glu Ser
                165                 170                 175

Ala Ala Asp Arg Ala Arg Asp Thr Trp Gly Leu Asp Lys Asp Arg Gln
            180                 185                 190

Thr Ile Phe Val Thr Gly Gly Ser Gln Gly Ser Val Ser Ile Asn Lys
        195                 200                 205
```

```
Ala Val Glu Gln Ala Val Asp Gln Leu Val Glu Ala Gly Phe Gln Val
    210                 215                 220

Leu His Ala Val Gly Lys Lys Asn Glu Leu Pro Ala Ala Lys Pro Gly
225                 230                 235                 240

Tyr His Pro Val Pro Phe Ile Asp Asp Met Gln Ala Ala Tyr Thr Val
                245                 250                 255

Ala Asp Leu Ile Val Cys Arg Ser Gly Ala Met Thr Val Ala Glu Val
            260                 265                 270

Thr Ala Ala Gly Val Pro Ala Ile Tyr Val Pro Leu Pro His Gly Asn
        275                 280                 285

Gly Glu Gln Ala Leu Asn Ala Gln Ala Val Ile Lys Ala Gly Ala Ala
    290                 295                 300

Arg Gln Ile Asp Asp Ala Asp Phe Thr Ala Gln Thr Leu Ile Asp Ala
305                 310                 315                 320

Thr Leu Asp Ile Leu Leu His Pro Ser Thr His Gln Ser Met Ser Asp
                325                 330                 335

Ala Ala Lys Thr Ser Thr Ala Gly Asn Ala Ser Thr Val Ile Ala Asp
            340                 345                 350

Met Ile Ala Ala Thr Ile Asn Ser Gln His Asn
        355                 360
```

Sequence Listing

<210> 43
<211> 2235
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2212)
<223> RXA02711

<400> 43

```
aaaacctcca ggcgattcca caagaagcag cagctccgcc gtatcagacc aacactgttc 60

cttatgctgc aaccaccgga caagcaggtg gcgcagggca gtg act ttc ccc agc   115
                                              Val Thr Phe Pro Ser
                                                1               5

aat ggc aga agt cgg ggc gag cgt gcg gga cgt gaa gat acg tcc cgc   163
Asn Gly Arg Ser Arg Gly Glu Arg Ala Gly Arg Glu Asp Thr Ser Arg
                  10                  15                  20

cgt tcg gcg tat cag gac gaa agc aga aga gcc gct aga gag cgc gaa   211
Arg Ser Ala Tyr Gln Asp Glu Ser Arg Arg Ala Ala Arg Glu Arg Glu
              25                  30                  35

ctt acg cga cgc agc ggt aaa gct aaa ggc gta aac caa gaa gaa gga   259
Leu Thr Arg Arg Ser Gly Lys Ala Lys Gly Val Asn Gln Glu Glu Gly
          40                  45                  50
```

```
gtg acc tac cgg cct aaa tct tca acc cag ggc ggc gca cgc aag cga   307
Val Thr Tyr Arg Pro Lys Ser Ser Thr Gln Gly Gly Ala Arg Lys Arg
     55                  60                  65

cgt gtg aac atg gtt acc gct atc gca ttg gtc atc gct ggc gta ctg   355
Arg Val Asn Met Val Thr Ala Ile Ala Leu Val Ile Ala Gly Val Leu
 70                  75                  80                  85

atc att cgc ctc ggc tgg gtc caa gtt gtc tgg gga cca gaa ctg tcc   403
Ile Ile Arg Leu Gly Trp Val Gln Val Val Trp Gly Pro Glu Leu Ser
                 90                  95                 100

ctc aat gct tcg gaa cag cgc acc cgc gtg tac gta gat cct gca cgt   451
Leu Asn Ala Ser Glu Gln Arg Thr Arg Val Tyr Val Asp Pro Ala Arg
            105                 110                 115

cgt gga agc atc gtg gac cgc gaa gga aac cag atg gcg tac acg atg   499
Arg Gly Ser Ile Val Asp Arg Glu Gly Asn Gln Met Ala Tyr Thr Met
        120                 125                 130

cag gca cgt tcg ctg acg gtt tct ccg aac atc atg cgt gag gaa tta   547
Gln Ala Arg Ser Leu Thr Val Ser Pro Asn Ile Met Arg Glu Glu Leu
    135                 140                 145

aag acc gga act gat ttg gcc ttg cgt ttg gcg gct gaa gaa acc gat   595
Lys Thr Gly Thr Asp Leu Ala Leu Arg Leu Ala Ala Glu Glu Thr Asp
150                 155                 160                 165

ccg gaa aac gtg gcc agc tat gtg acc atc gaa gaa ggc aac gcg tat   643
Pro Glu Asn Val Ala Ser Tyr Val Thr Ile Glu Glu Gly Asn Ala Tyr
                170                 175                 180

gtt ttt gcg tct gaa gaa cag cgc gaa acc att ctg tcc gac aag gta   691
Val Phe Ala Ser Glu Glu Gln Arg Glu Thr Ile Leu Ser Asp Lys Val
            185                 190                 195

gaa gag cgc att caa agc att gcg gat cgg atc cct gag atc atc aaa   739
Glu Glu Arg Ile Gln Ser Ile Ala Asp Arg Ile Pro Glu Ile Ile Lys
        200                 205                 210

tcc cat gac caa gat gtc act gga att tcc tct gag gag atc ctg gac   787
Ser His Asp Gln Asp Val Thr Gly Ile Ser Ser Glu Glu Ile Leu Asp
    215                 220                 225

aag ctc aat gct gat agc cag tat gag gtg ctc gtc cgc aat gtt gat   835
Lys Leu Asn Ala Asp Ser Gln Tyr Glu Val Leu Val Arg Asn Val Asp
230                 235                 240                 245

ccc gat gta gcg tca gaa atc acc gat gag atg ccc agc gtc gca gct   883
Pro Asp Val Ala Ser Glu Ile Thr Asp Glu Met Pro Ser Val Ala Ala
                250                 255                 260

gat cat caa gac atc cgc caa tac cca aac ggc gcg att ggt gaa aac   931
Asp His Gln Asp Ile Arg Gln Tyr Pro Asn Gly Ala Ile Gly Glu Asn
            265                 270                 275

atc atc ggt cga atc agc atg gac ggc gaa ggc cag ttc ggc ttt gag   979
Ile Ile Gly Arg Ile Ser Met Asp Gly Glu Gly Gln Phe Gly Phe Glu
        280                 285                 290

gct tcc aac gat tcc ctg ttg gca gga aac aac ggt cgc tca acc cag  1027
```

```
Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn Gly Arg Ser Thr Gln
    295                 300                 305

gac atg tcc att ttg gga caa gca ata ccg ggc acg ttg agg gat caa   1075
Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly Thr Leu Arg Asp Gln
310                 315                 320                 325

att cca gcc att gat ggt gcc agc gtt gaa ctc acc gtt gat ctg gat   1123
Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu Thr Val Asp Leu Asp
                330                 335                 340

ctg caa acc tat gtg cag cag gca ttg gag cag gcg aaa gct aac tcc   1171
Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln Ala Lys Ala Asn Ser
            345                 350                 355

ggt gca gaa aac gcc tcc gct gtg gtt ctt gat gcc aag acc gct gag   1219
Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp Ala Lys Thr Ala Glu
        360                 365                 370

gtt ttg gcg atg gca aac acc gat acc atc aac ccc aac gaa gac acg   1267
Val Leu Ala Met Ala Asn Thr Asp Thr Ile Asn Pro Asn Glu Asp Thr
    375                 380                 385

gga aag cag att gag cag ggc aag agc ttt gac aat cct tct gtc acc   1315
Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp Asn Pro Ser Val Thr
390                 395                 400                 405

cac ccc ttc gag cct ggt tct gta gcc aag gtg att act gca gca ggc   1363
His Pro Phe Glu Pro Gly Ser Val Ala Lys Val Ile Thr Ala Ala Gly
                410                 415                 420

gta att caa gag ggc ttg act act cca gat gaa gtg ttg cag gta ccg   1411
Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu Val Leu Gln Val Pro
            425                 430                 435

ggc agt att gaa atg gcc ggt gtt tct gtc ggt gat gcg tgg gac cac   1459
Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly Asp Ala Trp Asp His
        440                 445                 450

ggt gtc gtt ccc tac acc act gca gga att ttt ggt aag tcc tcg aat   1507
Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe Gly Lys Ser Ser Asn
    455                 460                 465

gta ggc act ctg atg ctt gcg cag cgt ctt ggt gaa gat aaa ttt gct   1555
Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly Glu Asp Lys Phe Ala
470                 475                 480                 485

gat tac ctg gaa cga ttc ggt gtg gga cag cca acg ggt att gag ctt   1603
Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro Thr Gly Ile Glu Leu
                490                 495                 500

ccg agc gaa tcc caa ggc ctg ctg ccc gca cgt gag cag tgg tct ggc   1651
Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg Glu Gln Trp Ser Gly
            505                 510                 515

ggt act ttt gct aac ctg ccc atc ggt cag ggt atg tcg atc acc acg   1699
Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly Met Ser Ile Thr Thr
        520                 525                 530

ttg caa atg gct gga atc tac caa gcc ttg gcc aac gat ggt gaa cgc   1747
Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala Asn Asp Gly Glu Arg
```

```
    535                 540                 545

att caa ccg cgg atc atc aag agc gtg act gat tct gac gga aca gtc   1795
Ile Gln Pro Arg Ile Ile Lys Ser Val Thr Asp Ser Asp Gly Thr Val
550                 555                 560                 565

cta gag cag cca gaa ccc gat aaa atc cag gtt gtc agc gct gaa gct   1843
Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val Val Ser Ala Glu Ala
                570                 575                 580

gcc cgc acc acg gtg gat atg ttt agg tct gtc acc cag gtt gat cca   1891
Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val Thr Gln Val Asp Pro
            585                 590                 595

act gga gtg caa caa ggt acc gct cca gac gcc tcc att gag ggt tat   1939
Thr Gly Val Gln Gln Gly Thr Ala Pro Asp Ala Ser Ile Glu Gly Tyr
        600                 605                 610

caa atc tca ggt aag aca ggt acg gcg cag aaa gtt gac ccc aac acg   1987
Gln Ile Ser Gly Lys Thr Gly Thr Ala Gln Lys Val Asp Pro Asn Thr
    615                 620                 625

ggc gcg tac tct aac tcg caa tac tgg att acc ttc gcg ggt att gca   2035
Gly Ala Tyr Ser Asn Ser Gln Tyr Trp Ile Thr Phe Ala Gly Ile Ala
630                 635                 640                 645

ccc gct gat gat cct cga ttt gtt gta gcc atc atg ctt gat gag cca   2083
Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile Met Leu Asp Glu Pro
                650                 655                 660

gaa cgc gga gtc cac ggt ggt ggc ggc caa acc gca gca cct ttg ttc   2131
Glu Arg Gly Val His Gly Gly Gly Gly Gln Thr Ala Ala Pro Leu Phe
            665                 670                 675

aaa gac atc gcc acc tgg ttg ctc aac cgc gac aac atc cca ctg tct   2179
Lys Asp Ile Ala Thr Trp Leu Leu Asn Arg Asp Asn Ile Pro Leu Ser
        680                 685                 690

gca gcc acc gaa ccg atc atc ctt caa gct caa taactcaaac agaagtgtct 2232
Ala Ala Thr Glu Pro Ile Ile Leu Gln Ala Gln
    695                 700

ttt                                                               2235


<210> 44
<211> 704
<212> PRT
<213> Corynebacterium glutamicum

<400> 44
Val Thr Phe Pro Ser Asn Gly Arg Ser Arg Gly Glu Arg Ala Gly Arg
  1               5                  10                  15

Glu Asp Thr Ser Arg Arg Ser Ala Tyr Gln Asp Glu Ser Arg Arg Ala
             20                  25                  30

Ala Arg Glu Arg Glu Leu Thr Arg Arg Ser Gly Lys Ala Lys Gly Val
         35                  40                  45

Asn Gln Glu Glu Gly Val Thr Tyr Arg Pro Lys Ser Ser Thr Gln Gly
```

```
     50                  55                  60

Gly Ala Arg Lys Arg Arg Val Asn Met Val Thr Ala Ile Ala Leu Val
 65                  70                  75                  80

Ile Ala Gly Val Leu Ile Ile Arg Leu Gly Trp Val Gln Val Val Trp
                 85                  90                  95

Gly Pro Glu Leu Ser Leu Asn Ala Ser Glu Gln Arg Thr Arg Val Tyr
            100                 105                 110

Val Asp Pro Ala Arg Arg Gly Ser Ile Val Asp Arg Glu Gly Asn Gln
        115                 120                 125

Met Ala Tyr Thr Met Gln Ala Arg Ser Leu Thr Val Ser Pro Asn Ile
    130                 135                 140

Met Arg Glu Glu Leu Lys Thr Gly Thr Asp Leu Ala Leu Arg Leu Ala
145                 150                 155                 160

Ala Glu Glu Thr Asp Pro Glu Asn Val Ala Ser Tyr Val Thr Ile Glu
                165                 170                 175

Glu Gly Asn Ala Tyr Val Phe Ala Ser Glu Glu Gln Arg Glu Thr Ile
            180                 185                 190

Leu Ser Asp Lys Val Glu Glu Arg Ile Gln Ser Ile Ala Asp Arg Ile
        195                 200                 205

Pro Glu Ile Ile Lys Ser His Asp Gln Asp Val Thr Gly Ile Ser Ser
    210                 215                 220

Glu Glu Ile Leu Asp Lys Leu Asn Ala Asp Ser Gln Tyr Glu Val Leu
225                 230                 235                 240

Val Arg Asn Val Asp Pro Asp Val Ala Ser Glu Ile Thr Asp Glu Met
                245                 250                 255

Pro Ser Val Ala Ala Asp His Gln Asp Ile Arg Gln Tyr Pro Asn Gly
            260                 265                 270

Ala Ile Gly Glu Asn Ile Ile Gly Arg Ile Ser Met Asp Gly Glu Gly
        275                 280                 285

Gln Phe Gly Phe Glu Ala Ser Asn Asp Ser Leu Leu Ala Gly Asn Asn
    290                 295                 300

Gly Arg Ser Thr Gln Asp Met Ser Ile Leu Gly Gln Ala Ile Pro Gly
305                 310                 315                 320

Thr Leu Arg Asp Gln Ile Pro Ala Ile Asp Gly Ala Ser Val Glu Leu
                325                 330                 335

Thr Val Asp Leu Asp Leu Gln Thr Tyr Val Gln Gln Ala Leu Glu Gln
            340                 345                 350

Ala Lys Ala Asn Ser Gly Ala Glu Asn Ala Ser Ala Val Val Leu Asp
        355                 360                 365

Ala Lys Thr Ala Glu Val Leu Ala Met Ala Asn Thr Asp Thr Ile Asn
    370                 375                 380
```

```
Pro Asn Glu Asp Thr Gly Lys Gln Ile Glu Gln Gly Lys Ser Phe Asp
385                 390                 395                 400

Asn Pro Ser Val Thr His Pro Phe Glu Pro Gly Ser Val Ala Lys Val
                405                 410                 415

Ile Thr Ala Ala Gly Val Ile Gln Glu Gly Leu Thr Thr Pro Asp Glu
            420                 425                 430

Val Leu Gln Val Pro Gly Ser Ile Glu Met Ala Gly Val Ser Val Gly
        435                 440                 445

Asp Ala Trp Asp His Gly Val Val Pro Tyr Thr Thr Ala Gly Ile Phe
    450                 455                 460

Gly Lys Ser Ser Asn Val Gly Thr Leu Met Leu Ala Gln Arg Leu Gly
465                 470                 475                 480

Glu Asp Lys Phe Ala Asp Tyr Leu Glu Arg Phe Gly Val Gly Gln Pro
                485                 490                 495

Thr Gly Ile Glu Leu Pro Ser Glu Ser Gln Gly Leu Leu Pro Ala Arg
            500                 505                 510

Glu Gln Trp Ser Gly Gly Thr Phe Ala Asn Leu Pro Ile Gly Gln Gly
        515                 520                 525

Met Ser Ile Thr Thr Leu Gln Met Ala Gly Ile Tyr Gln Ala Leu Ala
    530                 535                 540

Asn Asp Gly Glu Arg Ile Gln Pro Arg Ile Ile Lys Ser Val Thr Asp
545                 550                 555                 560

Ser Asp Gly Thr Val Leu Glu Gln Pro Glu Pro Asp Lys Ile Gln Val
                565                 570                 575

Val Ser Ala Glu Ala Ala Arg Thr Thr Val Asp Met Phe Arg Ser Val
            580                 585                 590

Thr Gln Val Asp Pro Thr Gly Val Gln Gln Gly Thr Ala Pro Asp Ala
        595                 600                 605

Ser Ile Glu Gly Tyr Gln Ile Ser Gly Lys Thr Gly Thr Ala Gln Lys
    610                 615                 620

Val Asp Pro Asn Thr Gly Ala Tyr Ser Asn Ser Gln Tyr Trp Ile Thr
625                 630                 635                 640

Phe Ala Gly Ile Ala Pro Ala Asp Asp Pro Arg Phe Val Val Ala Ile
                645                 650                 655

Met Leu Asp Glu Pro Glu Arg Gly Val His Gly Gly Gly Gln Thr
            660                 665                 670

Ala Ala Pro Leu Phe Lys Asp Ile Ala Thr Trp Leu Leu Asn Arg Asp
        675                 680                 685

Asn Ile Pro Leu Ser Ala Ala Thr Glu Pro Ile Ile Leu Gln Ala Gln
    690                 695                 700
```

CONFIDENTIAL

<210> 45
<211> 749
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(726)
<223> RXA02859

<400> 45

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cag tat acc gtt gat cag ctg ctg cac ggt ctt ctt tta gcc agc ggt   48
Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
  1               5                  10                  15

aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca   96
Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
             20                  25                  30

acc ctg gag aaa gta aac gcg ctg gcc aag gag ttg ggc act caa gac   144
Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
         35                  40                  45

acc ttc gtt gcc act tat tcc ggt ttg gat gcg ccg gga atg tcg acc   192
Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
     50                  55                  60

tcc gca tac gac atg tca ttg att tat cag cat gcg tgg cag aac ccg   240
Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65                  70                  75                  80

gtt ttc gag tcg att atc tcc acc gat cac att gat ttc cct ggt tgg   288
Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
                 85                  90                  95

ggc gac aat gag ggt ttc caa gtc tgg aac gat aac gcc ttg ttc atg   336
Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
            100                 105                 110

aac gat cct gat ggc atc ggc ggc aag acc ggc tac acc gac gac gcg   384
Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
        115                 120                 125

aac cac acc ttt gtc ggc ggt ctc gat cgg ggt ggt cgc cgc ctc gcc   432
Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
    130                 135                 140

gcc gta ctc ttg gat tcc acc gtc agc gac att cgt ccg tgg gaa caa   480
Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
145                 150                 155                 160

gca cga ttg ctt atc gac gcc tcc ctc ccc atc acg ccg ggg tcc ggc   528
Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
                165                 170                 175

gtg ggc cag ctg ggc tcc ggc agc gcg aac gat gtg gca ccg gcg acc   576
Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
```

```
            180                 185                 190

cca gaa tta cca gaa ccc acc gac aac ctg act tca ggt gag ggt ggg   624
Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
        195                 200                 205

tcg cag aac acg ctg ctt aag ctc gtg gtg ccc atc gga atc atc gtg   672
Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
    210                 215                 220

ctg ttg cta atc gcc gca cta gcg tgg aca ttc aga tct ccc aag aaa   720
Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
225                 230                 235                 240

aag aac taggtgttct tcttcacgac ctc                                749
Lys Asn
```

<210> 46
<211> 242
<212> PRT
<213> Corynebacterium glutamicum

<400> 46

```
Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
  1               5                  10                  15

Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
             20                  25                  30

Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
         35                  40                  45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
     50                  55                  60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65                  70                  75                  80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
                 85                  90                  95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
            100                 105                 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
        115                 120                 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
    130                 135                 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
145                 150                 155                 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
                165                 170                 175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
            180                 185                 190
```

```
Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
        195                 200                 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
    210                 215                 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
225                 230                 235                 240

Lys Asn
```

<210> 47
<211> 1149
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1126)
<223> RXA00569

<400> 47

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ctgccggctg ggtaagaaaa ggtcgtggcg gcgtttatga agtccccact gagcggatca 60

tcccgctact aaccatcatt tctgccagtg agaatcacta atg aga tta aag aag   115
                                              Met Arg Leu Lys Lys
                                                1               5

cag ctt ctt ggc agc ctg tta gtt gtc atc gtg gtt ttg tcc atc gcc   163
Gln Leu Leu Gly Ser Leu Leu Val Val Ile Val Val Leu Ser Ile Ala
                  10                  15                  20

gta gca acc acc aaa caa caa aaa ggc ttc gtc aca ggt cag ccc acc   211
Val Ala Thr Thr Lys Gln Gln Lys Gly Phe Val Thr Gly Gln Pro Thr
             25                  30                  35

ggt gcg ctt aac ctc tcc gac atc ctc gac tcc gaa gaa ctt ggc gag   259
Gly Ala Leu Asn Leu Ser Asp Ile Leu Asp Ser Glu Glu Leu Gly Glu
         40                  45                  50

tat cac ctc atg tca gcc gcc atc atc act ggt aac act gta gat ttc   307
Tyr His Leu Met Ser Ala Ala Ile Ile Thr Gly Asn Thr Val Asp Phe
     55                  60                  65

agc ggg ctc ggc gca ggt cca gac gac cct ttt gaa atc gca tcg att   355
Ser Gly Leu Gly Ala Gly Pro Asp Asp Pro Phe Glu Ile Ala Ser Ile
 70                  75                  80                  85

acg aag atc ttc acc ggt gag ctg ctt cga ctt cag att gag cga gga   403
Thr Lys Ile Phe Thr Gly Glu Leu Leu Arg Leu Gln Ile Glu Arg Gly
                 90                  95                 100

gag atc aca gaa tcc acg gcc gtc gga gac gtt ctt gga gaa cgt gta   451
Glu Ile Thr Glu Ser Thr Ala Val Gly Asp Val Leu Gly Glu Arg Val
            105                 110                 115

gcc gac tcc ctc atc cgg gac ata acc gtg gaa gaa cta gcc aat cac   499
Ala Asp Ser Leu Ile Arg Asp Ile Thr Val Glu Glu Leu Ala Asn His
        120                 125                 130
```

```
acc agc gga cta ccc cgt cta ggc aat gta gga ctt aga cct ttt atg   547
Thr Ser Gly Leu Pro Arg Leu Gly Asn Val Gly Leu Arg Pro Phe Met
    135                 140                 145

gct acg ttc ttt gac aag aat cct tac aaa gac ctc tct gca gat cga   595
Ala Thr Phe Phe Asp Lys Asn Pro Tyr Lys Asp Leu Ser Ala Asp Arg
150                 155                 160                 165

gtc atc tct atc agc aca acg tcc aaa ttg aat tcg cgc gga gaa ttt   643
Val Ile Ser Ile Ser Thr Thr Ser Lys Leu Asn Ser Arg Gly Glu Phe
                170                 175                 180

cac tac tca aat ctt ggt ttt gct ctg ctt ggc caa gtc ctt gcc cgc   691
His Tyr Ser Asn Leu Gly Phe Ala Leu Leu Gly Gln Val Leu Ala Arg
            185                 190                 195

aat gcc ggt tta acg ttt gac cag ctc tta gac cgt gat tta ctg gca   739
Asn Ala Gly Leu Thr Phe Asp Gln Leu Leu Asp Arg Asp Leu Leu Ala
        200                 205                 210

cca ctc aac ctc aat aac acc aag ctc atg acc cca gaa tcc ctc gct   787
Pro Leu Asn Leu Asn Asn Thr Lys Leu Met Thr Pro Glu Ser Leu Ala
    215                 220                 225

caa gat gca cct caa ggg ttc tca aca cct ggc aaa caa gtc gaa gcg   835
Gln Asp Ala Pro Gln Gly Phe Ser Thr Pro Gly Lys Gln Val Glu Ala
230                 235                 240                 245

tgg gag atg gat ggc ttt ctc ccc gca gct ggc ctg cgt tcc acc gcg   883
Trp Glu Met Asp Gly Phe Leu Pro Ala Ala Gly Leu Arg Ser Thr Ala
                250                 255                 260

cgc gac atg gca gtt ttc tgt cag tac tta ttc aca aaa ggc ccc gcc   931
Arg Asp Met Ala Val Phe Cys Gln Tyr Leu Phe Thr Lys Gly Pro Ala
            265                 270                 275

cct ttc acc tgg caa tcc ctt gaa tcg gcc cct gaa atc gtc tgg cat   979
Pro Phe Thr Trp Gln Ser Leu Glu Ser Ala Pro Glu Ile Val Trp His
        280                 285                 290

aac gga gag tcc ttt gga tat agt tcc gta ctc ttc ttt aac acc gct  1027
Asn Gly Glu Ser Phe Gly Tyr Ser Ser Val Leu Phe Phe Asn Thr Ala
    295                 300                 305

aca act act gcc atc ttc gtt gct gcc gac gtt gcc aca tct gtc ttc  1075
Thr Thr Thr Ala Ile Phe Val Ala Ala Asp Val Ala Thr Ser Val Phe
310                 315                 320                 325

cca att ggt cac gag ctt tta atg gca aac tcc act agg cag gaa tca  1123
Pro Ile Gly His Glu Leu Leu Met Ala Asn Ser Thr Arg Gln Glu Ser
                330                 335                 340

aaa tgatcgattc ccccgcctct atc                                   1149
Lys
```

<210> 48
<211> 342
<212> PRT

<213> Corynebacterium glutamicum

<400> 48

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Met Arg Leu Lys Lys Gln Leu Leu Gly Ser Leu Leu Val Val Ile Val
  1               5                  10                  15

Val Leu Ser Ile Ala Val Ala Thr Thr Lys Gln Gln Lys Gly Phe Val
             20                  25                  30

Thr Gly Gln Pro Thr Gly Ala Leu Asn Leu Ser Asp Ile Leu Asp Ser
         35                  40                  45

Glu Glu Leu Gly Glu Tyr His Leu Met Ser Ala Ala Ile Ile Thr Gly
     50                  55                  60

Asn Thr Val Asp Phe Ser Gly Leu Gly Ala Gly Pro Asp Asp Pro Phe
 65                  70                  75                  80

Glu Ile Ala Ser Ile Thr Lys Ile Phe Thr Gly Glu Leu Leu Arg Leu
                 85                  90                  95

Gln Ile Glu Arg Gly Glu Ile Thr Glu Ser Thr Ala Val Gly Asp Val
            100                 105                 110

Leu Gly Glu Arg Val Ala Asp Ser Leu Ile Arg Asp Ile Thr Val Glu
        115                 120                 125

Glu Leu Ala Asn His Thr Ser Gly Leu Pro Arg Leu Gly Asn Val Gly
    130                 135                 140

Leu Arg Pro Phe Met Ala Thr Phe Phe Asp Lys Asn Pro Tyr Lys Asp
145                 150                 155                 160

Leu Ser Ala Asp Arg Val Ile Ser Ile Ser Thr Thr Ser Lys Leu Asn
                165                 170                 175

Ser Arg Gly Glu Phe His Tyr Ser Asn Leu Gly Phe Ala Leu Leu Gly
            180                 185                 190

Gln Val Leu Ala Arg Asn Ala Gly Leu Thr Phe Asp Gln Leu Leu Asp
        195                 200                 205

Arg Asp Leu Leu Ala Pro Leu Asn Leu Asn Asn Thr Lys Leu Met Thr
    210                 215                 220

Pro Glu Ser Leu Ala Gln Asp Ala Pro Gln Gly Phe Ser Thr Pro Gly
225                 230                 235                 240

Lys Gln Val Glu Ala Trp Glu Met Asp Gly Phe Leu Pro Ala Ala Gly
                245                 250                 255

Leu Arg Ser Thr Ala Arg Asp Met Ala Val Phe Cys Gln Tyr Leu Phe
            260                 265                 270

Thr Lys Gly Pro Ala Pro Phe Thr Trp Gln Ser Leu Glu Ser Ala Pro
        275                 280                 285

Glu Ile Val Trp His Asn Gly Glu Ser Phe Gly Tyr Ser Ser Val Leu
    290                 295                 300

Phe Phe Asn Thr Ala Thr Thr Thr Ala Ile Phe Val Ala Ala Asp Val
```

```
305                 310                 315                 320

Ala Thr Ser Val Phe Pro Ile Gly His Glu Leu Leu Met Ala Asn Ser
                325                 330                 335

Thr Arg Gln Glu Ser Lys
            340
```

<210> 49
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXN03092

<400> 49

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ccgactgtca gcagtaacgc acagtcgaat aaataaagat tggctgacat tgttggagtc 60

ttgggttcac gattcccggg gttatcgcta ggctgttgga gtg tcc acc acg aat   115
                                            Val Ser Thr Thr Asn
                                              1               5

tct ctg aca aag ctc gtt gca tct aca gtc gcc gct ggc gtc ctt ggt   163
Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala Ala Gly Val Leu Gly
                10                  15                  20

gcg ctc gca ctt gtg cct ttc gct agt ctt tct ggc gtt gcg gtt gcg   211
Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser Gly Val Ala Val Ala
            25                  30                  35

cgt acc aat gac acg atg cag acc aac ctt tca gat ctg acg gat ggt   259
Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser Asp Leu Thr Asp Gly
        40                  45                  50

cgc ggg ccg ggc gtc acg acg att act gat tcc act gac cag ccg att   307
Arg Gly Pro Gly Val Thr Thr Ile Tnr Asp Ser Thr Asp Gln Pro Ile
    55                  60                  65

gct tat att tat gcg cag cgg cgg ttt gag gtt ggg ggt gat cag att   355
Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val Gly Gly Asp Gln Ile
70                  75                  80                  85

tct acg tcg atg aag gat gcg atc gtt tcg att gag gat cgc agg ttc   403
Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile Glu Asp Arg Arg Phe
                90                  95                  100

tat gag cat gat ggt gtg gat ttg cag ggc ttt ggt cgt gca atc ctg   451
Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe Gly Arg Ala Ile Leu
            105                 110                 115

acg aac ctg gct gcg ggt ggc gtg gag cag ggt gct tcg acg att aac   499
Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly Ala Ser Thr Ile Asn
        120                 125                 130

cag cag tat gtg aag aac ttc ttg ctg ttg gtg gaa gct gat gat gag   547
Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val Glu Ala Asp Asp Glu
    135                 140                 145
```

```
gcg gag cag gct gct gct gtg gaa acc tcc atc cct cgt aag ctc cgt   595
Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile Pro Arg Lys Leu Arg
150                 155                 160                 165

gag atg aag atg gcg tct gat ttg gaa aag acg ttg tcg aag gat gag   643
Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr Leu Ser Lys Asp Glu
                170                 175                 180

att ctg act cgt tat ctc aac att gtt cct ttt ggt aat ggt gct tat   691
Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe Gly Asn Gly Ala Tyr
            185                 190                 195

ggt gtt gag gct gcg gcg cgg acg tat ttc ggt acg tcg gct gcc gag   739
Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly Thr Ser Ala Ala Glu
        200                 205                 210

tta acc att cca cag tct gcg atg ctc gcg ggc att gtg cag tct tcg   787
Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly Ile Val Gln Ser Ser
    215                 220                 225

tct tat ctc aat cca tac acc aat cac gat gct gtg ttt gag cgt cgt   835
Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala Val Phe Glu Arg Arg
230                 235                 240                 245

aat act gtt ttg ggc gct atg gct gat gct ggc gcg att tcc cca gac   883
Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly Ala Ile Ser Pro Asp
                250                 255                 260

gag gct tcg gct ttc cag cag gaa cct ttg ggt gtc ctg gaa acc ccg   931
Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly Val Leu Glu Thr Pro
            265                 270                 275

caa ggc tta tcc aat ggt tgt atc ggc gct ggc gat cgg tgg ttt ttt   979
Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly Asp Arg Trp Phe Phe
        280                 285                 290

ttg caa taacgctctt gcaatatctt tct                                1008
Leu Gln
    295
```

<210> 50
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 50

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Val Ser Thr Thr Asn Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala
  1               5                  10                  15

Ala Gly Val Leu Gly Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser
             20                  25                  30

Gly Val Ala Val Ala Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser
         35                  40                  45

Asp Leu Thr Asp Gly Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser
     50                  55                  60

Thr Asp Gln Pro Ile Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val
```

```
 65                  70                  75                  80

Gly Gly Asp Gln Ile Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile
                 85                  90                  95

Glu Asp Arg Arg Phe Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe
            100                 105                 110

Gly Arg Ala Ile Leu Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly
        115                 120                 125

Ala Ser Thr Ile Asn Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val
    130                 135                 140

Glu Ala Asp Asp Glu Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile
145                 150                 155                 160

Pro Arg Lys Leu Arg Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr
                165                 170                 175

Leu Ser Lys Asp Glu Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe
            180                 185                 190

Gly Asn Gly Ala Tyr Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly
        195                 200                 205

Thr Ser Ala Ala Glu Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly
    210                 215                 220

Ile Val Gln Ser Ser Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala
225                 230                 235                 240

Val Phe Glu Arg Arg Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly
                245                 250                 255

Ala Ile Ser Pro Asp Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly
            260                 265                 270

Val Leu Glu Thr Pro Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly
        275                 280                 285

Asp Arg Trp Phe Phe Leu Gln
    290                 295


<210> 51
<211> 1033
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1033)
<223> FRXA00594

<400> 51
ccgactgtca gcagtaacgc acagtcgaat aaataaagat tggctgacat tgttggagtc 60

ttgggttcac gattcccggg gttatcgcta ggctgttgga gtg tcc acc acg aat   115
                                              Val Ser Thr Thr Asn
                                                1               5
```

```
tct ctg aca aag ctc gtt gca tct aca gtc gcc gct ggc gtc ctt ggt   163
Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala Ala Gly Val Leu Gly
                 10                  15                  20

gcg ctc gca ctt gtg cct ttc gct agt ctt tct ggc gtt gcg gtt gcg   211
Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser Gly Val Ala Val Ala
             25                  30                  35

cgt acc aat gac acg atg cag acc aac ctt tca gat ctg acg gat ggt   259
Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser Asp Leu Thr Asp Gly
         40                  45                  50

cgc ggg ccg ggc gtc acg acg att act gat tcc act gac cag ccg att   307
Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser Thr Asp Gln Pro Ile
     55                  60                  65

gct tat att tat gcg cag cgg cgg ttt gag gtt ggg ggt gat cag att   355
Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val Gly Gly Asp Gln Ile
 70                  75                  80                  85

tct acg tcg atg aag gat gcg atc gtt tcg att gag gat cgc agg ttc   403
Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile Glu Asp Arg Arg Phe
                 90                  95                 100

tat gag cat gat ggt gtg gat ttg cag ggc ttt ggt cgt gca atc ctg   451
Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe Gly Arg Ala Ile Leu
             105                 110                 115

acg aac ctg gct gcg ggt ggc gtg gag cag ggt gct tcg acg att aac   499
Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly Ala Ser Thr Ile Asn
         120                 125                 130

cag cag tat gtg aag aac ttc ttg ctg ttg gtg gaa gct gat gat gag   547
Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val Glu Ala Asp Asp Glu
     135                 140                 145

gcg gag cag gct gct gct gtg gaa acc tcc atc cct cgt aag ctc cgt   595
Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile Pro Arg Lys Leu Arg
150                 155                 160                 165

gag atg aag atg gcg tct gat ttg gaa aag acg ttg tcg aag gat gag   643
Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr Leu Ser Lys Asp Glu
                 170                 175                 180

att ctg act cgt tat ctc aac att gtt cct ttt ggt aat ggt gct tat   691
Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe Gly Asn Gly Ala Tyr
             185                 190                 195

ggt gtt gag gct gcg gcg cgg acg tat ttc ggt acg tcg gct gcc gag   739
Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly Thr Ser Ala Ala Glu
         200                 205                 210

tta acc att cca cag tct gcg atg ctc gcg ggc att gtg cag tct tcg   787
Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly Ile Val Gln Ser Ser
     215                 220                 225

tct tat ctc aat cca tac acc aat cac gat gct gtg ttt gag cgt cgt   835
Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala Val Phe Glu Arg Arg
230                 235                 240                 245
```

```
aat act gtt ttg ggc gct atg gct gat gct ggc gcg att tcc cca gac   883
Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly Ala Ile Ser Pro Asp
                250                 255                 260

gag gct tcg gct ttc cag cag gaa cct ttg ggt gtc ctg gaa acc ccg   931
Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly Val Leu Glu Thr Pro
            265                 270                 275

caa ggc tta tcc aat ggt tgt atc ggc gct ggc gat cgt ggt ttc ttc   979
Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly Asp Arg Gly Phe Phe
        280                 285                 290

tgc gat tac gct ctg caa tat ctt tct gag cag gga atc acc caa gat   1027
Cys Asp Tyr Ala Leu Gln Tyr Leu Ser Glu Gln Gly Ile Thr Gln Asp
    295                 300                 305

atg ctg                                                           1033
Met Leu
310
```

Sequence Listing

<210> 52
<211> 311
<212> PRT
<213> Corynebacterium glutamicum

<400> 52

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Val Ser Thr Thr Asn Ser Leu Thr Lys Leu Val Ala Ser Thr Val Ala
  1               5                  10                  15

Ala Gly Val Leu Gly Ala Leu Ala Leu Val Pro Phe Ala Ser Leu Ser
             20                  25                  30

Gly Val Ala Val Ala Arg Thr Asn Asp Thr Met Gln Thr Asn Leu Ser
         35                  40                  45

Asp Leu Thr Asp Gly Arg Gly Pro Gly Val Thr Thr Ile Thr Asp Ser
     50                  55                  60

Thr Asp Gln Pro Ile Ala Tyr Ile Tyr Ala Gln Arg Arg Phe Glu Val
 65                  70                  75                  80

Gly Gly Asp Gln Ile Ser Thr Ser Met Lys Asp Ala Ile Val Ser Ile
                 85                  90                  95

Glu Asp Arg Arg Phe Tyr Glu His Asp Gly Val Asp Leu Gln Gly Phe
            100                 105                 110

Gly Arg Ala Ile Leu Thr Asn Leu Ala Ala Gly Gly Val Glu Gln Gly
        115                 120                 125

Ala Ser Thr Ile Asn Gln Gln Tyr Val Lys Asn Phe Leu Leu Leu Val
    130                 135                 140

Glu Ala Asp Asp Glu Ala Glu Gln Ala Ala Ala Val Glu Thr Ser Ile
145                 150                 155                 160

Pro Arg Lys Leu Arg Glu Met Lys Met Ala Ser Asp Leu Glu Lys Thr
                165                 170                 175

Leu Ser Lys Asp Glu Ile Leu Thr Arg Tyr Leu Asn Ile Val Pro Phe
```

```
            180                 185                 190

Gly Asn Gly Ala Tyr Gly Val Glu Ala Ala Ala Arg Thr Tyr Phe Gly
        195                 200                 205

Thr Ser Ala Ala Glu Leu Thr Ile Pro Gln Ser Ala Met Leu Ala Gly
    210                 215                 220

Ile Val Gln Ser Ser Ser Tyr Leu Asn Pro Tyr Thr Asn His Asp Ala
225                 230                 235                 240

Val Phe Glu Arg Arg Asn Thr Val Leu Gly Ala Met Ala Asp Ala Gly
                245                 250                 255

Ala Ile Ser Pro Asp Glu Ala Ser Ala Phe Gln Gln Glu Pro Leu Gly
            260                 265                 270

Val Leu Glu Thr Pro Gln Gly Leu Ser Asn Gly Cys Ile Gly Ala Gly
        275                 280                 285

Asp Arg Gly Phe Phe Cys Asp Tyr Ala Leu Gln Tyr Leu Ser Glu Gln
    290                 295                 300

Gly Ile Thr Gln Asp Met Leu
305                 310


<210> 53
<211> 1545
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1522)
<223> RXA01828

<400> 53
catccctgat ggctaactac attctgatgg ccatcatctt gcgtatttct gacagtgccc 60

gccgacctgt catgtccaag caagcatcgg aggtggctgc gtg aac cgc tcg att   115
                                              Val Asn Arg Ser Ile
                                                1               5

cga atc aca tcc ctc ttc tct ttg ctc ctg atc ttg gtg ctc gta gca   163
Arg Ile Thr Ser Leu Phe Ser Leu Leu Leu Ile Leu Val Leu Val Ala
                10                  15                  20

aac ctc acc tgg att cag gct ttt agg gac gat gat ctt gct cag aac   211
Asn Leu Thr Trp Ile Gln Ala Phe Arg Asp Asp Asp Leu Ala Gln Asn
            25                  30                  35

cca ctg aac gca cgt ggt ttc ctg gag gcg aag tcc act ccg cgt gga   259
Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys Ser Thr Pro Arg Gly
        40                  45                  50

cag att tca act ggt ggc caa gta ctc gca gag tcc tcc cag gac gat   307
Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu Ser Ser Gln Asp Asp
    55                  60                  65

cag ggt ttt tac cag cgc agc tac atc acc aac ccg act gcc tac gca   355
```

```
Gln Gly Phe Tyr Gln Arg Ser Tyr Ile Thr Asn Pro Thr Ala Tyr Ala
 70                  75                  80                  85

ccg gtg gtt ggt tac ctc tct gat gtt tat gga gca gct ggc ctg gaa   403
Pro Val Val Gly Tyr Leu Ser Asp Val Tyr Gly Ala Ala Gly Leu Glu
                90                  95                 100

ttg gga tac aac tct atc ctc aac ggc agt gac tct tcc ctg ttt acc   451
Leu Gly Tyr Asn Ser Ile Leu Asn Gly Ser Asp Ser Ser Leu Phe Thr
            105                 110                 115

tcc cag tgg ctg gat gtc att tct ggc agc cct acc cat ggc gca aac   499
Ser Gln Trp Leu Asp Val Ile Ser Gly Ser Pro Thr His Gly Ala Asn
        120                 125                 130

att gag ctg acc ttg gat ccc aat gcg cag caa act gct tat gaa cag   547
Ile Glu Leu Thr Leu Asp Pro Asn Ala Gln Gln Thr Ala Tyr Glu Gln
    135                 140                 145

ctg agc caa agc ggc tac gag ggt gct gtg gtg gcg ctt cgc cca agc   595
Leu Ser Gln Ser Gly Tyr Glu Gly Ala Val Val Ala Leu Arg Pro Ser
150                 155                 160                 165

act ggt gag gtg ctg gcc atg gcg tca tcg cca agc tat gac ccc aac   643
Thr Gly Glu Val Leu Ala Met Ala Ser Ser Pro Ser Tyr Asp Pro Asn
                170                 175                 180

cag atc gtg gat cca gca acc gca gag gac gct tgg gct gag tac acc   691
Gln Ile Val Asp Pro Ala Thr Ala Glu Asp Ala Trp Ala Glu Tyr Thr
            185                 190                 195

tcc act gaa ggt gca ccg ctg ctc aac cat gca acg cag gaa tca ctg   739
Ser Thr Glu Gly Ala Pro Leu Leu Asn His Ala Thr Gln Glu Ser Leu
        200                 205                 210

cct cct gga tct att ttc aag atc atc act act gcg gca gct ttg gaa   787
Pro Pro Gly Ser Ile Phe Lys Ile Ile Thr Thr Ala Ala Ala Leu Glu
    215                 220                 225

aac ggc tac tct gct gat tcc acc gtg act gca gag gca gca gtg acc   835
Asn Gly Tyr Ser Ala Asp Ser Thr Val Thr Ala Glu Ala Ala Val Thr
230                 235                 240                 245

ctg cct ggc acc aac acc acc ttg acc aac tac ggc ggt cag aca tgt   883
Leu Pro Gly Thr Asn Thr Thr Leu Thr Asn Tyr Gly Gly Gln Thr Cys
                250                 255                 260

gcg ggc ggt ggc acc act acc ctg ctc acc gct ttc cag ctc tcc tgc   931
Ala Gly Gly Gly Thr Thr Thr Leu Leu Thr Ala Phe Gln Leu Ser Cys
            265                 270                 275

aat act gcg ttt gtg gag acc ggc att gat gtt ggc gcg gat gct ttg   979
Asn Thr Ala Phe Val Glu Thr Gly Ile Asp Val Gly Ala Asp Ala Leu
        280                 285                 290

cgc gcg tct gcc gag gac ttc gga gtg gga caa acc tac agc ttg gga  1027
Arg Ala Ser Ala Glu Asp Phe Gly Val Gly Gln Thr Tyr Ser Leu Gly
    295                 300                 305

cta gat aac gtt cct ggc ggc ttg ggt gaa atc ccc gac gat gcc gcc  1075
Leu Asp Asn Val Pro Gly Gly Leu Gly Glu Ile Pro Asp Asp Ala Ala
```

```
310                 315                 320                 325

ctt gga caa tcc agc att ggc cag cgc gac gtg caa atg aac gtg ctg   1123
Leu Gly Gln Ser Ser Ile Gly Gln Arg Asp Val Gln Met Asn Val Leu
                330                 335                 340

cag gcc gct gtc atg gca gga acc gta tcc aac ggt ggc gta cgc atg   1171
Gln Ala Ala Val Met Ala Gly Thr Val Ser Asn Gly Gly Val Arg Met
            345                 350                 355

gaa cca tat ttg gta tcc cgc gtc acc ggt cag gac ctg agc gaa ctg   1219
Glu Pro Tyr Leu Val Ser Arg Val Thr Gly Gln Asp Leu Ser Glu Leu
        360                 365                 370

agc acc cac aag ccg aaa tca gtt ggt gga gtc gag cca gaa att gca   1267
Ser Thr His Lys Pro Lys Ser Val Gly Gly Val Glu Pro Glu Ile Ala
    375                 380                 385

gaa cag ttg aag act ttg atg gaa gcc tca gag cgc aat act tcg ggc   1315
Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu Arg Asn Thr Ser Gly
390                 395                 400                 405

tac acc gga att cag atc gct tcc aag act ggt acc gcg gaa cat ggt   1363
Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly Thr Ala Glu His Gly
                410                 415                 420

gat gaa aac aca cca cca cac acc tgg tac gtg gca ttc aac aac gac   1411
Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val Ala Phe Asn Asn Asp
            425                 430                 435

att gct gtt gct gtg ttg gtg aaa gac ggc ggt gga ttt ggc acc agt   1459
Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly Gly Phe Gly Thr Ser
        440                 445                 450

gca act ggt ggt cag gtc gca gcc cca att ggc cga gct gtg ctt cag   1507
Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly Arg Ala Val Leu Gln
    455                 460                 465

gca gcc gga gga ttt taaaatatga gtcaagaaga cat                    1545
Ala Ala Gly Gly Phe
470
```

<210> 54
<211> 474
<212> PRT
<213> Corynebacterium glutamicum

<400> 54

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Val Asn Arg Ser Ile Arg Ile Thr Ser Leu Phe Ser Leu Leu Leu Ile
  1               5                  10                  15

Leu Val Leu Val Ala Asn Leu Thr Trp Ile Gln Ala Phe Arg Asp Asp
             20                  25                  30

Asp Leu Ala Gln Asn Pro Leu Asn Ala Arg Gly Phe Leu Glu Ala Lys
         35                  40                  45

Ser Thr Pro Arg Gly Gln Ile Ser Thr Gly Gly Gln Val Leu Ala Glu
     50                  55                  60
```

Ser Ser Gln Asp Asp Gln Gly Phe Tyr Gln Arg Ser Tyr Ile Thr Asn
65 70 75 80

Pro Thr Ala Tyr Ala Pro Val Val Gly Tyr Leu Ser Asp Val Tyr Gly
85 90 95

Ala Ala Gly Leu Glu Leu Gly Tyr Asn Ser Ile Leu Asn Gly Ser Asp
100 105 110

Ser Ser Leu Phe Thr Ser Gln Trp Leu Asp Val Ile Ser Gly Ser Pro
115 120 125

Thr His Gly Ala Asn Ile Glu Leu Thr Leu Asp Pro Asn Ala Gln Gln
130 135 140

Thr Ala Tyr Glu Gln Leu Ser Gln Ser Gly Tyr Glu Gly Ala Val Val
145 150 155 160

Ala Leu Arg Pro Ser Thr Gly Glu Val Leu Ala Met Ala Ser Ser Pro
165 170 175

Ser Tyr Asp Pro Asn Gln Ile Val Asp Pro Ala Thr Ala Glu Asp Ala
180 185 190

Trp Ala Glu Tyr Thr Ser Thr Glu Gly Ala Pro Leu Leu Asn His Ala
195 200 205

Thr Gln Glu Ser Leu Pro Pro Gly Ser Ile Phe Lys Ile Ile Thr Thr
210 215 220

Ala Ala Ala Leu Glu Asn Gly Tyr Ser Ala Asp Ser Thr Val Thr Ala
225 230 235 240

Glu Ala Ala Val Thr Leu Pro Gly Thr Asn Thr Thr Leu Thr Asn Tyr
245 250 255

Gly Gly Gln Thr Cys Ala Gly Gly Gly Thr Thr Thr Leu Leu Thr Ala
260 265 270

Phe Gln Leu Ser Cys Asn Thr Ala Phe Val Glu Thr Gly Ile Asp Val
275 280 285

Gly Ala Asp Ala Leu Arg Ala Ser Ala Glu Asp Phe Gly Val Gly Gln
290 295 300

Thr Tyr Ser Leu Gly Leu Asp Asn Val Pro Gly Gly Leu Gly Glu Ile
305 310 315 320

Pro Asp Asp Ala Ala Leu Gly Gln Ser Ser Ile Gly Gln Arg Asp Val
325 330 335

Gln Met Asn Val Leu Gln Ala Ala Val Met Ala Gly Thr Val Ser Asn
340 345 350

Gly Gly Val Arg Met Glu Pro Tyr Leu Val Ser Arg Val Thr Gly Gln
355 360 365

Asp Leu Ser Glu Leu Ser Thr His Lys Pro Lys Ser Val Gly Gly Val
370 375 380

Glu Pro Glu Ile Ala Glu Gln Leu Lys Thr Leu Met Glu Ala Ser Glu

385 390 395 400

Arg Asn Thr Ser Gly Tyr Thr Gly Ile Gln Ile Ala Ser Lys Thr Gly
405 410 415

Thr Ala Glu His Gly Asp Glu Asn Thr Pro Pro His Thr Trp Tyr Val
420 425 430

Ala Phe Asn Asn Asp Ile Ala Val Ala Val Leu Val Lys Asp Gly Gly
435 440 445

Gly Phe Gly Thr Ser Ala Thr Gly Gly Gln Val Ala Ala Pro Ile Gly
450 455 460

Arg Ala Val Leu Gln Ala Ala Gly Gly Phe
465 470

<210> 55
<211> 1208
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1185)
<223> RXA00612

<400> 55

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gcc gct gca gcc att cag cag ggc gct ggc cta gac acc atg ttg gat   48
Ala Ala Ala Ala Ile Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp
  1               5                  10                  15

gtt cct tct cga tat gag gtc aag ggc atg ggc tcc ggc ggt gcc gcg   96
Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
             20                  25                  30

aac tgt ccc gca aat act tac tgc gtg gaa aac gca gga tcc tac gcg   144
Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
         35                  40                  45

cct cgc atg act ctg cag gac gct ctc gcg cag tcc ccc aac act gca   192
Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
     50                  55                  60

ttc gtt gaa atg atc gag cag gtt ggc gtg gac acc gtt gtg gat ctt   240
Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
 65                  70                  75                  80

tca gta aag ctg ggc ctg cga agc tac acc gat gaa ggt tcc ttc gac   288
Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
                 85                  90                  95

ggc gaa agc tca atc gcg gac tac atg aag gac aac aac ctc ggt tct   336
Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
            100                 105                 110

tac act ctt gga cct acc gct gtt aac cct ctt gaa ttg tcc aat gtt   384
Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val
        115                 120                 125
```

```
gct gca acc att gca tcc ggt ggc atg tgg tgc gaa ccc aat ccc atc   432
Ala Ala Thr Ile Ala Ser Gly Gly Met Trp Cys Glu Pro Asn Pro Ile
    130                 135                 140

gcc agc gtc cat gac cgt gaa ggc aac gaa gtc tac att gac cgc cct   480
Ala Ser Val His Asp Arg Glu Gly Asn Glu Val Tyr Ile Asp Arg Pro
145                 150                 155                 160

gca tgt gag cgc gcc atc gat gcc gaa acg gct tca gct ttg gcc gtc   528
Ala Cys Glu Arg Ala Ile Asp Ala Glu Thr Ala Ser Ala Leu Ala Val
                165                 170                 175

ggc atg agc aag gat acg gtc agc gga act gcg gcc tct gca gcc agc   576
Gly Met Ser Lys Asp Thr Val Ser Gly Thr Ala Ala Ser Ala Ala Ser
            180                 185                 190

atg tac gga tgg tcc ttg cca acc gca gcg aag acc ggt acc acc gag   624
Met Tyr Gly Trp Ser Leu Pro Thr Ala Ala Lys Thr Gly Thr Thr Glu
        195                 200                 205

tcc aac cag tcc tca gca ttt atg ggc ttc aac agc aac ttt gcc gca   672
Ser Asn Gln Ser Ser Ala Phe Met Gly Phe Asn Ser Asn Phe Ala Ala
    210                 215                 220

gct cca tac atc tac aat gac ggc acc tcc acc acc cca ctg tgc agc   720
Ala Pro Tyr Ile Tyr Asn Asp Gly Thr Ser Thr Thr Pro Leu Cys Ser
225                 230                 235                 240

ggc ccc gtc cgc cag tgc agc agc ggt aac ctc ttc ggc ggt aac gaa   768
Gly Pro Val Arg Gln Cys Ser Ser Gly Asn Leu Phe Gly Gly Asn Glu
                245                 250                 255

cca gct caa aca tgg ttt aac atg gca agc aac gtc ccc gca gct tcg   816
Pro Ala Gln Thr Trp Phe Asn Met Ala Ser Asn Val Pro Ala Ala Ser
            260                 265                 270

caa gga aca ctg cca tcc agc agc gat tca ttc cgc ctc ggc act tcc   864
Gln Gly Thr Leu Pro Ser Ser Ser Asp Ser Phe Arg Leu Gly Thr Ser
        275                 280                 285

ggc gaa ctc ctc aac cag gtt gtc ggc caa agc gaa gcc tcc gct cga   912
Gly Glu Leu Leu Asn Gln Val Val Gly Gln Ser Glu Ala Ser Ala Arg
    290                 295                 300

cgc acc ctc gaa gcc aaa ggc tac aag gtc acc acg cgt tca gtc tcc   960
Arg Thr Leu Glu Ala Lys Gly Tyr Lys Val Thr Thr Arg Ser Val Ser
305                 310                 315                 320

ggc gcc ggc agc gcg cgc ggc acc gta gtc agc gca acc cct cag ggt  1008
Gly Ala Gly Ser Ala Arg Gly Thr Val Val Ser Ala Thr Pro Gln Gly
                325                 330                 335

gca gtg ctt atc gac ggt gga acc gtc att ttg gac atc tcc gac ggc  1056
Ala Val Leu Ile Asp Gly Gly Thr Val Ile Leu Asp Ile Ser Asp Gly
            340                 345                 350

aca agc cct gcc ccc gct gcc acc aac aat gat gac agc gac gat gga  1104
Thr Ser Pro Ala Pro Ala Ala Thr Asn Asn Asp Asp Ser Asp Asp Gly
        355                 360                 365

gac acc cct gct cca tca aca aac aac cgc gga aca acc att gaa gac  1152
```

```
Asp Thr Pro Ala Pro Ser Thr Asn Asn Arg Gly Thr Thr Ile Glu Asp
    370                 375                 380

gcc atc aat gac gcc atc aac cag ttc ttc cgc tagaaatacc tagttgctca 1205
Ala Ile Asn Asp Ala Ile Asn Gln Phe Phe Arg
385                 390                 395

aac                                                               1208


<210> 56
<211> 395
<212> PRT
<213> Corynebacterium glutamicum

<400> 56
Ala Ala Ala Ala Ile Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp
  1               5                  10                  15

Val Pro Ser Arg Tyr Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala
             20                  25                  30

Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala
         35                  40                  45

Pro Arg Met Thr Leu Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala
     50                  55                  60

Phe Val Glu Met Ile Glu Gln Val Gly Val Asp Thr Val Val Asp Leu
 65                  70                  75                  80

Ser Val Lys Leu Gly Leu Arg Ser Tyr Thr Asp Glu Gly Ser Phe Asp
                 85                  90                  95

Gly Glu Ser Ser Ile Ala Asp Tyr Met Lys Asp Asn Asn Leu Gly Ser
            100                 105                 110

Tyr Thr Leu Gly Pro Thr Ala Val Asn Pro Leu Glu Leu Ser Asn Val
        115                 120                 125

Ala Ala Thr Ile Ala Ser Gly Gly Met Trp Cys Glu Pro Asn Pro Ile
    130                 135                 140

Ala Ser Val His Asp Arg Glu Gly Asn Glu Val Tyr Ile Asp Arg Pro
145                 150                 155                 160

Ala Cys Glu Arg Ala Ile Asp Ala Glu Thr Ala Ser Ala Leu Ala Val
                165                 170                 175

Gly Met Ser Lys Asp Thr Val Ser Gly Thr Ala Ala Ser Ala Ala Ser
            180                 185                 190

Met Tyr Gly Trp Ser Leu Pro Thr Ala Ala Lys Thr Gly Thr Thr Glu
        195                 200                 205

Ser Asn Gln Ser Ser Ala Phe Met Gly Phe Asn Ser Asn Phe Ala Ala
    210                 215                 220

Ala Pro Tyr Ile Tyr Asn Asp Gly Thr Ser Thr Thr Pro Leu Cys Ser
225                 230                 235                 240
```

```
Gly Pro Val Arg Gln Cys Ser Ser Gly Asn Leu Phe Gly Gly Asn Glu
                245                 250                 255

Pro Ala Gln Thr Trp Phe Asn Met Ala Ser Asn Val Pro Ala Ala Ser
            260                 265                 270

Gln Gly Thr Leu Pro Ser Ser Ser Asp Ser Phe Arg Leu Gly Thr Ser
        275                 280                 285

Gly Glu Leu Leu Asn Gln Val Val Gly Gln Ser Glu Ala Ser Ala Arg
    290                 295                 300

Arg Thr Leu Glu Ala Lys Gly Tyr Lys Val Thr Thr Arg Ser Val Ser
305                 310                 315                 320

Gly Ala Gly Ser Ala Arg Gly Thr Val Val Ser Ala Thr Pro Gln Gly
                325                 330                 335

Ala Val Leu Ile Asp Gly Gly Thr Val Ile Leu Asp Ile Ser Asp Gly
            340                 345                 350

Thr Ser Pro Ala Pro Ala Ala Thr Asn Asn Asp Asp Ser Asp Asp Gly
        355                 360                 365

Asp Thr Pro Ala Pro Ser Thr Asn Asn Arg Gly Thr Thr Ile Glu Asp
    370                 375                 380

Ala Ile Asn Asp Ala Ile Asn Gln Phe Phe Arg
385                 390                 395


<210> 57
<211> 1404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1381)
<223> RXA01510

<400> 57
ccgcgcgtat ggttcgtgcg tgagacgacg gtcgatataa ggttggagtc ctgatatcgc 60

aagaagaatc gcaagaaaat ttgcaggaga aggagcgccc atg aaa aat gcg tgg   115
                                            Met Lys Asn Ala Trp
                                              1               5

tgg gtt ggc tca tcg gtt ggt gta ctg att gca gtg ggg gct gtc atc   163
Trp Val Gly Ser Ser Val Gly Val Leu Ile Ala Val Gly Ala Val Ile
                  10                  15                  20

ggt ggt ggc gtg tgg gtg aat cat tct ggt ttt ggt ttg gat cac ccg   211
Gly Gly Gly Val Trp Val Asn His Ser Gly Phe Gly Leu Asp His Pro
              25                  30                  35

gag ccc atg tcg gtg gag atg cct gag cag ctg ttt tct tct gcg att   259
Glu Pro Met Ser Val Glu Met Pro Glu Gln Leu Phe Ser Ser Ala Ile
          40                  45                  50

gat ccg gat gct ttg gaa gcc cca gat ttt gcc act ttg gag aag gat   307
```

```
Asp Pro Asp Ala Leu Glu Ala Pro Asp Phe Ala Thr Leu Glu Lys Asp
     55                  60                  65

ttg acc tcg cag gct gcg gat tct cgg ttg ggc act ttt gtc ggt gtt   355
Leu Thr Ser Gln Ala Ala Asp Ser Arg Leu Gly Thr Phe Val Gly Val
 70                  75                  80                  85

gcc agg gat gtg gaa tct ggt gag gtg gtg tgg gag cag aat cag ggg   403
Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp Glu Gln Asn Gln Gly
                 90                  95                 100

act gcg gtg agg ccg gcg tcg gcg acg aag att ttg acg gcg gcg gtg   451
Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile Leu Thr Ala Ala Val
            105                 110                 115

gcg ttg tat gag ctt ggc cgt gag gac acc atc aca acg aag gtt gtt   499
Ala Leu Tyr Glu Leu Gly Arg Glu Asp Thr Ile Thr Thr Lys Val Val
        120                 125                 130

gag ggg gag cag ccg gga acg gtg gtg att aag gcg ggt ggt gat gtc   547
Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys Ala Gly Gly Asp Val
    135                 140                 145

acg ttg agt gag gag atg ctc gat gat ttg gcc acc cag ctt gag ggg   595
Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala Thr Gln Leu Glu Gly
150                 155                 160                 165

caa gat att ggc act gtg ttg atc gat acg tct att tgg cct gat gag   643
Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser Ile Trp Pro Asp Glu
                170                 175                 180

ggc ttt gct agt acg tgg gat cca gtg gat gtt gat gct ggt tat atc   691
Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val Asp Ala Gly Tyr Ile
            185                 190                 195

gct gat gtg gag ccc gcg atg att gag gct gcc cgc att ggt ggg tcg   739
Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala Arg Ile Gly Gly Ser
        200                 205                 210

gag ggg gat ctg ccg agg tct cat act ccg gcg tta gat gtt gcg cag   787
Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala Leu Asp Val Ala Gln
    215                 220                 225

gcg ttg gcg gat cgt gtc ggc gcg gac acc gta gat gag ggc agc gct   835
Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val Asp Glu Gly Ser Ala
230                 235                 240                 245

ccg gac aaa acc gtg ctg gca tcc gtg gag tct gac acg ttg gat cag   883
Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser Asp Thr Leu Asp Gln
                250                 255                 260

cgt ctt gct cgg atg atg aag gat tct gac aat gtg atg gca gag ggt   931
Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn Val Met Ala Glu Gly
            265                 270                 275

atc gct aag gaa gtg gcc gcg tcg aag gat ttg gct acc gat tcg gcg   979
Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu Ala Thr Asp Ser Ala
        280                 285                 290

agt acc tcg aag atg acg ttg gag att ctc aag gac aag ggc ttc gat  1027
Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys Asp Lys Gly Phe Asp
```

```
    295                 300                 305

ttg agt ggc gtg tcc att gtg gat aat tcg ggt ttg agc ttt gac aac   1075
Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly Leu Ser Phe Asp Asn
310                 315                 320                 325

ctc att acg ccc cgc ctg ctt gat gat att ttg acc cgc gcc gcc acg   1123
Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu Thr Arg Ala Ala Thr
                330                 335                 340

gaa cct gag ttg agt tca cta ttg aca tcg ctg cct atc gcg cat gga   1171
Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu Pro Ile Ala His Gly
            345                 350                 355

acc gga acc ttg gag gat cgc tac gac gga ctc tca ggt gcg ggt tgg   1219
Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu Ser Gly Ala Gly Trp
        360                 365                 370

gtg cgg gcg aaa act ggc act ctg acg gat aca tcg gca ttg gca ggg   1267
Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr Ser Ala Leu Ala Gly
    375                 380                 385

gtg gtg acc tcg gag tcg ggg cgt gtg ttt acc ttt gct ttt gtg tct   1315
Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr Phe Ala Phe Val Ser
390                 395                 400                 405

aat ggt tcc gcg att gtg ccg gcg cgt gag gct ttg gat gag atg gcg   1363
Asn Gly Ser Ala Ile Val Pro Ala Arg Glu Ala Leu Asp Glu Met Ala
                410                 415                 420

tcg att ctg agg gac ttt taaggtggca tccctcatcg gga                1404
Ser Ile Leu Arg Asp Phe
            425
```

<210> 58
<211> 427
<212> PRT
<213> Corynebacterium glutamicum

<400> 58

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Met Lys Asn Ala Trp Trp Val Gly Ser Ser Val Gly Val Leu Ile Ala
  1               5                  10                  15

Val Gly Ala Val Ile Gly Gly Gly Val Trp Val Asn His Ser Gly Phe
             20                  25                  30

Gly Leu Asp His Pro Glu Pro Met Ser Val Glu Met Pro Glu Gln Leu
         35                  40                  45

Phe Ser Ser Ala Ile Asp Pro Asp Ala Leu Glu Ala Pro Asp Phe Ala
     50                  55                  60

Thr Leu Glu Lys Asp Leu Thr Ser Gln Ala Ala Asp Ser Arg Leu Gly
 65                  70                  75                  80

Thr Phe Val Gly Val Ala Arg Asp Val Glu Ser Gly Glu Val Val Trp
                 85                  90                  95

Glu Gln Asn Gln Gly Thr Ala Val Arg Pro Ala Ser Ala Thr Lys Ile
            100                 105                 110
```

Leu Thr Ala Ala Val Ala Leu Tyr Glu Leu Gly Arg Glu Asp Thr Ile
115 120 125

Thr Thr Lys Val Val Glu Gly Glu Gln Pro Gly Thr Val Val Ile Lys
130 135 140

Ala Gly Gly Asp Val Thr Leu Ser Glu Glu Met Leu Asp Asp Leu Ala
145 150 155 160

Thr Gln Leu Glu Gly Gln Asp Ile Gly Thr Val Leu Ile Asp Thr Ser
165 170 175

Ile Trp Pro Asp Glu Gly Phe Ala Ser Thr Trp Asp Pro Val Asp Val
180 185 190

Asp Ala Gly Tyr Ile Ala Asp Val Glu Pro Ala Met Ile Glu Ala Ala
195 200 205

Arg Ile Gly Gly Ser Glu Gly Asp Leu Pro Arg Ser His Thr Pro Ala
210 215 220

Leu Asp Val Ala Gln Ala Leu Ala Asp Arg Val Gly Ala Asp Thr Val
225 230 235 240

Asp Glu Gly Ser Ala Pro Asp Lys Thr Val Leu Ala Ser Val Glu Ser
245 250 255

Asp Thr Leu Asp Gln Arg Leu Ala Arg Met Met Lys Asp Ser Asp Asn
260 265 270

Val Met Ala Glu Gly Ile Ala Lys Glu Val Ala Ala Ser Lys Asp Leu
275 280 285

Ala Thr Asp Ser Ala Ser Thr Ser Lys Met Thr Leu Glu Ile Leu Lys
290 295 300

Asp Lys Gly Phe Asp Leu Ser Gly Val Ser Ile Val Asp Asn Ser Gly
305 310 315 320

Leu Ser Phe Asp Asn Leu Ile Thr Pro Arg Leu Leu Asp Asp Ile Leu
325 330 335

Thr Arg Ala Ala Thr Glu Pro Glu Leu Ser Ser Leu Leu Thr Ser Leu
340 345 350

Pro Ile Ala His Gly Thr Gly Thr Leu Glu Asp Arg Tyr Asp Gly Leu
355 360 365

Ser Gly Ala Gly Trp Val Arg Ala Lys Thr Gly Thr Leu Thr Asp Thr
370 375 380

Ser Ala Leu Ala Gly Val Val Thr Ser Glu Ser Gly Arg Val Phe Thr
385 390 395 400

Phe Ala Phe Val Ser Asn Gly Ser Ala Ile Val Pro Ala Arg Glu Ala
405 410 415

Leu Asp Glu Met Ala Ser Ile Leu Arg Asp Phe
420 425

<210> 59
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1939)
<223> RXN01608

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taatcttcac tccatgaaca aggtgcagcg caggtcactg atg gcg ttg tgc atg 115
Met Ala Leu Cys Met
1 5

acg gtg gca ttt gct gga gga agc ctg acc gcg tgc aca cct cgt cct 163
Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala Cys Thr Pro Arg Pro
10 15 20

gat acc gca gac ccc atc gca gag gaa ttc ctt caa gct tgg gca tcg 211
Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu Gln Ala Trp Ala Ser
25 30 35

caa gat ttc gac act att gcg gac atc acc gac caa gct gac ctt gcc 259
Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp Gln Ala Asp Leu Ala
40 45 50

aca gaa atg ctc agc acc agt ttc gat ggt ctg caa gca gac agc gtt 307
Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu Gln Ala Asp Ser Val
55 60 65

gaa ctg act ttg gat tcc gtg gat tcc cgg gac acc atc gcc acc gcc 355
Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp Thr Ile Ala Thr Ala
70 75 80 85

aat ttc tcc gtg gtg tgg aag ctt ccc cga gac aga gaa gtt tcc tac 403
Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp Arg Glu Val Ser Tyr
90 95 100

gac tca tcg atg acg ctg acc aag atg cgc aac gaa tgg aca gtg cgt 451
Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn Glu Trp Thr Val Arg
105 110 115

tgg gaa cct tcc ctc gtg cac ccc aaa ctg ggc gcc aac cag cac ctg 499
Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly Ala Asn Gln His Leu
120 125 130

gaa ttg cgc gcc att gaa gcg cag cga gcc aac gta att tcc tcc gat 547
Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn Val Ile Ser Ser Asp
135 140 145

gga gct ccg gtt ctc gcg ccg gga agt atc tac cga gtt ttg gtt gat 595
Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr Arg Val Leu Val Asp
150 155 160 165

ccc agc gca ggg gat gcc gat gtg gtg gtc aag agg gtg gca gat tat 643
Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys Arg Val Ala Asp Tyr
170 175 180

```
ttg aat gaa gcc cat gcg act gat gag aat gtg aac acc ctt gat gtc   691
Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val Asn Thr Leu Asp Val
            185                 190                 195

gaa gac att atg agc aat ctt ggc gat tcc acc tat tca ctc acc aca   739
Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr Tyr Ser Leu Thr Thr
        200                 205                 210

gtt gat gcc aat ttg ggt gcc cgc atg gaa cag gat cta gcg ggg att   787
Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln Asp Leu Ala Gly Ile
    215                 220                 225

ccg ggg ctg acg ttc aat gag gaa gca tcc atg gta gcc acc gac cca   835
Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met Val Ala Thr Asp Pro
230                 235                 240                 245

ggt ttt gct ccg gat att gtg tct cgc gtt gcg cgc att gtg gaa gat   883
Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala Arg Ile Val Glu Asp
                250                 255                 260

gaa tta gaa gga tcc aat ggt tgg cgc gcc tcc att gtc act tcc aat   931
Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser Ile Val Thr Ser Asn
            265                 270                 275

ggt gcg gtg att gat gat atc gcc tac gac gcc cca gag ctt gcc ccc   979
Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala Pro Glu Leu Ala Pro
        280                 285                 290

agc gtg agg atc agc ctg gat cac aac gtt caa cga gca gcg gaa gaa   1027
Ser Val Arg Ile Ser Leu Asp His Asn Val Gln Arg Ala Ala Glu Glu
    295                 300                 305

gcc gta gac ctg cgc gct gag atg aaa gcc atg atg gtg gtc atg agg   1075
Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met Met Val Val Met Arg
310                 315                 320                 325

cca tcc act ggt gaa atc ctc gca gtg gcc caa aca gat gaa gct gac   1123
Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln Thr Asp Glu Ala Asp
                330                 335                 340

aaa gac ggc gat gtt gcg ctg atg gga caa tac cca ccg gga tcg aca   1171
Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr Pro Pro Gly Ser Thr
            345                 350                 355

ttc aag atc atc act gca gcc gcg ggg ttg gcg cat gaa gga tta act   1219
Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala His Glu Gly Leu Thr
        360                 365                 370

cca gac agc att gtg cca tgc cct ggc acc atg aat atc tac ggc cga   1267
Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met Asn Ile Tyr Gly Arg
    375                 380                 385

att gtc acc aac tac aac agc ttc tcc ttg ggc aac acc tca ttg gat   1315
Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly Asn Thr Ser Leu Asp
390                 395                 400                 405

gat gct ttt gcc aat tca tgc aac acc act ttc gcg gat att ttc cac   1363
Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe Ala Asp Ile Phe His
                410                 415                 420
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Sequence Listing

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cac ttg gag cca ggc caa ctg aaa aat gtg gct aag cag ttt ggc ctc   1411
His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala Lys Gln Phe Gly Leu
            425                 430                 435

gga att gat tat caa atc cca ggc ctt gac acc atg acg gga tcg gtg   1459
Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr Met Thr Gly Ser Val
        440                 445                 450

cct gaa ggt gac atc gtg ttg gac cgt acc gaa tct ggt tac ggc cag   1507
Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu Ser Gly Tyr Gly Gln
    455                 460                 465

ggt ctt gac cta gca agt ccc ttt ggc atg gcg ttg gtc gcc tcc act   1555
Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala Leu Val Ala Ser Thr
470                 475                 480                 485

gca gcc acc ggt tca gtt ccc acg cca acg ctg att tct gga cat gaa   1603
Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu Ile Ser Gly His Glu
                490                 495                 500

act gtt gcc agt gaa gaa gtt ctg gcg ctt gat cca gaa gtc ctt gcc   1651
Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp Pro Glu Val Leu Ala
            505                 510                 515

aat gtg cag cgg atg atg aaa tcc gtg gtc aat gac ggt acc gct cgt   1699
Asn Val Gln Arg Met Met Lys Ser Val Val Asn Asp Gly Thr Ala Arg
        520                 525                 530

ggc atg cgc caa acc ggt ggc cag atc tac gca aag aca ggt gaa gcc   1747
Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala Lys Thr Gly Glu Ala
    535                 540                 545

gaa atc aac gaa ggc tcc cat gcg tgg ttc acc ggc tac cgc gaa gat   1795
Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr Gly Tyr Arg Glu Asp
550                 555                 560                 565

gac atc gct ttt gcc acc ctc gtg gtg ttg ggc gga ggc tcc gaa gcg   1843
Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly Gly Gly Ser Glu Ala
                570                 575                 580

gct gcc gct gtg aca gat cag ttc ttt gtg aaa ctc gat gag ctt cgc   1891
Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys Leu Asp Glu Leu Arg
            585                 590                 595

gca ggg gga gaa gtt gca gtc agt gaa gct gaa gag cag cca gtc ggc   1939
Ala Gly Gly Glu Val Ala Val Ser Glu Ala Glu Glu Gln Pro Val Gly
        600                 605                 610

taaaaaatag cctccatcca acc                                        1962
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<210> 60
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<213> Corynebacterium glutamicum

<400> 60

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Met Ala Leu Cys Met Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala
  1               5                  10                  15

Cys Thr Pro Arg Pro Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu
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20 25 30

Gln Ala Trp Ala Ser Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp
35 40 45

Gln Ala Asp Leu Ala Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu
50 55 60

Gln Ala Asp Ser Val Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp
65 70 75 80

Thr Ile Ala Thr Ala Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp
85 90 95

Arg Glu Val Ser Tyr Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn
100 105 110

Glu Trp Thr Val Arg Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly
115 120 125

Ala Asn Gln His Leu Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn
130 135 140

Val Ile Ser Ser Asp Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr
145 150 155 160

Arg Val Leu Val Asp Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys
165 170 175

Arg Val Ala Asp Tyr Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val
180 185 190

Asn Thr Leu Asp Val Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr
195 200 205

Tyr Ser Leu Thr Thr Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln
210 215 220

Asp Leu Ala Gly Ile Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met
225 230 235 240

Val Ala Thr Asp Pro Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala
245 250 255

Arg Ile Val Glu Asp Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser
260 265 270

Ile Val Thr Ser Asn Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala
275 280 285

Pro Glu Leu Ala Pro Ser Val Arg Ile Ser Leu Asp His Asn Val Gln
290 295 300

Arg Ala Ala Glu Glu Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met
305 310 315 320

Met Val Val Met Arg Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln
325 330 335

Thr Asp Glu Ala Asp Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr
340 345 350

Pro Pro Gly Ser Thr Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala
355 360 365

His Glu Gly Leu Thr Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met
370 375 380

Asn Ile Tyr Gly Arg Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly
385 390 395 400

Asn Thr Ser Leu Asp Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe
405 410 415

Ala Asp Ile Phe His His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala
420 425 430

Lys Gln Phe Gly Leu Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr
435 440 445

Met Thr Gly Ser Val Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu
450 455 460

Ser Gly Tyr Gly Gln Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala
465 470 475 480

Leu Val Ala Ser Thr Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu
485 490 495

Ile Ser Gly His Glu Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp
500 505 510

Pro Glu Val Leu Ala Asn Val Gln Arg Met Met Lys Ser Val Val Asn
515 520 525

Asp Gly Thr Ala Arg Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala
530 535 540

Lys Thr Gly Glu Ala Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr
545 550 555 560

Gly Tyr Arg Glu Asp Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly
565 570 575

Gly Gly Ser Glu Ala Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys
580 585 590

Leu Asp Glu Leu Arg Ala Gly Gly Glu Val Ala Val Ser Glu Ala Glu
595 600 605

Glu Gln Pro Val Gly
610

<210> 61
<211> 1962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1939)

<223> FRXA01608

<400> 61

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taatcttcac tccatgaaca aggtgcagcg caggtcactg atg gcg ttg tgc atg   115
                                              Met Ala Leu Cys Met
                                                1               5

acg gtg gca ttt gct gga gga agc ctg acc gcg tgc aca cct cgt cct   163
Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala Cys Thr Pro Arg Pro
                10                  15                  20

gat acc gca gac ccc atc gca gag gaa ttc ctt caa gct tgg gca tcg   211
Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu Gln Ala Trp Ala Ser
            25                  30                  35

caa gat ttc gac act att gcg gac atc acc gac caa gct gac ctt gcc   259
Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp Gln Ala Asp Leu Ala
        40                  45                  50

aca gaa atg ctc agc acc agt ttc gat ggt ctg caa gca gac agc gtt   307
Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu Gln Ala Asp Ser Val
    55                  60                  65

gaa ctg act ttg gat tcc gtg gat tcc cgg gac acc atc gcc acc gcc   355
Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp Thr Ile Ala Thr Ala
70                  75                  80                  85

aat ttc tcc gtg gtg tgg aag ctt ccc cga gac aga gaa gtt tcc tac   403
Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp Arg Glu Val Ser Tyr
                90                  95                  100

gac tca tcg atg acg ctg acc aag atg cgc aac gaa tgg aca gtg cgt   451
Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn Glu Trp Thr Val Arg
            105                 110                 115

tgg gaa cct tcc ctc gtg cac ccc aaa ctg ggc gcc aac cag cac ctg   499
Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly Ala Asn Gln His Leu
        120                 125                 130

gaa ttg cgc gcc att gaa gcg cag cga gcc aac gta att tcc tcc gat   547
Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn Val Ile Ser Ser Asp
    135                 140                 145

gga gct ccg gtt ctc gcg ccg gga agt atc tac cga gtt ttg gtt gat   595
Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr Arg Val Leu Val Asp
150                 155                 160                 165

ccc agc gca ggg gat gcc gat gtg gtg gtc aag agg gtg gca gat tat   643
Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys Arg Val Ala Asp Tyr
                170                 175                 180

ttg aat gaa gcc cat gcg act gat gag aat gtg aac acc ctt gat gtc   691
Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val Asn Thr Leu Asp Val
            185                 190                 195

gaa gac att atg agc aat ctt ggc gat tcc acc tat tca ctc acc aca   739
Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr Tyr Ser Leu Thr Thr
        200                 205                 210
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gtt gat gcc aat ttg ggt gcc cgc atg gaa cag gat cta gcg ggg att   787
Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln Asp Leu Ala Gly Ile
    215                 220                 225

ccg ggg ctg acg ttc aat gag gaa gca tcc atg gta gcc acc gac cca   835
Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met Val Ala Thr Asp Pro
230                 235                 240                 245

ggt ttt gct ccg gat att gtg tct cgc gtt gcg cgc att gtg gaa gat   883
Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala Arg Ile Val Glu Asp
                250                 255                 260

gaa tta gaa gga tcc aat ggt tgg cgc gcc tcc att gtc act tcc aat   931
Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser Ile Val Thr Ser Asn
            265                 270                 275

ggt gcg gtg att gat gat atc gcc tac gac gcc cca gag ctt gcc ccc   979
Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala Pro Glu Leu Ala Pro
        280                 285                 290

agc gtg agg atc agc ctg gat cac aac gtt caa cga gca gcg gaa gaa   1027
Ser Val Arg Ile Ser Leu Asp His Asn Val Gln Arg Ala Ala Glu Glu
    295                 300                 305

gcc gta gac ctg cgc gct gag atg aaa gcc atg atg gtg gtc atg agg   1075
Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met Met Val Val Met Arg
310                 315                 320                 325

cca tcc act ggt gaa atc ctc gca gtg gcc caa aca gat gaa gct gac   1123
Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln Thr Asp Glu Ala Asp
                330                 335                 340

aaa gac ggc gat gtt gcg ctg atg gga caa tac cca ccg gga tcg aca   1171
Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr Pro Pro Gly Ser Thr
            345                 350                 355

ttc aag atc atc act gca gcc gcg ggg ttg gcg cat gaa gga tta act   1219
Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala His Glu Gly Leu Thr
        360                 365                 370

cca gac agc att gtg cca tgc cct ggc acc atg aat atc tac ggc cga   1267
Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met Asn Ile Tyr Gly Arg
    375                 380                 385

att gtc acc aac tac aac agc ttc tcc ttg ggc aac acc tca ttg gat   1315
Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly Asn Thr Ser Leu Asp
390                 395                 400                 405

gat gct ttt gcc aat tca tgc aac acc act ttc gcg gat att ttc cac   1363
Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe Ala Asp Ile Phe His
                410                 415                 420

cac ttg gag cca ggc caa ctg aaa aat gtg gct aag cag ttt ggc ctc   1411
His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala Lys Gln Phe Gly Leu
            425                 430                 435

gga att gat tat caa atc cca ggc ctt gac acc atg acg gga tcg gtg   1459
Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr Met Thr Gly Ser Val
        440                 445                 450

cct gaa ggt gac atc gtg ttg gac cgt acc gaa tct ggt tac ggc cag   1507
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Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu Ser Gly Tyr Gly Gln
    455                 460                 465

ggt ctt gac cta gca agt ccc ttt ggc atg gcg ttg gtc gcc tcc act   1555
Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala Leu Val Ala Ser Thr
470                 475                 480                 485

gca gcc acc ggt tca gtt ccc acg cca acg ctg att tct gga cat gaa   1603
Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu Ile Ser Gly His Glu
                490                 495                 500

act gtt gcc agt gaa gaa gtt ctg gcg ctt gat cca gaa gtc ctt gcc   1651
Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp Pro Glu Val Leu Ala
            505                 510                 515

aat gtg cag cgg atg atg aaa tcc gtg gtc aat gac ggt acc gct cgt   1699
Asn Val Gln Arg Met Met Lys Ser Val Val Asn Asp Gly Thr Ala Arg
        520                 525                 530

ggc atg cgc caa acc ggt ggc cag atc tac gca aag aca ggt gaa gcc   1747
Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala Lys Thr Gly Glu Ala
    535                 540                 545

gaa atc aac gaa ggc tcc cat gcg tgg ttc acc ggc tac cgc gaa gat   1795
Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr Gly Tyr Arg Glu Asp
550                 555                 560                 565

gac atc gct ttt gcc acc ctc gtg gtg ttg ggc gga ggc tcc gaa gcg   1843
Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly Gly Gly Ser Glu Ala
                570                 575                 580

gct gcc gct gtg aca gat cag ttc ttt gtg aaa ctc gat gag ctt cgc   1891
Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys Leu Asp Glu Leu Arg
            585                 590                 595

gca ggg gga gaa gtt gca gtc agt gaa gct gaa gag cag cca gtc ggc   1939
Ala Gly Gly Glu Val Ala Val Ser Glu Ala Glu Glu Gln Pro Val Gly
        600                 605                 610

taaaaaatag cctccatcca acc                                        1962


<210> 62
<211> 613
<212> PRT
<213> Corynebacterium glutamicum

<400> 62
Met Ala Leu Cys Met Thr Val Ala Phe Ala Gly Gly Ser Leu Thr Ala
  1               5                  10                  15

Cys Thr Pro Arg Pro Asp Thr Ala Asp Pro Ile Ala Glu Glu Phe Leu
             20                  25                  30

Gln Ala Trp Ala Ser Gln Asp Phe Asp Thr Ile Ala Asp Ile Thr Asp
         35                  40                  45

Gln Ala Asp Leu Ala Thr Glu Met Leu Ser Thr Ser Phe Asp Gly Leu
     50                  55                  60

Gln Ala Asp Ser Val Glu Leu Thr Leu Asp Ser Val Asp Ser Arg Asp
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65 70 75 80

Thr Ile Ala Thr Ala Asn Phe Ser Val Val Trp Lys Leu Pro Arg Asp
85 90 95

Arg Glu Val Ser Tyr Asp Ser Ser Met Thr Leu Thr Lys Met Arg Asn
100 105 110

Glu Trp Thr Val Arg Trp Glu Pro Ser Leu Val His Pro Lys Leu Gly
115 120 125

Ala Asn Gln His Leu Glu Leu Arg Ala Ile Glu Ala Gln Arg Ala Asn
130 135 140

Val Ile Ser Ser Asp Gly Ala Pro Val Leu Ala Pro Gly Ser Ile Tyr
145 150 155 160

Arg Val Leu Val Asp Pro Ser Ala Gly Asp Ala Asp Val Val Val Lys
165 170 175

Arg Val Ala Asp Tyr Leu Asn Glu Ala His Ala Thr Asp Glu Asn Val
180 185 190

Asn Thr Leu Asp Val Glu Asp Ile Met Ser Asn Leu Gly Asp Ser Thr
195 200 205

Tyr Ser Leu Thr Thr Val Asp Ala Asn Leu Gly Ala Arg Met Glu Gln
210 215 220

Asp Leu Ala Gly Ile Pro Gly Leu Thr Phe Asn Glu Glu Ala Ser Met
225 230 235 240

Val Ala Thr Asp Pro Gly Phe Ala Pro Asp Ile Val Ser Arg Val Ala
245 250 255

Arg Ile Val Glu Asp Glu Leu Glu Gly Ser Asn Gly Trp Arg Ala Ser
260 265 270

Ile Val Thr Ser Asn Gly Ala Val Ile Asp Asp Ile Ala Tyr Asp Ala
275 280 285

Pro Glu Leu Ala Pro Ser Val Arg Ile Ser Leu Asp His Asn Val Gln
290 295 300

Arg Ala Ala Glu Glu Ala Val Asp Leu Arg Ala Glu Met Lys Ala Met
305 310 315 320

Met Val Val Met Arg Pro Ser Thr Gly Glu Ile Leu Ala Val Ala Gln
325 330 335

Thr Asp Glu Ala Asp Lys Asp Gly Asp Val Ala Leu Met Gly Gln Tyr
340 345 350

Pro Pro Gly Ser Thr Phe Lys Ile Ile Thr Ala Ala Ala Gly Leu Ala
355 360 365

His Glu Gly Leu Thr Pro Asp Ser Ile Val Pro Cys Pro Gly Thr Met
370 375 380

Asn Ile Tyr Gly Arg Ile Val Thr Asn Tyr Asn Ser Phe Ser Leu Gly
385 390 395 400

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Asn Thr Ser Leu Asp Asp Ala Phe Ala Asn Ser Cys Asn Thr Thr Phe
                405                 410                 415

Ala Asp Ile Phe His His Leu Glu Pro Gly Gln Leu Lys Asn Val Ala
            420                 425                 430

Lys Gln Phe Gly Leu Gly Ile Asp Tyr Gln Ile Pro Gly Leu Asp Thr
        435                 440                 445

Met Thr Gly Ser Val Pro Glu Gly Asp Ile Val Leu Asp Arg Thr Glu
    450                 455                 460

Ser Gly Tyr Gly Gln Gly Leu Asp Leu Ala Ser Pro Phe Gly Met Ala
465                 470                 475                 480

Leu Val Ala Ser Thr Ala Ala Thr Gly Ser Val Pro Thr Pro Thr Leu
                485                 490                 495

Ile Ser Gly His Glu Thr Val Ala Ser Glu Glu Val Leu Ala Leu Asp
            500                 505                 510

Pro Glu Val Leu Ala Asn Val Gln Arg Met Met Lys Ser Val Val Asn
        515                 520                 525

Asp Gly Thr Ala Arg Gly Met Arg Gln Thr Gly Gly Gln Ile Tyr Ala
    530                 535                 540

Lys Thr Gly Glu Ala Glu Ile Asn Glu Gly Ser His Ala Trp Phe Thr
545                 550                 555                 560

Gly Tyr Arg Glu Asp Asp Ile Ala Phe Ala Thr Leu Val Val Leu Gly
                565                 570                 575

Gly Gly Ser Glu Ala Ala Ala Ala Val Thr Asp Gln Phe Phe Val Lys
            580                 585                 590

Leu Asp Glu Leu Arg Ala Gly Gly Glu Val Ala Val Ser Glu Ala Glu
        595                 600                 605

Glu Gln Pro Val Gly
    610
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Confidential

<210> 63
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1255)
<223> RXA01270

<400> 63
gcatgcacat gcagaaagcc tcgctcctaa taatctcgat agagatcgat ttatgcaacg 60

tgctggaaaa ctagcttcaa cagattcgga gatcatctaa atg act aat gaa cga 115
                                                Met Thr Asn Glu Arg
                                                  1   5

```
att ttt cta tca tcg cca gat gta aca cag tta gag gaa gac gca ttg   163
Ile Phe Leu Ser Ser Pro Asp Val Thr Gln Leu Glu Glu Asp Ala Leu
                 10                  15                  20

gta cgc gca atc cga tca gga tgg att gca ccg ctt ggt cca gaa gtt   211
Val Arg Ala Ile Arg Ser Gly Trp Ile Ala Pro Leu Gly Pro Glu Val
             25                  30                  35

gat gcg ttt gag caa gaa ctt gct gag tat tgt ggc cgc aaa tat gtt   259
Asp Ala Phe Glu Gln Glu Leu Ala Glu Tyr Cys Gly Arg Lys Tyr Val
         40                  45                  50

gtt gca ctt tca tcg ggt act gca gcc ctc cac tta ggt cta tta gca   307
Val Ala Leu Ser Ser Gly Thr Ala Ala Leu His Leu Gly Leu Leu Ala
     55                  60                  65

cta ggc gtt gga gaa gga gac ttg gtt ctt aca tca tca atg act ttt   355
Leu Gly Val Gly Glu Gly Asp Leu Val Leu Thr Ser Ser Met Thr Phe
 70                  75                  80                  85

gca gcg acc acc aac gca att gtt tat acg ggt gct gag cca att ttc   403
Ala Ala Thr Thr Asn Ala Ile Val Tyr Thr Gly Ala Glu Pro Ile Phe
                 90                  95                 100

gtg gac tgc gat gaa tct gga aat atg gat cca gat ctt tta gaa aaa   451
Val Asp Cys Asp Glu Ser Gly Asn Met Asp Pro Asp Leu Leu Glu Lys
             105                 110                 115

gcc ttt gct gag cta aag agt gaa gga aag gaa gta aag gct gta gta   499
Ala Phe Ala Glu Leu Lys Ser Glu Gly Lys Glu Val Lys Ala Val Val
         120                 125                 130

cct gtc gat cta ctt ggc aaa gtt gtt cag cac gag aag att aaa aag   547
Pro Val Asp Leu Leu Gly Lys Val Val Gln His Glu Lys Ile Lys Lys
     135                 140                 145

att gct gat gaa tac ggg gca gta gtg ctt tct gat gcc gct gaa tcc   595
Ile Ala Asp Glu Tyr Gly Ala Val Val Leu Ser Asp Ala Ala Glu Ser
150                 155                 160                 165

ttg ggc gcc att cgc aat gga aag tct gct gca gca tat gga gtg gcg   643
Leu Gly Ala Ile Arg Asn Gly Lys Ser Ala Ala Ala Tyr Gly Val Ala
                 170                 175                 180

gca gcg gtt tcc ttc aac gga aac aaa att atg act acc agc ggt ggt   691
Ala Ala Val Ser Phe Asn Gly Asn Lys Ile Met Thr Thr Ser Gly Gly
             185                 190                 195

gga gct ttg tta act gat gac aag gat att gca gac aac gtc cgc tat   739
Gly Ala Leu Leu Thr Asp Asp Lys Asp Ile Ala Asp Asn Val Arg Tyr
         200                 205                 210

ctt gcg aca caa gct cgc caa cct gta gtt cat tac gaa cac acc gat   787
Leu Ala Thr Gln Ala Arg Gln Pro Val Val His Tyr Glu His Thr Asp
     215                 220                 225

gtt ggg tat aac tat cgc ctt tca aat atc ctc gct gca ctg gga cga   835
Val Gly Tyr Asn Tyr Arg Leu Ser Asn Ile Leu Ala Ala Leu Gly Arg
230                 235                 240                 245

gct caa ctt tcc cga ctc gac aag atg att gag cgt cga cgt caa cac   883
```

```
Ala Gln Leu Ser Arg Leu Asp Lys Met Ile Glu Arg Arg Arg Gln His
                250                 255                 260

cgt gcg ttc tat cga gaa ttg ttt gca ggt gtt tct gga gta gag atc   931
Arg Ala Phe Tyr Arg Glu Leu Phe Ala Gly Val Ser Gly Val Glu Ile
            265                 270                 275

ttt ggc gag cca tca ggg gtc gat ggt ggc gac act att gat aat ttc   979
Phe Gly Glu Pro Ser Gly Val Asp Gly Gly Asp Thr Ile Asp Asn Phe
        280                 285                 290

tgg ctc act tct att ctt att gat aaa gaa gtt gcg gga ttt agc tct   1027
Trp Leu Thr Ser Ile Leu Ile Asp Lys Glu Val Ala Gly Phe Ser Ser
    295                 300                 305

gaa gat ctt cga tca gtt cta aat cag gcg aat att gag tct cgt ccc   1075
Glu Asp Leu Arg Ser Val Leu Asn Gln Ala Asn Ile Glu Ser Arg Pro
310                 315                 320                 325

ttg tgg aaa cca atg cat ctc cag cca gta ttt aag aag tat cgt agc   1123
Leu Trp Lys Pro Met His Leu Gln Pro Val Phe Lys Lys Tyr Arg Ser
                330                 335                 340

ttc acc aat gaa gaa gga cag agg cta ttt gat tca ggg ctt tct ctc   1171
Phe Thr Asn Glu Glu Gly Gln Arg Leu Phe Asp Ser Gly Leu Ser Leu
            345                 350                 355

cca agc ggt tca gta ctt gat aat gcg tca atg aat cgt gtt gag act   1219
Pro Ser Gly Ser Val Leu Asp Asn Ala Ser Met Asn Arg Val Glu Thr
        360                 365                 370

aca att ggc cag ttt ttg gag agt cag cat gcg atc taagtacaaa        1265
Thr Ile Gly Gln Phe Leu Glu Ser Gln His Ala Ile
    375                 380                 385

aactatggcg tag                                                   1278


<210> 64
<211> 385
<212> PRT
<213> Corynebacterium glutamicum

<400> 64
Met Thr Asn Glu Arg Ile Phe Leu Ser Ser Pro Asp Val Thr Gln Leu
  1               5                  10                  15

Glu Glu Asp Ala Leu Val Arg Ala Ile Arg Ser Gly Trp Ile Ala Pro
             20                  25                  30

Leu Gly Pro Glu Val Asp Ala Phe Glu Gln Glu Leu Ala Glu Tyr Cys
         35                  40                  45

Gly Arg Lys Tyr Val Val Ala Leu Ser Ser Gly Thr Ala Ala Leu His
     50                  55                  60

Leu Gly Leu Leu Ala Leu Gly Val Gly Glu Gly Asp Leu Val Leu Thr
 65                  70                  75                  80

Ser Ser Met Thr Phe Ala Ala Thr Thr Asn Ala Ile Val Tyr Thr Gly
                 85                  90                  95
```

Ala Glu Pro Ile Phe Val Asp Cys Asp Glu Ser Gly Asn Met Asp Pro
100 105 110

Asp Leu Leu Glu Lys Ala Phe Ala Glu Leu Lys Ser Glu Gly Lys Glu
115 120 125

Val Lys Ala Val Val Pro Val Asp Leu Leu Gly Lys Val Val Gln His
130 135 140

Glu Lys Ile Lys Lys Ile Ala Asp Glu Tyr Gly Ala Val Val Leu Ser
145 150 155 160

Asp Ala Ala Glu Ser Leu Gly Ala Ile Arg Asn Gly Lys Ser Ala Ala
165 170 175

Ala Tyr Gly Val Ala Ala Ala Val Ser Phe Asn Gly Asn Lys Ile Met
180 185 190

Thr Thr Ser Gly Gly Gly Ala Leu Leu Thr Asp Asp Lys Asp Ile Ala
195 200 205

Asp Asn Val Arg Tyr Leu Ala Thr Gln Ala Arg Gln Pro Val Val His
210 215 220

Tyr Glu His Thr Asp Val Gly Tyr Asn Tyr Arg Leu Ser Asn Ile Leu
225 230 235 240

Ala Ala Leu Gly Arg Ala Gln Leu Ser Arg Leu Asp Lys Met Ile Glu
245 250 255

Arg Arg Arg Gln His Arg Ala Phe Tyr Arg Glu Leu Phe Ala Gly Val
260 265 270

Ser Gly Val Glu Ile Phe Gly Glu Pro Ser Gly Val Asp Gly Gly Asp
275 280 285

Thr Ile Asp Asn Phe Trp Leu Thr Ser Ile Leu Ile Asp Lys Glu Val
290 295 300

Ala Gly Phe Ser Ser Glu Asp Leu Arg Ser Val Leu Asn Gln Ala Asn
305 310 315 320

Ile Glu Ser Arg Pro Leu Trp Lys Pro Met His Leu Gln Pro Val Phe
325 330 335

Lys Lys Tyr Arg Ser Phe Thr Asn Glu Glu Gly Gln Arg Leu Phe Asp
340 345 350

Ser Gly Leu Ser Leu Pro Ser Gly Ser Val Leu Asp Asn Ala Ser Met
355 360 365

Asn Arg Val Glu Thr Thr Ile Gly Gln Phe Leu Glu Ser Gln His Ala
370 375 380

Ile
385

<210> 65
<211> 1797

Substitute Sheet

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1774)
<223> RXN00549

<400> 65
aaagagcagc ggcaaaaggc gcttaaagag cgactctaag ggctacgctg taagaaacac 60

catcattggt gccattgttg ctgtcatttt gattccagta atg gtc ttc atg ggt 115
Met Val Phe Met Gly
1 5

gct tac atc atg gtt gat gtt cca gaa ccg gaa gag ttg gtt tca ccc 163
Ala Tyr Ile Met Val Asp Val Pro Glu Pro Glu Glu Leu Val Ser Pro
10 15 20

cag gtt tcg cag att tac gca tct gac ggt gag act gaa ttg gca cgc 211
Gln Val Ser Gln Ile Tyr Ala Ser Asp Gly Glu Thr Glu Leu Ala Arg
25 30 35

atc gtt cct cca gaa ggc aac cgc cag atg gtg acg atc gat cag gtg 259
Ile Val Pro Pro Glu Gly Asn Arg Gln Met Val Thr Ile Asp Gln Val
40 45 50

cct gac act gtg aaa aat gcg gtg gtg gct gcg gaa gac cga gag ttt 307
Pro Asp Thr Val Lys Asn Ala Val Val Ala Ala Glu Asp Arg Glu Phe
55 60 65

tac aca aac ccc ggt ttt tcc att act ggc tat gcc cga gca gca ctt 355
Tyr Thr Asn Pro Gly Phe Ser Ile Thr Gly Tyr Ala Arg Ala Ala Leu
70 75 80 85

ggc gta atc act ggt gat tct tca gcg ggt ggt ggt tcc acc att act 403
Gly Val Ile Thr Gly Asp Ser Ser Ala Gly Gly Gly Ser Thr Ile Thr
90 95 100

cag cag tat gtg aag aag gct gtg gtt ggt gat gag cgt tcg ctg atc 451
Gln Gln Tyr Val Lys Lys Ala Val Val Gly Asp Glu Arg Ser Leu Ile
105 110 115

cgt aag gct aag gaa ttg gtc tat tcc gcg aag atg gcc aat gag tgg 499
Arg Lys Ala Lys Glu Leu Val Tyr Ser Ala Lys Met Ala Asn Glu Trp
120 125 130

tct aag gac gag gtc ctt gag gct tat ctc aac act gtg tac ttc ggt 547
Ser Lys Asp Glu Val Leu Glu Ala Tyr Leu Asn Thr Val Tyr Phe Gly
135 140 145

cga aat gcc tat ggt gtg cag gct gca gct cat gca ttc ttt gat aag 595
Arg Asn Ala Tyr Gly Val Gln Ala Ala Ala His Ala Phe Phe Asp Lys
150 155 160 165

cca gta gaa gag ctc acg gct gct gag ggc gca gtg ctg gcg gcc agt 643
Pro Val Glu Glu Leu Thr Ala Ala Glu Gly Ala Val Leu Ala Ala Ser
170 175 180

att cag ctg cca agc cag ttg gat cct tgg aca aat cca gtt gag gcg 691
Ile Gln Leu Pro Ser Gln Leu Asp Pro Trp Thr Asn Pro Val Glu Ala

```
            185                 190                 195

gaa acg cgt tgg aac tat gtc atg gac ggc ctg gtg gaa att ggc gct   739
Glu Thr Arg Trp Asn Tyr Val Met Asp Gly Leu Val Glu Ile Gly Ala
        200                 205                 210

atc tcg gca gag gag cgc gca gtt gct acc tac cct gaa acc act gac   787
Ile Ser Ala Glu Glu Arg Ala Val Ala Thr Tyr Pro Glu Thr Thr Asp
    215                 220                 225

cct gcg tcc aac agt gcg tac acc gaa gcc acc ggc act aat ggt ttg   835
Pro Ala Ser Asn Ser Ala Tyr Thr Glu Ala Thr Gly Thr Asn Gly Leu
230                 235                 240                 245

att aag aac caa gtg atg gcg gag ttg tct gag ctt ggt atc act gag   883
Ile Lys Asn Gln Val Met Ala Glu Leu Ser Glu Leu Gly Ile Thr Glu
                250                 255                 260

gat gat gtg caa acc tgt ggt ttg cag gtc acc acc acc att gat cca   931
Asp Asp Val Gln Thr Cys Gly Leu Gln Val Thr Thr Thr Ile Asp Pro
            265                 270                 275

aag act cag gaa ggt gcc gtt gaa gcg gta caa aac cag ttg gat ctt   979
Lys Thr Gln Glu Gly Ala Val Glu Ala Val Gln Asn Gln Leu Asp Leu
        280                 285                 290

ctg tct gag aac aac cgt gca gcg gta gtc tcc att gat cct tct aat   1027
Leu Ser Glu Asn Asn Arg Ala Ala Val Val Ser Ile Asp Pro Ser Asn
    295                 300                 305

ggt gcg gtt cgt gct tat tac ggc ggc gag aat gcg act ggt tgg gac   1075
Gly Ala Val Arg Ala Tyr Tyr Gly Gly Glu Asn Ala Thr Gly Trp Asp
310                 315                 320                 325

ttt gca aac gct ccg ctt cag acc ggt tct aca ttc aag atc ttt ggt   1123
Phe Ala Asn Ala Pro Leu Gln Thr Gly Ser Thr Phe Lys Ile Phe Gly
                330                 335                 340

ctg gca gca gca ctt cag caa ggt att cca ctg tct cag cca tac agc   1171
Leu Ala Ala Ala Leu Gln Gln Gly Ile Pro Leu Ser Gln Pro Tyr Ser
            345                 350                 355

tct gcg ccg gtg act gtg ggt gat gct caa atc gga aac gtc ggt ggc   1219
Ser Ala Pro Val Thr Val Gly Asp Ala Gln Ile Gly Asn Val Gly Gly
        360                 365                 370

agc ggt tgt ggt tcc tgt tcc atc gag cag gcg ttg ttg cat tct tac   1267
Ser Gly Cys Gly Ser Cys Ser Ile Glu Gln Ala Leu Leu His Ser Tyr
    375                 380                 385

aac acc agc ttc att cgt ttg cag cag gat ctg gaa aat ggt tca cag   1315
Asn Thr Ser Phe Ile Arg Leu Gln Gln Asp Leu Glu Asn Gly Ser Gln
390                 395                 400                 405

gat act gcg gac atg gcg cat gct ttg ggt atc gcg aag tct ttg cca   1363
Asp Thr Ala Asp Met Ala His Ala Leu Gly Ile Ala Lys Ser Leu Pro
                410                 415                 420

act atc cct gag aca ctg act gaa aac gga gag acc cct tat gag ggc   1411
Thr Ile Pro Glu Thr Leu Thr Glu Asn Gly Glu Thr Pro Tyr Glu Gly
            425                 430                 435
```

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atc atc ttg ggt cag tat gag tcc cgc cca ctt gat atg gct tct gcg   1459
Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro Leu Asp Met Ala Ser Ala
        440                 445                 450

atg gca act atc gct aat gaa ggt gtc tgg cac cgc ccg cac ttc gtg   1507
Met Ala Thr Ile Ala Asn Glu Gly Val Trp His Arg Pro His Phe Val
    455                 460                 465

tcc aag gtg gag act gtc agc ggt gag gtt ctc tac gag ttc gag gat   1555
Ser Lys Val Glu Thr Val Ser Gly Glu Val Leu Tyr Glu Phe Glu Asp
470                 475                 480                 485

ggc gac ggc gag cgt cgt gtt tct gaa aag gtt gca ctg aat ctg ctc   1603
Gly Asp Gly Glu Arg Arg Val Ser Glu Lys Val Ala Leu Asn Leu Leu
                490                 495                 500

aag gcc atg ggg cca atc gct gca tac tcc aac gga aac gct ctg gct   1651
Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser Asn Gly Asn Ala Leu Ala
            505                 510                 515

gat ggc cag gtt tct gca tcc aag act ggt acc act cag ctt ggt gat   1699
Asp Gly Gln Val Ser Ala Ser Lys Thr Gly Thr Thr Gln Leu Gly Asp
        520                 525                 530

acc ggt gca aac aag gat gcg tgg atg ttg ggt gcg gca cct cag cta   1747
Thr Gly Ala Asn Lys Asp Ala Trp Met Leu Gly Ala Ala Pro Gln Leu
    535                 540                 545

gct act gcg gtg tgg gtc gga act gct tgataacact gcattgtata         1794
Ala Thr Ala Val Trp Val Gly Thr Ala
550                 555

aca                                                               1797
```

<210> 66
<211> 558
<212> PRT
<213> Corynebacterium glutamicum

<400> 66

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Met Val Phe Met Gly Ala Tyr Ile Met Val Asp Val Pro Glu Pro Glu
  1               5                  10                  15

Glu Leu Val Ser Pro Gln Val Ser Gln Ile Tyr Ala Ser Asp Gly Glu
             20                  25                  30

Thr Glu Leu Ala Arg Ile Val Pro Pro Glu Gly Asn Arg Gln Met Val
         35                  40                  45

Thr Ile Asp Gln Val Pro Asp Thr Val Lys Asn Ala Val Val Ala Ala
     50                  55                  60

Glu Asp Arg Glu Phe Tyr Thr Asn Pro Gly Phe Ser Ile Thr Gly Tyr
 65                  70                  75                  80

Ala Arg Ala Ala Leu Gly Val Ile Thr Gly Asp Ser Ser Ala Gly Gly
                 85                  90                  95

Gly Ser Thr Ile Thr Gln Gln Tyr Val Lys Lys Ala Val Val Gly Asp
```

```
            100                 105                 110

Glu Arg Ser Leu Ile Arg Lys Ala Lys Glu Leu Val Tyr Ser Ala Lys
        115                 120                 125

Met Ala Asn Glu Trp Ser Lys Asp Glu Val Leu Glu Ala Tyr Leu Asn
    130                 135                 140

Thr Val Tyr Phe Gly Arg Asn Ala Tyr Gly Val Gln Ala Ala Ala His
145                 150                 155                 160

Ala Phe Phe Asp Lys Pro Val Glu Glu Leu Thr Ala Ala Glu Gly Ala
                165                 170                 175

Val Leu Ala Ala Ser Ile Gln Leu Pro Ser Gln Leu Asp Pro Trp Thr
            180                 185                 190

Asn Pro Val Glu Ala Glu Thr Arg Trp Asn Tyr Val Met Asp Gly Leu
        195                 200                 205

Val Glu Ile Gly Ala Ile Ser Ala Glu Glu Arg Ala Val Ala Thr Tyr
    210                 215                 220

Pro Glu Thr Thr Asp Pro Ala Ser Asn Ser Ala Tyr Thr Glu Ala Thr
225                 230                 235                 240

Gly Thr Asn Gly Leu Ile Lys Asn Gln Val Met Ala Glu Leu Ser Glu
                245                 250                 255

Leu Gly Ile Thr Glu Asp Asp Val Gln Thr Cys Gly Leu Gln Val Thr
            260                 265                 270

Thr Thr Ile Asp Pro Lys Thr Gln Glu Gly Ala Val Glu Ala Val Gln
        275                 280                 285

Asn Gln Leu Asp Leu Leu Ser Glu Asn Asn Arg Ala Ala Val Val Ser
    290                 295                 300

Ile Asp Pro Ser Asn Gly Ala Val Arg Ala Tyr Tyr Gly Gly Glu Asn
305                 310                 315                 320

Ala Thr Gly Trp Asp Phe Ala Asn Ala Pro Leu Gln Thr Gly Ser Thr
                325                 330                 335

Phe Lys Ile Phe Gly Leu Ala Ala Ala Leu Gln Gln Gly Ile Pro Leu
            340                 345                 350

Ser Gln Pro Tyr Ser Ser Ala Pro Val Thr Val Gly Asp Ala Gln Ile
        355                 360                 365

Gly Asn Val Gly Gly Ser Gly Cys Gly Ser Cys Ser Ile Glu Gln Ala
    370                 375                 380

Leu Leu His Ser Tyr Asn Thr Ser Phe Ile Arg Leu Gln Gln Asp Leu
385                 390                 395                 400

Glu Asn Gly Ser Gln Asp Thr Ala Asp Met Ala His Ala Leu Gly Ile
                405                 410                 415

Ala Lys Ser Leu Pro Thr Ile Pro Glu Thr Leu Thr Glu Asn Gly Glu
            420                 425                 430
```

```
Thr Pro Tyr Glu Gly Ile Ile Leu Gly Gln Tyr Glu Ser Arg Pro Leu
        435                 440                 445

Asp Met Ala Ser Ala Met Ala Thr Ile Ala Asn Glu Gly Val Trp His
    450                 455                 460

Arg Pro His Phe Val Ser Lys Val Glu Thr Val Ser Gly Glu Val Leu
465                 470                 475                 480

Tyr Glu Phe Glu Asp Gly Asp Gly Glu Arg Arg Val Ser Glu Lys Val
                485                 490                 495

Ala Leu Asn Leu Leu Lys Ala Met Gly Pro Ile Ala Ala Tyr Ser Asn
            500                 505                 510

Gly Asn Ala Leu Ala Asp Gly Gln Val Ser Ala Ser Lys Thr Gly Thr
        515                 520                 525

Thr Gln Leu Gly Asp Thr Gly Ala Asn Lys Asp Ala Trp Met Leu Gly
    530                 535                 540

Ala Ala Pro Gln Leu Ala Thr Ala Val Trp Val Gly Thr Ala
545                 550                 555


<210> 67
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXN00550

<400> 67
aaggatgcgt ggatgttggg tgcggcacct cagctagcta ctgcggtgtg ggtcggaact 60

gcttgataac actgcattgt ataacacctg gggtggcagt atg tat ggt tct aac   115
                                              Met Tyr Gly Ser Asn
                                                1               5

tcc cct gcc acg atc tgg aag cag acc atg gat aac gcc ctc gag aac   163
Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp Asn Ala Leu Glu Asn
                10                  15                  20

tcc cct ctc gaa act tgg gat atc gct cca gca ttg ggg tac ggt aac   211
Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala Leu Gly Tyr Gly Asn
            25                  30                  35

cca cca gtt ccg gaa tat gtg tgg act cca agt cca aac atc gcg act   259
Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser Pro Asn Ile Ala Thr
        40                  45                  50

aat gat cca gaa gga gca acc gag gaa gct cca gtg gag gat cca aat   307
Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro Val Glu Asp Pro Asn
    55                  60                  65

gca gta atc gat acc cct gct gta gat ccc act gca cct gca gag gag   355
Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr Ala Pro Ala Glu Glu
```

```
 70                  75                  80                  85

acc ggt aac ggt cag gta gaa atc ctg ccg ggg ctg act atc ccg gga   403
Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly Leu Thr Ile Pro Gly
                 90                  95                 100

gat ctc tta ggg atc ggc taaaatccgg tcgtagccta aac                 444
Asp Leu Leu Gly Ile Gly
            105


<210> 68
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 68
Met Tyr Gly Ser Asn Ser Pro Ala Thr Ile Trp Lys Gln Thr Met Asp
  1               5                  10                  15

Asn Ala Leu Glu Asn Ser Pro Leu Glu Thr Trp Asp Ile Ala Pro Ala
             20                  25                  30

Leu Gly Tyr Gly Asn Pro Pro Val Pro Glu Tyr Val Trp Thr Pro Ser
         35                  40                  45

Pro Asn Ile Ala Thr Asn Asp Pro Glu Gly Ala Thr Glu Glu Ala Pro
     50                  55                  60

Val Glu Asp Pro Asn Ala Val Ile Asp Thr Pro Ala Val Asp Pro Thr
 65                  70                  75                  80

Ala Pro Ala Glu Glu Thr Gly Asn Gly Gln Val Glu Ile Leu Pro Gly
                 85                  90                  95

Leu Thr Ile Pro Gly Asp Leu Leu Gly Ile Gly
            100                 105


<210> 69
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(646)
<223> RXN03091

<400> 69
gcaaggctta tccaatggtt gtatcggcgc tggcgatcgg tggtttttgt tgcaataacg 60

ctcttgcaat atctttctga gcaggggaat cacccaagat atg ctg gcg aag gac   115
                                               Met Leu Ala Lys Asp
                                                 1               5

tcc tac acc atc aaa ttg act ttg gat cca gat gtt cag gat gca gcg   163
Ser Tyr Thr Ile Lys Leu Thr Leu Asp Pro Asp Val Gln Asp Ala Ala
                 10                  15                  20

cac aat gcg gtg tcc tcc cac gtt gat cca acc acc cca ggt gtc gct   211
```

```
His Asn Ala Val Ser Ser His Val Asp Pro Thr Thr Pro Gly Val Ala
            25                  30                  35

gaa gtt gtg aac gtc att gag cct ggc gag aac tcc cgc gat att ttg   259
Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn Ser Arg Asp Ile Leu
        40                  45                  50

gct att act tct tcc cgc aac tac ggc ctt gac ctg gat gct ggt gaa   307
Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp Leu Asp Ala Gly Glu
    55                  60                  65

acg atg ctg cct cag gca acg tcc cgt gtg ggt aat ggt gcc ggt tcc   355
Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly Asn Gly Ala Gly Ser
70                  75                  80                  85

att ttc aag atc ttt acc gcc gct gca gcc att cag cag ggc gct ggc   403
Ile Phe Lys Ile Phe Thr Ala Ala Ala Ala Ile Gln Gln Gly Ala Gly
                90                  95                  100

cta gac acc atg ttg gat gtt cct tct cga tat gag gtc aag ggc atg   451
Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr Glu Val Lys Gly Met
            105                 110                 115

ggc tcc ggc ggt gcc gcg aac tgt ccc gca aat act tac tgc gtg gaa   499
Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn Thr Tyr Cys Val Glu
        120                 125                 130

aac gca gga tcc tac gcg cct cgc atg act ctg cag gac gct ctc gcg   547
Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu Gln Asp Ala Leu Ala
    135                 140                 145

cag tcc ccc aac act gca ttc gtt gaa atg atc gag cag gtt ggc gtg   595
Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile Glu Gln Val Gly Val
150                 155                 160                 165

gac acc cgt tgt gga tct ttc agt aaa gct ggg cct gcg aag cta cac   643
Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly Pro Ala Lys Leu His
                170                 175                 180

cga tgaaggttcc ttcgacggcg aaa                                    669
Arg
```

Sequence Listing

<210> 70
<211> 182
<212> PRT
<213> Corynebacterium glutamicum

<400> 70

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Met Leu Ala Lys Asp Ser Tyr Thr Ile Lys Leu Thr Leu Asp Pro Asp
  1               5                  10                  15

Val Gln Asp Ala Ala His Asn Ala Val Ser Ser His Val Asp Pro Thr
            20                  25                  30

Thr Pro Gly Val Ala Glu Val Val Asn Val Ile Glu Pro Gly Glu Asn
        35                  40                  45

Ser Arg Asp Ile Leu Ala Ile Thr Ser Ser Arg Asn Tyr Gly Leu Asp
    50                  55                  60
```

```
Leu Asp Ala Gly Glu Thr Met Leu Pro Gln Ala Thr Ser Arg Val Gly
 65                  70                  75                  80

Asn Gly Ala Gly Ser Ile Phe Lys Ile Phe Thr Ala Ala Ala Ala Ile
                85                  90                  95

Gln Gln Gly Ala Gly Leu Asp Thr Met Leu Asp Val Pro Ser Arg Tyr
            100                 105                 110

Glu Val Lys Gly Met Gly Ser Gly Gly Ala Ala Asn Cys Pro Ala Asn
        115                 120                 125

Thr Tyr Cys Val Glu Asn Ala Gly Ser Tyr Ala Pro Arg Met Thr Leu
    130                 135                 140

Gln Asp Ala Leu Ala Gln Ser Pro Asn Thr Ala Phe Val Glu Met Ile
145                 150                 155                 160

Glu Gln Val Gly Val Asp Thr Arg Cys Gly Ser Phe Ser Lys Ala Gly
                165                 170                 175

Pro Ala Lys Leu His Arg
            180
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Sequence Listing

<210> 71
<211> 824
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(801)
<223> RXN03178

<400> 71

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ccc acc acc gtg gtc acg ggc acg atg gaa gcc gcc aac atc gag ggc   48
Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
  1               5                  10                  15

tcc cgc gtg ggt gtc ggc gag gcc ggc cag tat acc gtt gat cag ctg   96
Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
             20                  25                  30

ctg cac ggt ctt ctt tta gcc agc ggt aac gat gcg gcg tat atg ttg   144
Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
         35                  40                  45

gct cag gaa ctt ggt ggg gat caa gca acc ctg gag aaa gta aac gcg   192
Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
     50                  55                  60

ctg gcc aag gag ttg ggc act caa gac acc ttc gtt gcc act tat tcc   240
Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
 65                  70                  75                  80

ggt ttg gat gcg ccg gga atg tcg acc tcc gca tac gac atg tca ttg   288
Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
                85                  90                  95
```

```
att tat cag cat gcg tgg cag aac ccg gtt ttc gag tcg att atc tcc   336
Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
            100                 105                 110

acc gat cac att gat ttc cct ggt tgg ggc gac aat gag ggt ttc caa   384
Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
        115                 120                 125

gtc tgg aac gat aac gcc ttg ttc atg aac gat cct gat ggc atc ggc   432
Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
    130                 135                 140

ggc aag acc ggc tac acc gac gac gcg aac cac acc ttt gtc ggc ggt   480
Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
145                 150                 155                 160

ctc gat cgg ggt ggt cgc cgc ctc gcc gcc gta ctc ttg gat tcc acc   528
Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
                165                 170                 175

gtc agc gac att cgt ccg tgg gaa caa gca cga ttg ctt atc gac gcc   576
Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
            180                 185                 190

tcc ctc ccc atc acg ccg ggg tcc ggc gtg ggc cag ctg ggc tcc ggc   624
Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
        195                 200                 205

agc gcg aac gat gtg gca ccg gcg acc cca gaa tta cca gaa ccc acc   672
Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
    210                 215                 220

gac aac ctg act tca ggt gag ggt ggg tcg cag aac acg ctt ctt aag   720
Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
225                 230                 235                 240

ctc gtg gtg ccc atc gga atc atc gtg ctg ttg cta atc gcc gca cta   768
Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
                245                 250                 255

gcg tgg aca ttc aga tct ccc aag aaa aag aac taggtgttct tcttcacgac 821
Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
            260                 265

ctc                                                               824
```

<210> 72
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 72

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Pro Thr Thr Val Val Thr Gly Thr Met Glu Ala Ala Asn Ile Glu Gly
  1               5                  10                  15

Ser Arg Val Gly Val Gly Glu Ala Gly Gln Tyr Thr Val Asp Gln Leu
             20                  25                  30

Leu His Gly Leu Leu Leu Ala Ser Gly Asn Asp Ala Ala Tyr Met Leu
         35                  40                  45
```

```
Ala Gln Glu Leu Gly Gly Asp Gln Ala Thr Leu Glu Lys Val Asn Ala
     50                  55                  60

Leu Ala Lys Glu Leu Gly Thr Gln Asp Thr Phe Val Ala Thr Tyr Ser
 65                  70                  75                  80

Gly Leu Asp Ala Pro Gly Met Ser Thr Ser Ala Tyr Asp Met Ser Leu
                 85                  90                  95

Ile Tyr Gln His Ala Trp Gln Asn Pro Val Phe Glu Ser Ile Ile Ser
            100                 105                 110

Thr Asp His Ile Asp Phe Pro Gly Trp Gly Asp Asn Glu Gly Phe Gln
        115                 120                 125

Val Trp Asn Asp Asn Ala Leu Phe Met Asn Asp Pro Asp Gly Ile Gly
    130                 135                 140

Gly Lys Thr Gly Tyr Thr Asp Asp Ala Asn His Thr Phe Val Gly Gly
145                 150                 155                 160

Leu Asp Arg Gly Gly Arg Arg Leu Ala Ala Val Leu Leu Asp Ser Thr
                165                 170                 175

Val Ser Asp Ile Arg Pro Trp Glu Gln Ala Arg Leu Leu Ile Asp Ala
            180                 185                 190

Ser Leu Pro Ile Thr Pro Gly Ser Gly Val Gly Gln Leu Gly Ser Gly
        195                 200                 205

Ser Ala Asn Asp Val Ala Pro Ala Thr Pro Glu Leu Pro Glu Pro Thr
    210                 215                 220

Asp Asn Leu Thr Ser Gly Glu Gly Gly Ser Gln Asn Thr Leu Leu Lys
225                 230                 235                 240

Leu Val Val Pro Ile Gly Ile Ile Val Leu Leu Leu Ile Ala Ala Leu
                245                 250                 255

Ala Trp Thr Phe Arg Ser Pro Lys Lys Lys Asn
            260                 265
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<210> 73
<211> 749
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(726)
<223> FRXA02859

<400> 73

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cag tat acc gtt gat cag ctg ctg cac ggt ctt ctt tta gcc agc ggt   48
Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
  1               5                  10                  15

aac gat gcg gcg tat ctg ttg gct cag gaa ctt ggt ggg gat caa gca   96
Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
```

```
                20                  25                  30

acc ctg gag aaa gta aac gcg ctg gcc aag gag ttg ggc act caa gac   144
Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
          35                  40                  45

acc ttc gtt gcc act tat tcc ggt ttg gat gcg ccg gga atg tcg acc   192
Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
     50                  55                  60

tcc gca tac gac atg tca ttg att tat cag cat gcg tgg cag aac ccg   240
Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65                  70                  75                  80

gtt ttc gag tcg att atc tcc acc gat cac att gat ttc cct ggt tgg   288
Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
                 85                  90                  95

ggc gac aat gag ggt ttc caa gtc tgg aac gat aac gcc ttg ttc atg   336
Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
            100                 105                 110

aac gat cct gat ggc atc ggc ggc aag acc ggc tac acc gac gac gcg   384
Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
        115                 120                 125

aac cac acc ttt gtc ggc ggt ctc gat cgg ggt ggt cgc cgc ctc gcc   432
Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
    130                 135                 140

gcc gta ctc ttg gat tcc acc gtc agc gac att cgt ccg tgg gaa caa   480
Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
145                 150                 155                 160

gca cga ttg ctt atc gac gcc tcc ctc ccc atc acg ccg ggg tcc ggc   528
Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
                165                 170                 175

gtg ggc cag ctg ggc tcc ggc agc gcg aac gat gtg gca ccg gcg acc   576
Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
            180                 185                 190

cca gaa tta cca gaa ccc acc gac aac ctg act tca ggt gag ggt ggg   624
Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
        195                 200                 205

tcg cag aac acg ctg ctt aag ctc gtg gtg ccc atc gga atc atc gtg   672
Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
    210                 215                 220

ctg ttg cta atc gcc gca cta gcg tgg aca ttc aga tct ccc aag aaa   720
Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
225                 230                 235                 240

aag aac taggtgttct tcttcacgac ctc                               749
Lys Asn
```

<210> 74
<211> 242

<212> PRT
<213> Corynebacterium glutamicum

<400> 74

```
Gln Tyr Thr Val Asp Gln Leu Leu His Gly Leu Leu Leu Ala Ser Gly
  1               5                  10                  15

Asn Asp Ala Ala Tyr Leu Leu Ala Gln Glu Leu Gly Gly Asp Gln Ala
             20                  25                  30

Thr Leu Glu Lys Val Asn Ala Leu Ala Lys Glu Leu Gly Thr Gln Asp
         35                  40                  45

Thr Phe Val Ala Thr Tyr Ser Gly Leu Asp Ala Pro Gly Met Ser Thr
     50                  55                  60

Ser Ala Tyr Asp Met Ser Leu Ile Tyr Gln His Ala Trp Gln Asn Pro
 65                  70                  75                  80

Val Phe Glu Ser Ile Ile Ser Thr Asp His Ile Asp Phe Pro Gly Trp
                 85                  90                  95

Gly Asp Asn Glu Gly Phe Gln Val Trp Asn Asp Asn Ala Leu Phe Met
            100                 105                 110

Asn Asp Pro Asp Gly Ile Gly Gly Lys Thr Gly Tyr Thr Asp Asp Ala
        115                 120                 125

Asn His Thr Phe Val Gly Gly Leu Asp Arg Gly Gly Arg Arg Leu Ala
    130                 135                 140

Ala Val Leu Leu Asp Ser Thr Val Ser Asp Ile Arg Pro Trp Glu Gln
145                 150                 155                 160

Ala Arg Leu Leu Ile Asp Ala Ser Leu Pro Ile Thr Pro Gly Ser Gly
                165                 170                 175

Val Gly Gln Leu Gly Ser Gly Ser Ala Asn Asp Val Ala Pro Ala Thr
            180                 185                 190

Pro Glu Leu Pro Glu Pro Thr Asp Asn Leu Thr Ser Gly Glu Gly Gly
        195                 200                 205

Ser Gln Asn Thr Leu Leu Lys Leu Val Val Pro Ile Gly Ile Ile Val
    210                 215                 220

Leu Leu Leu Ile Ala Ala Leu Ala Trp Thr Phe Arg Ser Pro Lys Lys
225                 230                 235                 240

Lys Asn
```

<210> 75
<211> 1437
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1414)

<223> RXN01267

<400> 75

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tgctagtttt aaagaggcgt tgaggggtag tatcgcgtaa gtttattagt ggttagcgta 60

gatttttcga attgaagatg tttctgaaag gtatttagat atg tat gca gaa att   115
                                            Met Tyr Ala Glu Ile
                                              1               5

aat ggc ggt ttt att cca gag ggc acc gtg cgg gta agc ggc gca aaa   163
Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg Val Ser Gly Ala Lys
                10                  15                  20

aac tct gct act aga ctt ctc gcg gcg gca ctg cta acc gat gag gtg   211
Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu Leu Thr Asp Glu Val
            25                  30                  35

gtg cat ctt ggt aat ttc cca acc aag ctt gtg gat gtt gaa cat aaa   259
Val His Leu Gly Asn Phe Pro Thr Lys Leu Val Asp Val Glu His Lys
        40                  45                  50

att cgc ttt att gaa gag ctt ggc gga aaa gtg cat gtc gac cat gat   307
Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val His Val Asp His Asp
    55                  60                  65

gag caa att tta gta gtt gat gct aag gat ctt gca gcg cga gaa atg   355
Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu Ala Ala Arg Glu Met
70                  75                  80                  85

act act gat gaa ctg aat att ccg att cga act act tat ctc cta gca   403
Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr Thr Tyr Leu Leu Ala
                90                  95                  100

gca gcg cag att ggg cgt ggg gaa att gct cga gtt cct ttt cct ggg   451
Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg Val Pro Phe Pro Gly
            105                 110                 115

ggg tgt gct att gga gga ggt cct gct ggc gga cga gga tat gat ctt   499
Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly Arg Gly Tyr Asp Leu
        120                 125                 130

cat ctt atg gtc tgg gaa cag cta ggt tgt aaa att ctt gaa aaa gat   547
His Leu Met Val Trp Glu Gln Leu Gly Cys Lys Ile Leu Glu Lys Asp
    135                 140                 145

gat cac att gaa gta act gca ccc cag ggc ttt atc ggg gga gtt att   595
Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe Ile Gly Gly Val Ile
150                 155                 160                 165

gac ttt cct att tct act gtg gga ggc act gaa aac gcg tta cta tgc   643
Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu Asn Ala Leu Leu Cys
                170                 175                 180

gca agt att gct tca ggg gat act aaa att gcc aat gct tat att acc   691
Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala Asn Ala Tyr Ile Thr
            185                 190                 195

cct gag ata act gat ctt att gaa ctt ctg cga cgt atg ggt gcg gag   739
Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg Arg Met Gly Ala Glu
        200                 205                 210
```

```
atc act gtc tac ggt acc agc cgt att cat gta aag ggt cga gca ggt   787
Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val Lys Gly Arg Ala Gly
    215                 220                 225

ctt ttg cag ggc gca tat atg gac gta atg ccg gat cgt att gag gca   835
Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro Asp Arg Ile Glu Ala
230                 235                 240                 245

ttg acg tgg atc gtg tat gga att att tca ggc gga agg att acc gtc   883
Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly Gly Arg Ile Thr Val
                250                 255                 260

gaa ggt gtt cca ttt agc tcg atg gaa gtt cct ttt atc cac ctt gag   931
Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro Phe Ile His Leu Glu
            265                 270                 275

aag gct gga gtg gat ctt ttc cgt aat tca agt tcc gta tat att aca   979
Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser Ser Val Tyr Ile Thr
        280                 285                 290

cca gaa tgc ttg cct tca ggc tca gtt cag cca ttt gag cta gcg tgt   1027
Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro Phe Glu Leu Ala Cys
    295                 300                 305

gga act cac ccc gga gta att tcg gac atg cag gca ctt ttt gtt ctt   1075
Gly Thr His Pro Gly Val Ile Ser Asp Met Gln Ala Leu Phe Val Leu
310                 315                 320                 325

tta gga tta aaa ggt gca gga act tca cgc gtc tat gac tat cga tac   1123
Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val Tyr Asp Tyr Arg Tyr
                330                 335                 340

cca gaa aga att gca ttt gtt gag gaa ttg aca aat cta gtt tcg ggc   1171
Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr Asn Leu Val Ser Gly
            345                 350                 355

gac aaa tta agt gca gag gct ggc aag atc act atc cag gga gat gct   1219
Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr Ile Gln Gly Asp Ala
        360                 365                 370

act ttc cgg cca gga tat gcg aac tca act gat cta cgt ggt tct atg   1267
Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp Leu Arg Gly Ser Met
    375                 380                 385

gct gtt gtt tta gcg gcg ctt tgc gct gat gga aag tcc acg att aat   1315
Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly Lys Ser Thr Ile Asn
390                 395                 400                 405

aac gtc cat atg gcg tta cgt ggg tac aac gag ttg gat aaa aaa ctt   1363
Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu Leu Asp Lys Lys Leu
                410                 415                 420

cgt tta ctt ggt gcg gat tta act atc aga gaa ggc gaa gtt cct tca   1411
Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu Gly Glu Val Pro Ser
            425                 430                 435

cct taagaacgaa agttttacat tga                                    1437
Pro
```

<210> 76
<211> 438
<212> PRT
<213> Corynebacterium glutamicum

<400> 76

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Met Tyr Ala Glu Ile Asn Gly Gly Phe Ile Pro Glu Gly Thr Val Arg
 1               5                  10                  15

Val Ser Gly Ala Lys Asn Ser Ala Thr Arg Leu Leu Ala Ala Ala Leu
            20                  25                  30

Leu Thr Asp Glu Val Val His Leu Gly Asn Phe Pro Thr Lys Leu Val
        35                  40                  45

Asp Val Glu His Lys Ile Arg Phe Ile Glu Glu Leu Gly Gly Lys Val
    50                  55                  60

His Val Asp His Asp Glu Gln Ile Leu Val Val Asp Ala Lys Asp Leu
65                  70                  75                  80

Ala Ala Arg Glu Met Thr Thr Asp Glu Leu Asn Ile Pro Ile Arg Thr
                85                  90                  95

Thr Tyr Leu Leu Ala Ala Ala Gln Ile Gly Arg Gly Glu Ile Ala Arg
            100                 105                 110

Val Pro Phe Pro Gly Gly Cys Ala Ile Gly Gly Gly Pro Ala Gly Gly
        115                 120                 125

Arg Gly Tyr Asp Leu His Leu Met Val Trp Glu Gln Leu Gly Cys Lys
    130                 135                 140

Ile Leu Glu Lys Asp Asp His Ile Glu Val Thr Ala Pro Gln Gly Phe
145                 150                 155                 160

Ile Gly Gly Val Ile Asp Phe Pro Ile Ser Thr Val Gly Gly Thr Glu
                165                 170                 175

Asn Ala Leu Leu Cys Ala Ser Ile Ala Ser Gly Asp Thr Lys Ile Ala
            180                 185                 190

Asn Ala Tyr Ile Thr Pro Glu Ile Thr Asp Leu Ile Glu Leu Leu Arg
        195                 200                 205

Arg Met Gly Ala Glu Ile Thr Val Tyr Gly Thr Ser Arg Ile His Val
    210                 215                 220

Lys Gly Arg Ala Gly Leu Leu Gln Gly Ala Tyr Met Asp Val Met Pro
225                 230                 235                 240

Asp Arg Ile Glu Ala Leu Thr Trp Ile Val Tyr Gly Ile Ile Ser Gly
                245                 250                 255

Gly Arg Ile Thr Val Glu Gly Val Pro Phe Ser Ser Met Glu Val Pro
            260                 265                 270

Phe Ile His Leu Glu Lys Ala Gly Val Asp Leu Phe Arg Asn Ser Ser
        275                 280                 285

Ser Val Tyr Ile Thr Pro Glu Cys Leu Pro Ser Gly Ser Val Gln Pro
```

```
    290                 295                 300

Phe Glu Leu Ala Cys Gly Thr His Pro Gly Val Ile Ser Asp Met Gln
305                 310                 315                 320

Ala Leu Phe Val Leu Leu Gly Leu Lys Gly Ala Gly Thr Ser Arg Val
                325                 330                 335

Tyr Asp Tyr Arg Tyr Pro Glu Arg Ile Ala Phe Val Glu Glu Leu Thr
            340                 345                 350

Asn Leu Val Ser Gly Asp Lys Leu Ser Ala Glu Ala Gly Lys Ile Thr
        355                 360                 365

Ile Gln Gly Asp Ala Thr Phe Arg Pro Gly Tyr Ala Asn Ser Thr Asp
    370                 375                 380

Leu Arg Gly Ser Met Ala Val Val Leu Ala Ala Leu Cys Ala Asp Gly
385                 390                 395                 400

Lys Ser Thr Ile Asn Asn Val His Met Ala Leu Arg Gly Tyr Asn Glu
                405                 410                 415

Leu Asp Lys Lys Leu Arg Leu Leu Gly Ala Asp Leu Thr Ile Arg Glu
            420                 425                 430

Gly Glu Val Pro Ser Pro
        435
```

Sequence Listing

<210> 77
<211> 1032
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1009)
<223> RXN00045

<400> 77

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tgcgatggca gttcctcacc agagcctcag cgacgaagaa actgctcgca ttcacgccat 60

tgttgatgaa ttcctgtaca ccgcttaagg cccacacctc atg act gat ccc act   115
                                            Met Thr Asp Pro Thr
                                              1               5

tgc acc ctt gcc ctt gat att ggt gcc aca aag att gcc tac gca cta   163
Cys Thr Leu Ala Leu Asp Ile Gly Ala Thr Lys Ile Ala Tyr Ala Leu
                 10                  15                  20

gtc ccc gat aac acc ccg acg aca aca ttg tcc acg gga cgc ttg gga   211
Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser Thr Gly Arg Leu Gly
             25                  30                  35

aca aaa gaa ggc gac agc cct atc gag cag atc cgg ctg gtt ctt ctg   259
Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile Arg Leu Val Leu Leu
         40                  45                  50

gca ggc tta aaa gct gcc gag gaa cac ggt ctc agt gtc gcc cgc atc   307
Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu Ser Val Ala Arg Ile
```

```
     55                  60                  65

ggc atg ggc gct cct ggt gta att ctg gga cca gag gga acc atc gtg   355
Gly Met Gly Ala Pro Gly Val Ile Leu Gly Pro Glu Gly Thr Ile Val
 70                  75                  80                  85

tac aac ggt gaa acc ctc aca gag tgg gca ggc act gac ctg cga gga   403
Tyr Asn Gly Glu Thr Leu Thr Glu Trp Ala Gly Thr Asp Leu Arg Gly
                 90                  95                 100

tta tcc cga gaa gtc ctc aac gtt cca ttc gcg gca cac aat gat gtc   451
Leu Ser Arg Glu Val Leu Asn Val Pro Phe Ala Ala His Asn Asp Val
            105                 110                 115

cgc gta tgg gcc tac ggt gag cac cac tta ggc acc ggc aaa gac ctc   499
Arg Val Trp Ala Tyr Gly Glu His His Leu Gly Thr Gly Lys Asp Leu
        120                 125                 130

acc ggc agg gta ctc tac gtg tcc ctc ggc act gga gtc ggc gga gca   547
Thr Gly Arg Val Leu Tyr Val Ser Leu Gly Thr Gly Val Gly Gly Ala
    135                 140                 145

atc atc gaa gac gga atc atg atg agt agc ccc act gga act gcg gga   595
Ile Ile Glu Asp Gly Ile Met Met Ser Ser Pro Thr Gly Thr Ala Gly
150                 155                 160                 165

gaa ttc gca gaa gtt gtg tgc tct gac cat gca gga tta gcc gtt cgg   643
Glu Phe Ala Glu Val Val Cys Ser Asp His Ala Gly Leu Ala Val Arg
                170                 175                 180

tgc gaa aat gta gca agt ggc acc ggc cta acc agg tac tac aac gag   691
Cys Glu Asn Val Ala Ser Gly Thr Gly Leu Thr Arg Tyr Tyr Asn Glu
            185                 190                 195

gcc gcc gca act caa ctt gac ctt ccc gcc atc atg gag cgc ttc cac   739
Ala Ala Ala Thr Gln Leu Asp Leu Pro Ala Ile Met Glu Arg Phe His
        200                 205                 210

caa ggt gac ggc ctg gca cag caa atc att act gga aat ctc cga ggc   787
Gln Gly Asp Gly Leu Ala Gln Gln Ile Ile Thr Gly Asn Leu Arg Gly
    215                 220                 225

ttt ggc caa gcg cta ggc gca tta gtc aca gtg ctg gac ctt tcc gca   835
Phe Gly Gln Ala Leu Gly Ala Leu Val Thr Val Leu Asp Leu Ser Ala
230                 235                 240                 245

gta gta gtt gga ggc gga gtc gca ggc atc ggc gca ccc gtc atg gat   883
Val Val Val Gly Gly Gly Val Ala Gly Ile Gly Ala Pro Val Met Asp
                250                 255                 260

ccc atc acc gca ggg att ttc gat cga gtg tta acc ccc aac aaa tcc   931
Pro Ile Thr Ala Gly Ile Phe Asp Arg Val Leu Thr Pro Asn Lys Ser
            265                 270                 275

gta caa gtt tta agc acg tcc ctt ggt gcc caa gca gcc gtc atc gca   979
Val Gln Val Leu Ser Thr Ser Leu Gly Ala Gln Ala Ala Val Ile Ala
        280                 285                 290

gca gca aaa tat gcc cgc gat aac gcc ttt taagcaccta aaacgctgtt     1029
Ala Ala Lys Tyr Ala Arg Asp Asn Ala Phe
    295                 300
```

ctc 1032

<210> 78
<211> 303
<212> PRT
<213> Corynebacterium glutamicum

<400> 78

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Met Thr Asp Pro Thr Cys Thr Leu Ala Leu Asp Ile Gly Ala Thr Lys
  1               5                  10                  15

Ile Ala Tyr Ala Leu Val Pro Asp Asn Thr Pro Thr Thr Thr Leu Ser
             20                  25                  30

Thr Gly Arg Leu Gly Thr Lys Glu Gly Asp Ser Pro Ile Glu Gln Ile
         35                  40                  45

Arg Leu Val Leu Leu Ala Gly Leu Lys Ala Ala Glu Glu His Gly Leu
     50                  55                  60

Ser Val Ala Arg Ile Gly Met Gly Ala Pro Gly Val Ile Leu Gly Pro
 65                  70                  75                  80

Glu Gly Thr Ile Val Tyr Asn Gly Glu Thr Leu Thr Glu Trp Ala Gly
                 85                  90                  95

Thr Asp Leu Arg Gly Leu Ser Arg Glu Val Leu Asn Val Pro Phe Ala
            100                 105                 110

Ala His Asn Asp Val Arg Val Trp Ala Tyr Gly Glu His His Leu Gly
        115                 120                 125

Thr Gly Lys Asp Leu Thr Gly Arg Val Leu Tyr Val Ser Leu Gly Thr
    130                 135                 140

Gly Val Gly Gly Ala Ile Ile Glu Asp Gly Ile Met Met Ser Ser Pro
145                 150                 155                 160

Thr Gly Thr Ala Gly Glu Phe Ala Glu Val Val Cys Ser Asp His Ala
                165                 170                 175

Gly Leu Ala Val Arg Cys Glu Asn Val Ala Ser Gly Thr Gly Leu Thr
            180                 185                 190

Arg Tyr Tyr Asn Glu Ala Ala Ala Thr Gln Leu Asp Leu Pro Ala Ile
        195                 200                 205

Met Glu Arg Phe His Gln Gly Asp Gly Leu Ala Gln Gln Ile Ile Thr
    210                 215                 220

Gly Asn Leu Arg Gly Phe Gly Gln Ala Leu Gly Ala Leu Val Thr Val
225                 230                 235                 240

Leu Asp Leu Ser Ala Val Val Val Gly Gly Gly Val Ala Gly Ile Gly
                245                 250                 255

Ala Pro Val Met Asp Pro Ile Thr Ala Gly Ile Phe Asp Arg Val Leu
            260                 265                 270
```

```
Thr Pro Asn Lys Ser Val Gln Val Leu Ser Thr Ser Leu Gly Ala Gln
        275                 280                 285

Ala Ala Val Ile Ala Ala Ala Lys Tyr Ala Arg Asp Asn Ala Phe
    290                 295                 300


<210> 79
<211> 1812
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1789)
<223> RXN02704

<400> 79
cgtctttgga catgttcaaa ggcatgggcc agcgtggcga cctctttgca cacaacatca 60

ttggcacaat caaaggatta acggaagaga aaggctgatc atg acc acc gga gcc   115
                                            Met Thr Thr Gly Ala
                                              1               5

tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg   163
Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
                10                  15                  20

ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg   211
Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala
            25                  30                  35

cgc cct tta act gac tac atc atg atc ttg tgc atc gtg gtc att ttg   259
Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys Ile Val Val Ile Leu
        40                  45                  50

tcg tgc ctc ggt gta gtc atg gtg tat tcc tcc tca atg aca tgg tcg   307
Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser Ser Met Thr Trp Ser
    55                  60                  65

ttg agg gaa ggt ggc tcc gtg tgg ggt act gcc gtg cgc cag ggc atc   355
Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala Val Arg Gln Gly Ile
70                  75                  80                  85

atg atc gtg ttg ggt ttc ttt gcc atg tgg gtg gcg ttg atg acg cgc   403
Met Ile Val Leu Gly Phe Phe Ala Met Trp Val Ala Leu Met Thr Arg
                90                  95                  100

ccg caa acc att aga aac cta tcc aac ctg ata ttg att gtg tct att   451
Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile Leu Ile Val Ser Ile
            105                 110                 115

gtc ttg ctg ctt gcc gtg cag att cct ggc att ggt aca ggt aaa gaa   499
Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile Gly Thr Gly Lys Glu
        120                 125                 130

gag gtc ggg tcg cag tcg tgg att gct ctt gga cct att cag ttt cag   547
Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly Pro Ile Gln Phe Gln
    135                 140                 145

cct tcg gag atc gcc aaa gtg gcc att gcc gtg tgg gga gcg cac tac   595
```

```
Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val Trp Gly Ala His Tyr
150                 155                 160                 165

ctc gca ggc aag ggc cct gtg cag cac tgg ttc aat aat cac ttg atg   643
Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe Asn Asn His Leu Met
                170                 175                 180

cgt ttt ggt ggc gtc ggt gca ttc atg gcg ttt ttg atc ttc atg gaa   691
Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe Leu Ile Phe Met Glu
            185                 190                 195

ggc gac gcc ggc atg gcg atg tct ttc gtg ctg gtt gta ttg ttc atg   739
Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu Val Val Leu Phe Met
        200                 205                 210

ctg ttt ttt gcg ggc atc gcc atg ggt tgg atc gcg att gcc ggc gta   787
Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile Ala Ile Ala Gly Val
    215                 220                 225

ctg att atc gca gcc ctc gca gtc ctg gca ttg ggc gga ggc ttc cgt   835
Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu Gly Gly Gly Phe Arg
230                 235                 240                 245

tca agc cga ttc gag gtg tat ttc gat gcg ctg ttt ggc aat ttc cac   883
Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu Phe Gly Asn Phe His
                250                 255                 260

gat gtg cga ggc att gcc ttc cag tcc tat cag ggc ttc ctc tct ctt   931
Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln Gly Phe Leu Ser Leu
            265                 270                 275

gca gat ggt tcc ggc ttg gga gtt ggt ttg ggc caa tca agg gcg aag   979
Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly Gln Ser Arg Ala Lys
        280                 285                 290

tgg ttc tac ctg ccc gaa gct aaa aat gac ttc atc ttt gcc atc att   1027
Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe Ile Phe Ala Ile Ile
    295                 300                 305

ggt gag gag ctg ggg ctg tgg ggt ggc gct ctg gtc atc gca ctt ttc   1075
Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu Val Ile Ala Leu Phe
310                 315                 320                 325

gcg ggg ctg ctg tac ttc ggt ctg cgc aca gcc aag aag agc cac gat   1123
Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala Lys Lys Ser His Asp
                330                 335                 340

cca ttc ttg ggc ttg atg gct gca acc ttg acg gca tcc gtg gtg tcg   1171
Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr Ala Ser Val Val Ser
            345                 350                 355

cag gcg ttc atc aac att ggc tac gtg gtt ggt ctg ctg cca gtt acc   1219
Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly Leu Leu Pro Val Thr
        360                 365                 370

ggt att cag ctg ccc atg att tcc gcc ggt ggt acc tcc gcg atc att   1267
Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly Thr Ser Ala Ile Ile
    375                 380                 385

acc ttg gct tcc atg ggc ttg ctc att agc tgt gca cgc cac gaa cca   1315
Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys Ala Arg His Glu Pro
```

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390                 395                 400                 405

gag aca gtt tct gcg atg gct tcc tat gga cgc ccc gca atc gat cga   1363
Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg Pro Ala Ile Asp Arg
                410                 415                 420

ctt ctg gga ttg cgt gag cct tca agt act ttg acc acc agt aat gca   1411
Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu Thr Thr Ser Asn Ala
            425                 430                 435

tcc ttg cgt tcc aac aaa acc aag gcc gct aaa caa aag ccg agt cct   1459
Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys Gln Lys Pro Ser Pro
        440                 445                 450

cag aaa gag tct cgg gac cgc ttc ggc gag cct gtg acc gca cgc cga   1507
Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro Val Thr Ala Arg Arg
    455                 460                 465

gcg cag gcg cca cga agt ggg cga gct gga gta caa tcg gaa gct ccg   1555
Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val Gln Ser Glu Ala Pro
470                 475                 480                 485

cga cgc tcg act ggt agc gtc aaa ggt cga agc agt ggt cag gac aac   1603
Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser Ser Gly Gln Asp Asn
                490                 495                 500

ggt cga agc aac gaa ggt acg gcg cgt agc caa tca act act ggt ggg   1651
Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln Ser Thr Thr Gly Gly
            505                 510                 515

cgc gca gcc gat cgc agc gtt gat cga agt cgt caa agc agg cct acc   1699
Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg Gln Ser Arg Pro Thr
        520                 525                 530

gag cgc cgt tcc gag agt cgc gcg atg att ggc gtg aca acc gca acc   1747
Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly Val Thr Thr Ala Thr
    535                 540                 545

gca gat aaa tgt gaa atc agg aga act acg aat aaa gat ggc           1789
Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn Lys Asp Gly
550                 555                 560

taactcccca aaacccatgc ggg                                        1812
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<210> 80
<211> 563
<212> PRT
<213> Corynebacterium glutamicum

<400> 80

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Met Thr Thr Gly Ala Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala
  1               5                  10                  15

Lys Thr Arg Thr Gly Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp
             20                  25                  30

Asn Asp Leu Leu Ala Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys
         35                  40                  45

Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser
```

```
     50                  55                  60

Ser Met Thr Trp Ser Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala
 65                  70                  75                  80

Val Arg Gln Gly Ile Met Ile Val Leu Gly Phe Phe Ala Met Trp Val
                 85                  90                  95

Ala Leu Met Thr Arg Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile
            100                 105                 110

Leu Ile Val Ser Ile Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile
        115                 120                 125

Gly Thr Gly Lys Glu Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly
    130                 135                 140

Pro Ile Gln Phe Gln Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val
145                 150                 155                 160

Trp Gly Ala His Tyr Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe
                165                 170                 175

Asn Asn His Leu Met Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe
            180                 185                 190

Leu Ile Phe Met Glu Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu
        195                 200                 205

Val Val Leu Phe Met Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile
    210                 215                 220

Ala Ile Ala Gly Val Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu
225                 230                 235                 240

Gly Gly Gly Phe Arg Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu
                245                 250                 255

Phe Gly Asn Phe His Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln
            260                 265                 270

Gly Phe Leu Ser Leu Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly
        275                 280                 285

Gln Ser Arg Ala Lys Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe
    290                 295                 300

Ile Phe Ala Ile Ile Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu
305                 310                 315                 320

Val Ile Ala Leu Phe Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala
                325                 330                 335

Lys Lys Ser His Asp Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr
            340                 345                 350

Ala Ser Val Val Ser Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly
        355                 360                 365

Leu Leu Pro Val Thr Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly
    370                 375                 380
```

SUBSTITUTE SHEET (RULE 26)

Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys
385 390 395 400

Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg
405 410 415

Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu
420 425 430

Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys
435 440 445

Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro
450 455 460

Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val
465 470 475 480

Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser
485 490 495

Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln
500 505 510

Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg
515 520 525

Gln Ser Arg Pro Thr Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly
530 535 540

Val Thr Thr Ala Thr Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn
545 550 555 560

Lys Asp Gly

EFS-Web Text Copy

<210> 81
<211> 1812
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1789)
<223> FRXA02704

<400> 81
cgtctttgga catgttcaaa ggcatgggcc agcgtggcga cctctttgca cacaacatca 60

ttggcacaat caaaggatta acggaagaga aaggctgatc atg acc acc gga gcc 115
Met Thr Thr Gly Ala
1 5

tca aaa aaa ccc gca cgt ccg aac act ggc gct aaa acc aga acg ggg 163
Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala Lys Thr Arg Thr Gly
10 15 20

ctg gga att agg gag cgt att tcc ggt gca tgg aat gat ctt ctc gcg 211
Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp Asn Asp Leu Leu Ala

```
                25                  30                  35

cgc cct tta act gac tac atc atg atc ttg tgc atc gtg gtc att ttg   259
Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys Ile Val Val Ile Leu
         40                  45                  50

tcg tgc ctc ggt gta gtc atg gtg tat tcc tcc tca atg aca tgg tcg   307
Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser Ser Met Thr Trp Ser
     55                  60                  65

ttg agg gaa ggt ggc tcc gtg tgg ggt act gcc gtg cgc cag ggc atc   355
Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala Val Arg Gln Gly Ile
 70                  75                  80                  85

atg atc gtg ttg ggt ttc ttt gcc atg tgg gtg gcg ttg atg acg cgc   403
Met Ile Val Leu Gly Phe Phe Ala Met Trp Val Ala Leu Met Thr Arg
                90                  95                 100

ccg caa acc att aga aac cta tcc aac ctg ata ttg att gtg tct att   451
Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile Leu Ile Val Ser Ile
            105                 110                 115

gtc ttg ctg ctt gcc gtg cag att cct ggc att ggt aca ggt aaa gaa   499
Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile Gly Thr Gly Lys Glu
        120                 125                 130

gag gtc ggg tcg cag tcg tgg att gct ctt gga cct att cag ttt cag   547
Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly Pro Ile Gln Phe Gln
    135                 140                 145

cct tcg gag atc gcc aaa gtg gcc att gcc gtg tgg gga gcg cac tac   595
Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val Trp Gly Ala His Tyr
150                 155                 160                 165

ctc gca ggc aag ggc cct gtg cag cac tgg ttc aat aat cac ttg atg   643
Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe Asn Asn His Leu Met
                170                 175                 180

cgt ttt ggt ggc gtc ggt gca ttc atg gcg ttt ttg atc ttc atg gaa   691
Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe Leu Ile Phe Met Glu
            185                 190                 195

ggc gac gcc ggc atg gcg atg tct ttc gtg ctg gtt gta ttg ttc atg   739
Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu Val Val Leu Phe Met
        200                 205                 210

ctg ttt ttt gcg ggc atc gcc atg ggt tgg atc gcg att gcc ggc gta   787
Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile Ala Ile Ala Gly Val
    215                 220                 225

ctg att atc gca gcc ctc gca gtc ctg gca ttg ggc gga ggc ttc cgt   835
Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu Gly Gly Gly Phe Arg
230                 235                 240                 245

tca agc cga ttc gag gtg tat ttc gat gcg ctg ttt ggc aat ttc cac   883
Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu Phe Gly Asn Phe His
                250                 255                 260

gat gtg cga ggc att gcc ttc cag tcc tat cag ggc ttc ctc tct ctt   931
Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln Gly Phe Leu Ser Leu
            265                 270                 275
```

```
gca gat ggt tcc ggc ttg gga gtt ggt ttg ggc caa tca agg gcg aag   979
Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly Gln Ser Arg Ala Lys
        280                 285                 290

tgg ttc tac ctg ccc gaa gct aaa aat gac ttc atc ttt gcc atc att   1027
Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe Ile Phe Ala Ile Ile
    295                 300                 305

ggt gag gag ctg ggg ctg tgg ggt ggc gct ctg gtc atc gca ctt ttc   1075
Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu Val Ile Ala Leu Phe
310                 315                 320                 325

gcg ggg ctg ctg tac ttc ggt ctg cgc aca gcc aag aag agc cac gat   1123
Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala Lys Lys Ser His Asp
                330                 335                 340

cca ttc ttg ggc ttg atg gct gca acc ttg acg gca tcc gtg gtg tcg   1171
Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr Ala Ser Val Val Ser
            345                 350                 355

cag gcg ttc atc aac att ggc tac gtg gtt ggt ctg ctg cca gtt acc   1219
Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly Leu Leu Pro Val Thr
        360                 365                 370

ggt att cag ctg ccc atg att tcc gcc ggt ggt acc tcc gcg atc att   1267
Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly Thr Ser Ala Ile Ile
    375                 380                 385

acc ttg gct tcc atg ggc ttg ctc att agc tgt gca cgc cac gaa cca   1315
Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys Ala Arg His Glu Pro
390                 395                 400                 405

gag aca gtt tct gcg atg gct tcc tat gga cgc ccc gca atc gat cga   1363
Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg Pro Ala Ile Asp Arg
                410                 415                 420

ctt ctg gga ttg cgt gag cct tca agt act ttg acc acc agt aat gca   1411
Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu Thr Thr Ser Asn Ala
            425                 430                 435

tcc ttg cgt tcc aac aaa acc aag gcc gct aaa caa aag ccg agt cct   1459
Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys Gln Lys Pro Ser Pro
        440                 445                 450

cag aaa gag tct cgg gac cgc ttc ggc gag cct gtg acc gca cgc cga   1507
Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro Val Thr Ala Arg Arg
    455                 460                 465

gcg cag gcg cca cga agt ggg cga gct gga gta caa tcg gaa gct ccg   1555
Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val Gln Ser Glu Ala Pro
470                 475                 480                 485

cga cgc tcg act ggt agc gtc aaa ggt cga agc agt ggt cag gac aac   1603
Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser Ser Gly Gln Asp Asn
                490                 495                 500

ggt cga agc aac gaa ggt acg gcg cgt agc caa tca act act ggt ggg   1651
Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln Ser Thr Thr Gly Gly
            505                 510                 515
```

Sequence Listing

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cgc gca gcc gat cgc agc gtt gat cga agt cgt caa agc agg cct acc   1699
Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg Gln Ser Arg Pro Thr
        520                 525                 530

gag cgc cgt tcc gag agt cgc gcg atg att ggc gtg aca acc gca acc   1747
Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly Val Thr Thr Ala Thr
    535                 540                 545

gca gat aaa tgt gaa atc agg aga act acg aat aaa gat ggc           1789
Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn Lys Asp Gly
550                 555                 560

taactcccca aaacccatgc ggg                                        1812
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<210> 82
<211> 563
<212> PRT
<213> Corynebacterium glutamicum

<400> 82

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Met Thr Thr Gly Ala Ser Lys Lys Pro Ala Arg Pro Asn Thr Gly Ala
  1               5                  10                  15

Lys Thr Arg Thr Gly Leu Gly Ile Arg Glu Arg Ile Ser Gly Ala Trp
             20                  25                  30

Asn Asp Leu Leu Ala Arg Pro Leu Thr Asp Tyr Ile Met Ile Leu Cys
         35                  40                  45

Ile Val Val Ile Leu Ser Cys Leu Gly Val Val Met Val Tyr Ser Ser
     50                  55                  60

Ser Met Thr Trp Ser Leu Arg Glu Gly Gly Ser Val Trp Gly Thr Ala
 65                  70                  75                  80

Val Arg Gln Gly Ile Met Ile Val Leu Gly Phe Phe Ala Met Trp Val
                 85                  90                  95

Ala Leu Met Thr Arg Pro Gln Thr Ile Arg Asn Leu Ser Asn Leu Ile
            100                 105                 110

Leu Ile Val Ser Ile Val Leu Leu Leu Ala Val Gln Ile Pro Gly Ile
        115                 120                 125

Gly Thr Gly Lys Glu Glu Val Gly Ser Gln Ser Trp Ile Ala Leu Gly
    130                 135                 140

Pro Ile Gln Phe Gln Pro Ser Glu Ile Ala Lys Val Ala Ile Ala Val
145                 150                 155                 160

Trp Gly Ala His Tyr Leu Ala Gly Lys Gly Pro Val Gln His Trp Phe
                165                 170                 175

Asn Asn His Leu Met Arg Phe Gly Gly Val Gly Ala Phe Met Ala Phe
            180                 185                 190

Leu Ile Phe Met Glu Gly Asp Ala Gly Met Ala Met Ser Phe Val Leu
        195                 200                 205

Val Val Leu Phe Met Leu Phe Phe Ala Gly Ile Ala Met Gly Trp Ile
```

```
    210                 215                 220

Ala Ile Ala Gly Val Leu Ile Ile Ala Ala Leu Ala Val Leu Ala Leu
225                 230                 235                 240

Gly Gly Gly Phe Arg Ser Ser Arg Phe Glu Val Tyr Phe Asp Ala Leu
                245                 250                 255

Phe Gly Asn Phe His Asp Val Arg Gly Ile Ala Phe Gln Ser Tyr Gln
            260                 265                 270

Gly Phe Leu Ser Leu Ala Asp Gly Ser Gly Leu Gly Val Gly Leu Gly
        275                 280                 285

Gln Ser Arg Ala Lys Trp Phe Tyr Leu Pro Glu Ala Lys Asn Asp Phe
    290                 295                 300

Ile Phe Ala Ile Ile Gly Glu Glu Leu Gly Leu Trp Gly Gly Ala Leu
305                 310                 315                 320

Val Ile Ala Leu Phe Ala Gly Leu Leu Tyr Phe Gly Leu Arg Thr Ala
                325                 330                 335

Lys Lys Ser His Asp Pro Phe Leu Gly Leu Met Ala Ala Thr Leu Thr
            340                 345                 350

Ala Ser Val Val Ser Gln Ala Phe Ile Asn Ile Gly Tyr Val Val Gly
        355                 360                 365

Leu Leu Pro Val Thr Gly Ile Gln Leu Pro Met Ile Ser Ala Gly Gly
    370                 375                 380

Thr Ser Ala Ile Ile Thr Leu Ala Ser Met Gly Leu Leu Ile Ser Cys
385                 390                 395                 400

Ala Arg His Glu Pro Glu Thr Val Ser Ala Met Ala Ser Tyr Gly Arg
                405                 410                 415

Pro Ala Ile Asp Arg Leu Leu Gly Leu Arg Glu Pro Ser Ser Thr Leu
            420                 425                 430

Thr Thr Ser Asn Ala Ser Leu Arg Ser Asn Lys Thr Lys Ala Ala Lys
        435                 440                 445

Gln Lys Pro Ser Pro Gln Lys Glu Ser Arg Asp Arg Phe Gly Glu Pro
    450                 455                 460

Val Thr Ala Arg Arg Ala Gln Ala Pro Arg Ser Gly Arg Ala Gly Val
465                 470                 475                 480

Gln Ser Glu Ala Pro Arg Arg Ser Thr Gly Ser Val Lys Gly Arg Ser
                485                 490                 495

Ser Gly Gln Asp Asn Gly Arg Ser Asn Glu Gly Thr Ala Arg Ser Gln
            500                 505                 510

Ser Thr Thr Gly Gly Arg Ala Ala Asp Arg Ser Val Asp Arg Ser Arg
        515                 520                 525

Gln Ser Arg Pro Thr Glu Arg Arg Ser Glu Ser Arg Ala Met Ile Gly
    530                 535                 540
```

```
Val Thr Thr Ala Thr Ala Asp Lys Cys Glu Ile Arg Arg Thr Thr Asn
545                 550                 555                 560

Lys Asp Gly
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<210> 83
<211> 1449
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1426)
<223> RXA02722

<400> 83

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ttttttttagt atcaactctt cgaaaggcga gacatcgaca atg acc tca ccg aac   115
                                              Met Thr Ser Pro Asn
                                                1               5

aac tac ctc gcc aag att aag gtc gtc ggc gtg ggc ggc ggc gga gtc   163
Asn Tyr Leu Ala Lys Ile Lys Val Val Gly Val Gly Gly Gly Gly Val
                  10                  15                  20

aac gcc gtc aac cgc atg att gaa gaa ggc ctc aaa ggc gtg gag ttc   211
Asn Ala Val Asn Arg Met Ile Glu Glu Gly Leu Lys Gly Val Glu Phe
              25                  30                  35

atc gcg gtg aac acc gac tcg cag gct ctc atg ttc tct gat gcc gac   259
Ile Ala Val Asn Thr Asp Ser Gln Ala Leu Met Phe Ser Asp Ala Asp
          40                  45                  50

gta aag ctc gat atc gga cgt gaa gct acc cgt ggt ctt ggt gcc ggc   307
Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg Gly Leu Gly Ala Gly
      55                  60                  65

gcg aac cca gaa gtt gga cgt gcc tcg gca gag gat cac aag aac gaa   355
Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu Asp His Lys Asn Glu
  70                  75                  80                  85

atc gaa gaa acc atc aag ggc gcc gac atg gtc ttc gtt acc gcc ggc   403
Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val Phe Val Thr Ala Gly
                  90                  95                 100

gaa ggt ggt ggc acc gga act ggt gct gca cca gtc gtg gca ggg atc   451
Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro Val Val Ala Gly Ile
              105                 110                 115

gcc aag aag atg ggc gca ctg acc att ggt gtt gtg acc aag cct ttc   499
Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val Val Thr Lys Pro Phe
          120                 125                 130

gag ttc gaa ggc cgt cgc cgt act cgc cag gca gaa gaa ggc atc gca   547
Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala Glu Glu Gly Ile Ala
      135                 140                 145
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```
gca ctg aag gag gtc tgc gac acc ctc atc gtt att cca aac gac cgc   595
Ala Leu Lys Glu Val Cys Asp Thr Leu Ile Val Ile Pro Asn Asp Arg
150                 155                 160                 165

ctg ctt gag ctg ggc gat gcg aac ctg tcc atc atg gaa gcg ttc cgc   643
Leu Leu Glu Leu Gly Asp Ala Asn Leu Ser Ile Met Glu Ala Phe Arg
                170                 175                 180

gca gcc gat gaa gtt ctc cac aat ggt gtt cag ggt att acc aac ctg   691
Ala Ala Asp Glu Val Leu His Asn Gly Val Gln Gly Ile Thr Asn Leu
            185                 190                 195

atc acc atc cct ggt gtg atc aac gtg gac ttc gcg gac gtt cgc tcc   739
Ile Thr Ile Pro Gly Val Ile Asn Val Asp Phe Ala Asp Val Arg Ser
        200                 205                 210

gtc atg tcc gaa gct ggt tcc gca ctc atg ggt gtg ggc tct gca cgt   787
Val Met Ser Glu Ala Gly Ser Ala Leu Met Gly Val Gly Ser Ala Arg
    215                 220                 225

ggg gac aac cgc gtt gtc tct gca acc gag cag gcc atc aac tct cca   835
Gly Asp Asn Arg Val Val Ser Ala Thr Glu Gln Ala Ile Asn Ser Pro
230                 235                 240                 245

ctt ctc gaa gca aca atg gac ggc gca act ggc gtc ctg ctg tcc ttt   883
Leu Leu Glu Ala Thr Met Asp Gly Ala Thr Gly Val Leu Leu Ser Phe
                250                 255                 260

gct ggt gga tcc gac ctg ggc ctc atg gaa gtc aac gca gct gca tcc   931
Ala Gly Gly Ser Asp Leu Gly Leu Met Glu Val Asn Ala Ala Ala Ser
            265                 270                 275

atg gtc cgt gag cgt tcc gat gaa gat gtc aac ctc atc ttc ggt acc   979
Met Val Arg Glu Arg Ser Asp Glu Asp Val Asn Leu Ile Phe Gly Thr
        280                 285                 290

atc atc gac gac aac ctg ggc gac gaa gtc cgc gta acc gtc atc gcg   1027
Ile Ile Asp Asp Asn Leu Gly Asp Glu Val Arg Val Thr Val Ile Ala
    295                 300                 305

acc ggt ttt gac gca gct cgc gca agc gcc gct gag aac cgc cgc gca   1075
Thr Gly Phe Asp Ala Ala Arg Ala Ser Ala Ala Glu Asn Arg Arg Ala
310                 315                 320                 325

ggc atc tca gct gca cct gca gct gag cca gtc cag cag cag gtc cca   1123
Gly Ile Ser Ala Ala Pro Ala Ala Glu Pro Val Gln Gln Gln Val Pro
                330                 335                 340

acc acc aac gca acc ctt cca cca gag aag gaa agc atc ttc ggt ggt   1171
Thr Thr Asn Ala Thr Leu Pro Pro Glu Lys Glu Ser Ile Phe Gly Gly
            345                 350                 355

gca cgt gag gag aac gat cct tac ctg tcc cgc tct gct ggt gca cgt   1219
Ala Arg Glu Glu Asn Asp Pro Tyr Leu Ser Arg Ser Ala Gly Ala Arg
        360                 365                 370

cat cgc att gag gag acc cgc tcc ggc ggt gga ctc ttc acc acc ggc   1267
His Arg Ile Glu Glu Thr Arg Ser Gly Gly Gly Leu Phe Thr Thr Gly
    375                 380                 385

aat gat cgc gat tac cgt cgt gat gag cgc cgc gaa gat cac cgt gac   1315
```

```
Asn Asp Arg Asp Tyr Arg Arg Asp Glu Arg Arg Glu Asp His Arg Asp
390                 395                 400                 405

gag cgc cgc gat gag cgc cgc gat gac cgt tcc tac gac cgc cgt gat   1363
Glu Arg Arg Asp Glu Arg Arg Asp Asp Arg Ser Tyr Asp Arg Arg Asp
                410                 415                 420

gat cgt cgt gac gat cgc cgc gat gac cgc gga gac gac ctg gat gta   1411
Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Gly Asp Asp Leu Asp Val
            425                 430                 435

ccc agc ttc ctc cag taattaagaa ggagaataga ctt                    1449
Pro Ser Phe Leu Gln
        440
```

<210> 84
<211> 442
<212> PRT
<213> Corynebacterium glutamicum

<400> 84

```
Met Thr Ser Pro Asn Asn Tyr Leu Ala Lys Ile Lys Val Val Gly Val
  1               5                  10                  15

Gly Gly Gly Gly Val Asn Ala Val Asn Arg Met Ile Glu Glu Gly Leu
             20                  25                  30

Lys Gly Val Glu Phe Ile Ala Val Asn Thr Asp Ser Gln Ala Leu Met
         35                  40                  45

Phe Ser Asp Ala Asp Val Lys Leu Asp Ile Gly Arg Glu Ala Thr Arg
     50                  55                  60

Gly Leu Gly Ala Gly Ala Asn Pro Glu Val Gly Arg Ala Ser Ala Glu
 65                  70                  75                  80

Asp His Lys Asn Glu Ile Glu Glu Thr Ile Lys Gly Ala Asp Met Val
                 85                  90                  95

Phe Val Thr Ala Gly Glu Gly Gly Gly Thr Gly Thr Gly Ala Ala Pro
            100                 105                 110

Val Val Ala Gly Ile Ala Lys Lys Met Gly Ala Leu Thr Ile Gly Val
        115                 120                 125

Val Thr Lys Pro Phe Glu Phe Glu Gly Arg Arg Arg Thr Arg Gln Ala
    130                 135                 140

Glu Glu Gly Ile Ala Ala Leu Lys Glu Val Cys Asp Thr Leu Ile Val
145                 150                 155                 160

Ile Pro Asn Asp Arg Leu Leu Glu Leu Gly Asp Ala Asn Leu Ser Ile
                165                 170                 175

Met Glu Ala Phe Arg Ala Ala Asp Glu Val Leu His Asn Gly Val Gln
            180                 185                 190

Gly Ile Thr Asn Leu Ile Thr Ile Pro Gly Val Ile Asn Val Asp Phe
        195                 200                 205
```

Ala Asp Val Arg Ser Val Met Ser Glu Ala Gly Ser Ala Leu Met Gly
210 215 220

Val Gly Ser Ala Arg Gly Asp Asn Arg Val Val Ser Ala Thr Glu Gln
225 230 235 240

Ala Ile Asn Ser Pro Leu Leu Glu Ala Thr Met Asp Gly Ala Thr Gly
245 250 255

Val Leu Leu Ser Phe Ala Gly Gly Ser Asp Leu Gly Leu Met Glu Val
260 265 270

Asn Ala Ala Ala Ser Met Val Arg Glu Arg Ser Asp Glu Asp Val Asn
275 280 285

Leu Ile Phe Gly Thr Ile Ile Asp Asp Asn Leu Gly Asp Glu Val Arg
290 295 300

Val Thr Val Ile Ala Thr Gly Phe Asp Ala Ala Arg Ala Ser Ala Ala
305 310 315 320

Glu Asn Arg Arg Ala Gly Ile Ser Ala Ala Pro Ala Ala Glu Pro Val
325 330 335

Gln Gln Gln Val Pro Thr Thr Asn Ala Thr Leu Pro Pro Glu Lys Glu
340 345 350

Ser Ile Phe Gly Gly Ala Arg Glu Glu Asn Asp Pro Tyr Leu Ser Arg
355 360 365

Ser Ala Gly Ala Arg His Arg Ile Glu Glu Thr Arg Ser Gly Gly Gly
370 375 380

Leu Phe Thr Thr Gly Asn Asp Arg Asp Tyr Arg Arg Asp Glu Arg Arg
385 390 395 400

Glu Asp His Arg Asp Glu Arg Arg Asp Glu Arg Arg Asp Asp Arg Ser
405 410 415

Tyr Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Arg Asp Asp Arg Gly
420 425 430

Asp Asp Leu Asp Val Pro Ser Phe Leu Gln
435 440

<210> 85
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)
<223> RXA00009

<400> 85
gacgacatgc gcaggcgagt aatcgaactg caattgggca aactagtccg cgatgatgcc 60

cacggcgtct acggcgaaat gcgatagggg agtacttcac atg gct ttt gga tat 115
Met Ala Phe Gly Tyr

```
                                                    1               5

gta ctg cgt gaa gct gtt cgc ggc atg ggc cgc aac gtc acc atg acc   163
Val Leu Arg Glu Ala Val Arg Gly Met Gly Arg Asn Val Thr Met Thr
                10                  15                  20

atc gcg ctc atc atc acc acc tct att tcc ttg gca ctt ctt gcc act   211
Ile Ala Leu Ile Ile Thr Thr Ser Ile Ser Leu Ala Leu Leu Ala Thr
            25                  30                  35

gga ttt ttg gtg acc aac atg acc gac cgc acc aag gac atc tac ctg   259
Gly Phe Leu Val Thr Asn Met Thr Asp Arg Thr Lys Asp Ile Tyr Leu
        40                  45                  50

gat cgc gtc gaa gtg atg atc caa ctc gat gag gac acc tct gcc aac   307
Asp Arg Val Glu Val Met Ile Gln Leu Asp Glu Asp Thr Ser Ala Asn
    55                  60                  65

gat ccc gaa tgc acc gcg gag tcc tgc acc gaa gtt cgt gat gtc tta   355
Asp Pro Glu Cys Thr Ala Glu Ser Cys Thr Glu Val Arg Asp Val Leu
70                  75                  80                  85

gaa gga ctc gac ggc atc gat tcc atc acc tac cgt tcc cgc gag gcc   403
Glu Gly Leu Asp Gly Ile Asp Ser Ile Thr Tyr Arg Ser Arg Glu Ala
                90                  95                  100

tcc tac gaa cga ttc gta gaa gtt ttc aaa gat act gac cca gtt ctc   451
Ser Tyr Glu Arg Phe Val Glu Val Phe Lys Asp Thr Asp Pro Val Leu
            105                 110                 115

gtc gct gaa acc tct ccc gac gca ttg cca gca gcg ttc cac gtc cga   499
Val Ala Glu Thr Ser Pro Asp Ala Leu Pro Ala Ala Phe His Val Arg
        120                 125                 130

ctt gaa gat cca ctt gcc gtt gag att ctc gat ccg gtc cgc gat ctt   547
Leu Glu Asp Pro Leu Ala Val Glu Ile Leu Asp Pro Val Arg Asp Leu
    135                 140                 145

cct caa gta agc aac gtg atc gac cag gtg gat gat ctg cgc gga gca   595
Pro Gln Val Ser Asn Val Ile Asp Gln Val Asp Asp Leu Arg Gly Ala
150                 155                 160                 165

acc gaa aac ctt gac tcc atc cgc aac gcc acc ttc ctc atc gcg gct   643
Thr Glu Asn Leu Asp Ser Ile Arg Asn Ala Thr Phe Leu Ile Ala Ala
                170                 175                 180

gtg caa gtt ttg gca tcg atc ttc ctg att gcc aac atg gtg caa atc   691
Val Gln Val Leu Ala Ser Ile Phe Leu Ile Ala Asn Met Val Gln Ile
            185                 190                 195

gct gca ttc aat cgt cgt gaa gaa act gaa atc atg cgc atc gtc ggc   739
Ala Ala Phe Asn Arg Arg Glu Glu Thr Glu Ile Met Arg Ile Val Gly
        200                 205                 210

gca tcg cgg ttc tac act cag gga cca ttc gtc ttc gaa gcg att cta   787
Ala Ser Arg Phe Tyr Thr Gln Gly Pro Phe Val Phe Glu Ala Ile Leu
    215                 220                 225

tcc acc ctc att ggt gcg gtt ttc gcc gtc ggc gcg ctc ttc ttg ggt   835
Ser Thr Leu Ile Gly Ala Val Phe Ala Val Gly Ala Leu Phe Leu Gly
230                 235                 240                 245
```

```
aaa gaa ctc gtc att gat aaa gca ctc cgc gga ctc tac gat tcc cag   883
Lys Glu Leu Val Ile Asp Lys Ala Leu Arg Gly Leu Tyr Asp Ser Gln
                250                 255                 260

ctc atc gca cca gtt acc acc aca gat att tgg ctg gtc gca ccg ata   931
Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp Leu Val Ala Pro Ile
            265                 270                 275

att tcc ggc att ggc gtg gtg atc gcc ggc att atc gca caa ctc acc   979
Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile Ile Ala Gln Leu Thr
        280                 285                 290

ctg cgc ttc tac gtg agg aaa taagactatt gaactccttg ccg             1023
Leu Arg Phe Tyr Val Arg Lys
    295                 300
```

<210> 86
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 86

```
Met Ala Phe Gly Tyr Val Leu Arg Glu Ala Val Arg Gly Met Gly Arg
  1               5                  10                  15

Asn Val Thr Met Thr Ile Ala Leu Ile Ile Thr Thr Ser Ile Ser Leu
             20                  25                  30

Ala Leu Leu Ala Thr Gly Phe Leu Val Thr Asn Met Thr Asp Arg Thr
         35                  40                  45

Lys Asp Ile Tyr Leu Asp Arg Val Glu Val Met Ile Gln Leu Asp Glu
     50                  55                  60

Asp Thr Ser Ala Asn Asp Pro Glu Cys Thr Ala Glu Ser Cys Thr Glu
 65                  70                  75                  80

Val Arg Asp Val Leu Glu Gly Leu Asp Gly Ile Asp Ser Ile Thr Tyr
                 85                  90                  95

Arg Ser Arg Glu Ala Ser Tyr Glu Arg Phe Val Glu Val Phe Lys Asp
            100                 105                 110

Thr Asp Pro Val Leu Val Ala Glu Thr Ser Pro Asp Ala Leu Pro Ala
        115                 120                 125

Ala Phe His Val Arg Leu Glu Asp Pro Leu Ala Val Glu Ile Leu Asp
    130                 135                 140

Pro Val Arg Asp Leu Pro Gln Val Ser Asn Val Ile Asp Gln Val Asp
145                 150                 155                 160

Asp Leu Arg Gly Ala Thr Glu Asn Leu Asp Ser Ile Arg Asn Ala Thr
                165                 170                 175

Phe Leu Ile Ala Ala Val Gln Val Leu Ala Ser Ile Phe Leu Ile Ala
            180                 185                 190

Asn Met Val Gln Ile Ala Ala Phe Asn Arg Arg Glu Glu Thr Glu Ile
```

```
        195                 200                 205

Met Arg Ile Val Gly Ala Ser Arg Phe Tyr Thr Gln Gly Pro Phe Val
    210                 215                 220

Phe Glu Ala Ile Leu Ser Thr Leu Ile Gly Ala Val Phe Ala Val Gly
225                 230                 235                 240

Ala Leu Phe Leu Gly Lys Glu Leu Val Ile Asp Lys Ala Leu Arg Gly
                245                 250                 255

Leu Tyr Asp Ser Gln Leu Ile Ala Pro Val Thr Thr Thr Asp Ile Trp
            260                 265                 270

Leu Val Ala Pro Ile Ile Ser Gly Ile Gly Val Val Ile Ala Gly Ile
        275                 280                 285

Ile Ala Gln Leu Thr Leu Arg Phe Tyr Val Arg Lys
    290                 295                 300


<210> 87
<211> 810
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXA00010

<400> 87
cttaagaatt accggttatt tgtcgttgag ttctcctctg agcactcagg gtagtcactt 60

ccgtttcttt agccacagga gtttcgctaa agtgtgaccc gtg atc acc ttc gag   115
                                            Val Ile Thr Phe Glu
                                              1               5

aac gtc acc aag aac tac aag aca tca acc cgc cct gca tta gac aat   163
Asn Val Thr Lys Asn Tyr Lys Thr Ser Thr Arg Pro Ala Leu Asp Asn
                  10                  15                  20

gtg tcc cta cac att gaa aaa ggc gag ttc gtg ttc ctc atc ggc cca   211
Val Ser Leu His Ile Glu Lys Gly Glu Phe Val Phe Leu Ile Gly Pro
              25                  30                  35

tcc ggc tcc gga aaa tca acc ttc ctg cgc ctg atg acg cgg gag gaa   259
Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Leu Met Thr Arg Glu Glu
          40                  45                  50

aac gtc agc tcc gga tcg ctg aca ctg gct gat ttt cag gtg aac aaa   307
Asn Val Ser Ser Gly Ser Leu Thr Leu Ala Asp Phe Gln Val Asn Lys
      55                  60                  65

ctt cgc ggc acg caa gta aac aaa ctg cgc caa cgc atc gga tat gtg   355
Leu Arg Gly Thr Gln Val Asn Lys Leu Arg Gln Arg Ile Gly Tyr Val
  70                  75                  80                  85

ttc caa gat ttc cga ctc tta aaa aac aag aat gtc tac gac aac gtc   403
Phe Gln Asp Phe Arg Leu Leu Lys Asn Lys Asn Val Tyr Asp Asn Val
                  90                  95                 100
```

```
gca ttc gca ttg gag gtc atc ggg aag aag aag gac aag att caa gaa   451
Ala Phe Ala Leu Glu Val Ile Gly Lys Lys Lys Asp Lys Ile Gln Glu
            105                 110                 115

ctt gtc ccc gaa act ctg gaa atg gtt ggc ctt gcc gga aaa gcc aac   499
Leu Val Pro Glu Thr Leu Glu Met Val Gly Leu Ala Gly Lys Ala Asn
        120                 125                 130

cgc atg ccc aac gaa cta tcc ggt ggt gag cag cag cgc gtg gcc atc   547
Arg Met Pro Asn Glu Leu Ser Gly Gly Glu Gln Gln Arg Val Ala Ile
    135                 140                 145

gcc cga gct ttc gtg aac cgc cca ctc gtc ttg ctt gct gat gaa cca   595
Ala Arg Ala Phe Val Asn Arg Pro Leu Val Leu Leu Ala Asp Glu Pro
150                 155                 160                 165

acc ggc aac ctc gac ccc gat acc tcc gat gag atc atg att ttg ctc   643
Thr Gly Asn Leu Asp Pro Asp Thr Ser Asp Glu Ile Met Ile Leu Leu
                170                 175                 180

aac cgc atc aat cgc ctc ggc acc acg gtg gtc atg tcc acc cac aac   691
Asn Arg Ile Asn Arg Leu Gly Thr Thr Val Val Met Ser Thr His Asn
            185                 190                 195

gcc cga act gtc gac gac atg cgc agg cga gta atc gaa ctg caa ttg   739
Ala Arg Thr Val Asp Asp Met Arg Arg Arg Val Ile Glu Leu Gln Leu
        200                 205                 210

ggc aaa cta gtc cgc gat gat gcc cac ggc gtc tac ggc gaa atg cga   787
Gly Lys Leu Val Arg Asp Asp Ala His Gly Val Tyr Gly Glu Met Arg
    215                 220                 225

taggggagta cttcacatgg ctt                                        810
```

<210> 88
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 88

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Val Ile Thr Phe Glu Asn Val Thr Lys Asn Tyr Lys Thr Ser Thr Arg
  1               5                  10                  15

Pro Ala Leu Asp Asn Val Ser Leu His Ile Glu Lys Gly Glu Phe Val
             20                  25                  30

Phe Leu Ile Gly Pro Ser Gly Ser Gly Lys Ser Thr Phe Leu Arg Leu
         35                  40                  45

Met Thr Arg Glu Glu Asn Val Ser Ser Gly Ser Leu Thr Leu Ala Asp
     50                  55                  60

Phe Gln Val Asn Lys Leu Arg Gly Thr Gln Val Asn Lys Leu Arg Gln
 65                  70                  75                  80

Arg Ile Gly Tyr Val Phe Gln Asp Phe Arg Leu Leu Lys Asn Lys Asn
                 85                  90                  95

Val Tyr Asp Asn Val Ala Phe Ala Leu Glu Val Ile Gly Lys Lys Lys
```

```
            100                 105                 110

Asp Lys Ile Gln Glu Leu Val Pro Glu Thr Leu Glu Met Val Gly Leu
        115                 120                 125

Ala Gly Lys Ala Asn Arg Met Pro Asn Glu Leu Ser Gly Gly Glu Gln
    130                 135                 140

Gln Arg Val Ala Ile Ala Arg Ala Phe Val Asn Arg Pro Leu Val Leu
145                 150                 155                 160

Leu Ala Asp Glu Pro Thr Gly Asn Leu Asp Pro Asp Thr Ser Asp Glu
                165                 170                 175

Ile Met Ile Leu Leu Asn Arg Ile Asn Arg Leu Gly Thr Thr Val Val
            180                 185                 190

Met Ser Thr His Asn Ala Arg Thr Val Asp Asp Met Arg Arg Arg Val
        195                 200                 205

Ile Glu Leu Gln Leu Gly Lys Leu Val Arg Asp Asp Ala His Gly Val
    210                 215                 220

Tyr Gly Glu Met Arg
225
```

Sequence Listing

<210> 89
<211> 1605
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1582)
<223> RXA00143

<400> 89

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ggacacccgg tgtataccca ctgggacctc ataaatccac tgacttggag aagcccctgt 60

gagtctgacc acaagccatt ttattccttt tccccgagaa atg gtc tgg gat tgg   115
                                              Met Val Trp Asp Trp
                                                1               5

cat acc cgc aag ggc gct gtc gca cgt ctg act ccc cca ttc atc cca   163
His Thr Arg Lys Gly Ala Val Ala Arg Leu Thr Pro Pro Phe Ile Pro
                10                  15                  20

ctt aac ccc att acg cag gca gaa cgc ctc gcc gac ggc acc acc atc   211
Leu Asn Pro Ile Thr Gln Ala Glu Arg Leu Ala Asp Gly Thr Thr Ile
            25                  30                  35

ttc agt ctc ccc gcg gga ctt aaa tgg gtg gca cgc cac gat tta tcc   259
Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala Arg His Asp Leu Ser
        40                  45                  50

ggg ttt ttg aac ggg tca cgc ttc acc gac gtc tgc ctc acc gcc cct   307
Gly Phe Leu Asn Gly Ser Arg Phe Thr Asp Val Cys Leu Thr Ala Pro
    55                  60                  65

gtg aag gcc ctc gca aac tgg cgc cac gtg cat aat ttc gtc gac caa   355
```

```
Val Lys Ala Leu Ala Asn Trp Arg His Val His Asn Phe Val Asp Gln
 70                  75                  80                  85

gac ggc ggc aca ctc atc aca gat tcc gtg agc acc cgc cta ccg gca   403
Asp Gly Gly Thr Leu Ile Thr Asp Ser Val Ser Thr Arg Leu Pro Ala
                 90                  95                 100

tcc aca ctc acg ggc atg ttc gcc tat cgc caa act cag ctc atc gaa   451
Ser Thr Leu Thr Gly Met Phe Ala Tyr Arg Gln Thr Gln Leu Ile Glu
            105                 110                 115

gac cta aaa ttc tta agt aga aca agc acg ctt ttc gac ggc tcc ccc   499
Asp Leu Lys Phe Leu Ser Arg Thr Ser Thr Leu Phe Asp Gly Ser Pro
        120                 125                 130

ctc acc gta gcc atc acc ggc tcc agg ggg ctc gtc ggc cgc gcg ctg   547
Leu Thr Val Ala Ile Thr Gly Ser Arg Gly Leu Val Gly Arg Ala Leu
    135                 140                 145

aca gcg cag ctg caa acc ggc ggc cac gaa gtc atc caa ctc gtg cgc   595
Thr Ala Gln Leu Gln Thr Gly Gly His Glu Val Ile Gln Leu Val Arg
150                 155                 160                 165

aaa gaa ccc aaa cct ggc caa cgt ttc tgg gat cca ctc aac cca gca   643
Lys Glu Pro Lys Pro Gly Gln Arg Phe Trp Asp Pro Leu Asn Pro Ala
                170                 175                 180

tcc gat ctc ctc gac ggc gcg gat gtt ttg gtt cac ctt gcc ggc gaa   691
Ser Asp Leu Leu Asp Gly Ala Asp Val Leu Val His Leu Ala Gly Glu
            185                 190                 195

ccg atc ttc ggg cga ttc aac gac tcc cac aaa gaa gcc atc cgc gag   739
Pro Ile Phe Gly Arg Phe Asn Asp Ser His Lys Glu Ala Ile Arg Glu
        200                 205                 210

tcc cgc gta ctt ccc acc aaa ttc ctc gca gaa tta gtt gcc gaa tcc   787
Ser Arg Val Leu Pro Thr Lys Phe Leu Ala Glu Leu Val Ala Glu Ser
    215                 220                 225

acc cag tgc acc acc atg att tcc gcc tct gca gtt gga ttc tat ggt   835
Thr Gln Cys Thr Thr Met Ile Ser Ala Ser Ala Val Gly Phe Tyr Gly
230                 235                 240                 245

cac gac cgc ggc gac gag atc ctg acc gaa gaa tcc gaa tcc ggc gat   883
His Asp Arg Gly Asp Glu Ile Leu Thr Glu Glu Ser Glu Ser Gly Asp
                250                 255                 260

gat ttc ctc gcc gag gtc tgt agg gat tgg gaa cac gcc act gct cct   931
Asp Phe Leu Ala Glu Val Cys Arg Asp Trp Glu His Ala Thr Ala Pro
            265                 270                 275

gcc tca gat gca gga aag cgc gta gcc ttc att cgc acc ggc gtg gcc   979
Ala Ser Asp Ala Gly Lys Arg Val Ala Phe Ile Arg Thr Gly Val Ala
        280                 285                 290

ctc agt gga cgc ggt ggc atg ctt ccc ctg ctg aaa acc ctg ttc tcc   1027
Leu Ser Gly Arg Gly Gly Met Leu Pro Leu Leu Lys Thr Leu Phe Ser
    295                 300                 305

acc gga cta ggc gga aaa ttc ggc gat ggc acc tcc tgg ttc agc tgg   1075
Thr Gly Leu Gly Gly Lys Phe Gly Asp Gly Thr Ser Trp Phe Ser Trp
```

```
310                 315                 320                 325

atc gcc atc gat gac ctc acc gac atc tac tac cgc gcc atc gtg gac   1123
Ile Ala Ile Asp Asp Leu Thr Asp Ile Tyr Tyr Arg Ala Ile Val Asp
                330                 335                 340

gcc cag atc tcc ggc ccc atc aac gcg gta gcc ccc aat cca gtc tcc   1171
Ala Gln Ile Ser Gly Pro Ile Asn Ala Val Ala Pro Asn Pro Val Ser
            345                 350                 355

aat gcg gac atg acc aag att ctg gcc acc agc atg cac cgt ccc gca   1219
Asn Ala Asp Met Thr Lys Ile Leu Ala Thr Ser Met His Arg Pro Ala
        360                 365                 370

ttc atc caa att cct tcc ctc ggc ccc aaa att ctg ctc gga agc caa   1267
Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile Leu Leu Gly Ser Gln
    375                 380                 385

ggc gct gaa gag cta gcc ctg gcg tcc caa cgc acc gcc cca gca gca   1315
Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg Thr Ala Pro Ala Ala
390                 395                 400                 405

ctg gaa aac ctc agc cac acc ttc cgc tac acc gac atc ggg gcc gcc   1363
Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr Asp Ile Gly Ala Ala
                410                 415                 420

atc gca cac gaa ctt ggc tac gaa caa ctc gca gat ttc gcc caa cag   1411
Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala Asp Phe Ala Gln Gln
            425                 430                 435

caa gaa atc gaa gcc gaa cgc aaa cag gaa cga gcc gaa ctc aaa gcc   1459
Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg Ala Glu Leu Lys Ala
        440                 445                 450

gcc aag aag atc gcc aag aaa gcc cca gtc cta gag gaa tcc ccc acc   1507
Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu Glu Glu Ser Pro Thr
    455                 460                 465

aac ctg gaa gat ccc gaa gaa gta gag caa agt atc ctt tca tca atc   1555
Asn Leu Glu Asp Pro Glu Glu Val Glu Gln Ser Ile Leu Ser Ser Ile
470                 475                 480                 485

ctc aat ttc cgc cgt aag cgc aac gac taaaaccacc atctgtagtg         1602
Leu Asn Phe Arg Arg Lys Arg Asn Asp
                490

tgg                                                              1605
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<210> 90
<211> 494
<212> PRT
<213> Corynebacterium glutamicum

<400> 90

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Met Val Trp Asp Trp His Thr Arg Lys Gly Ala Val Ala Arg Leu Thr
  1               5                  10                  15

Pro Pro Phe Ile Pro Leu Asn Pro Ile Thr Gln Ala Glu Arg Leu Ala
             20                  25                  30
```

```
Asp Gly Thr Thr Ile Phe Ser Leu Pro Ala Gly Leu Lys Trp Val Ala
         35                  40                  45

Arg His Asp Leu Ser Gly Phe Leu Asn Gly Ser Arg Phe Thr Asp Val
     50                  55                  60

Cys Leu Thr Ala Pro Val Lys Ala Leu Ala Asn Trp Arg His Val His
 65                  70                  75                  80

Asn Phe Val Asp Gln Asp Gly Gly Thr Leu Ile Thr Asp Ser Val Ser
                 85                  90                  95

Thr Arg Leu Pro Ala Ser Thr Leu Thr Gly Met Phe Ala Tyr Arg Gln
            100                 105                 110

Thr Gln Leu Ile Glu Asp Leu Lys Phe Leu Ser Arg Thr Ser Thr Leu
        115                 120                 125

Phe Asp Gly Ser Pro Leu Thr Val Ala Ile Thr Gly Ser Arg Gly Leu
    130                 135                 140

Val Gly Arg Ala Leu Thr Ala Gln Leu Gln Thr Gly Gly His Glu Val
145                 150                 155                 160

Ile Gln Leu Val Arg Lys Glu Pro Lys Pro Gly Gln Arg Phe Trp Asp
                165                 170                 175

Pro Leu Asn Pro Ala Ser Asp Leu Leu Asp Gly Ala Asp Val Leu Val
            180                 185                 190

His Leu Ala Gly Glu Pro Ile Phe Gly Arg Phe Asn Asp Ser His Lys
        195                 200                 205

Glu Ala Ile Arg Glu Ser Arg Val Leu Pro Thr Lys Phe Leu Ala Glu
    210                 215                 220

Leu Val Ala Glu Ser Thr Gln Cys Thr Thr Met Ile Ser Ala Ser Ala
225                 230                 235                 240

Val Gly Phe Tyr Gly His Asp Arg Gly Asp Glu Ile Leu Thr Glu Glu
                245                 250                 255

Ser Glu Ser Gly Asp Asp Phe Leu Ala Glu Val Cys Arg Asp Trp Glu
            260                 265                 270

His Ala Thr Ala Pro Ala Ser Asp Ala Gly Lys Arg Val Ala Phe Ile
        275                 280                 285

Arg Thr Gly Val Ala Leu Ser Gly Arg Gly Gly Met Leu Pro Leu Leu
    290                 295                 300

Lys Thr Leu Phe Ser Thr Gly Leu Gly Gly Lys Phe Gly Asp Gly Thr
305                 310                 315                 320

Ser Trp Phe Ser Trp Ile Ala Ile Asp Asp Leu Thr Asp Ile Tyr Tyr
                325                 330                 335

Arg Ala Ile Val Asp Ala Gln Ile Ser Gly Pro Ile Asn Ala Val Ala
            340                 345                 350

Pro Asn Pro Val Ser Asn Ala Asp Met Thr Lys Ile Leu Ala Thr Ser
```

```
        355                 360                 365

Met His Arg Pro Ala Phe Ile Gln Ile Pro Ser Leu Gly Pro Lys Ile
    370                 375                 380

Leu Leu Gly Ser Gln Gly Ala Glu Glu Leu Ala Leu Ala Ser Gln Arg
385                 390                 395                 400

Thr Ala Pro Ala Ala Leu Glu Asn Leu Ser His Thr Phe Arg Tyr Thr
                405                 410                 415

Asp Ile Gly Ala Ala Ile Ala His Glu Leu Gly Tyr Glu Gln Leu Ala
            420                 425                 430

Asp Phe Ala Gln Gln Gln Glu Ile Glu Ala Glu Arg Lys Gln Glu Arg
        435                 440                 445

Ala Glu Leu Lys Ala Ala Lys Lys Ile Ala Lys Lys Ala Pro Val Leu
    450                 455                 460

Glu Glu Ser Pro Thr Asn Leu Glu Asp Pro Glu Glu Val Glu Gln Ser
465                 470                 475                 480

Ile Leu Ser Ser Ile Leu Asn Phe Arg Arg Lys Arg Asn Asp
                485                 490
```

Sequence Listing

<210> 91
<211> 1684
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1684)
<223> RXA00277

<400> 91

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atgtggtgga caatgttcga cgattggttc ggaccttatc tctggtccta cggtccacca 60

cagctgcagt acatgccaga ggaagaaggg acagaaaacg atg aag gat aat gaa   115
                                            Met Lys Asp Asn Glu
                                              1               5

gat ttc gat cca gat tca cca gca acc gaa gct gtt gcc ttc aac cct   163
Asp Phe Asp Pro Asp Ser Pro Ala Thr Glu Ala Val Ala Phe Asn Pro
                 10                  15                  20

ttc gac gat gac gat gag gat gat tcc ccc gct acc tca gcc gtt gcc   211
Phe Asp Asp Asp Asp Glu Asp Asp Ser Pro Ala Thr Ser Ala Val Ala
             25                  30                  35

ttt aac cct ttt gaa gat gac gat gac gac gat gag ttc caa ggc gaa   259
Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp Glu Phe Gln Gly Glu
         40                  45                  50

ggc cta gaa ttc ctg ctg cgc gac ctc gac aat ctg cga gcc acc caa   307
Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn Leu Arg Ala Thr Gln
     55                  60                  65

ggt caa atg gtg gtg gaa caa cca gca gtt gaa gac agc ctc ggg tca   355
```

```
Gly Gln Met Val Val Glu Gln Pro Ala Val Glu Asp Ser Leu Gly Ser
 70                  75                  80                  85

gca tct gcg cat acg gag aca act gcg gcc tca ctg cgt ccc cgc cca   403
Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser Leu Arg Pro Arg Pro
                90                  95                 100

gag gtg gat cca agt gag agg agt cgt cga caa gca att tcg ctg ttc   451
Glu Val Asp Pro Ser Glu Arg Ser Arg Arg Gln Ala Ile Ser Leu Phe
            105                 110                 115

cgc gaa cgg cgc cgc gta agg cgc caa tcc cgc cca gtt gct gat ggc   499
Arg Glu Arg Arg Arg Val Arg Arg Gln Ser Arg Pro Val Ala Asp Gly
        120                 125                 130

atg gtg gaa ttg ccg ttc atc acc ccc aaa ccg gaa gat gag ctg ctc   547
Met Val Glu Leu Pro Phe Ile Thr Pro Lys Pro Glu Asp Glu Leu Leu
    135                 140                 145

atc gac ccg gaa aag aag cgc aaa cct ggt gtg gca gcg ccg caa ctt   595
Ile Asp Pro Glu Lys Lys Arg Lys Pro Gly Val Ala Ala Pro Gln Leu
150                 155                 160                 165

gtc gcg ggc gat atc gtc gca gag caa tat gaa gtc ctc ggc gtc atc   643
Val Ala Gly Asp Ile Val Ala Glu Gln Tyr Glu Val Leu Gly Val Ile
                170                 175                 180

gcg cac ggc ggc atg ggt tgg att tac ctc gcc aac gac cgc aat gtg   691
Ala His Gly Gly Met Gly Trp Ile Tyr Leu Ala Asn Asp Arg Asn Val
            185                 190                 195

tcc ggc cgc atc gtg gtg ctc aaa ggc atg atg gcg caa tct tcc gtt   739
Ser Gly Arg Ile Val Val Leu Lys Gly Met Met Ala Gln Ser Ser Val
        200                 205                 210

caa gac caa ggc acc gct gaa gcc gaa cgc gaa ttc ctc gcc gac atc   787
Gln Asp Gln Gly Thr Ala Glu Ala Glu Arg Glu Phe Leu Ala Asp Ile
    215                 220                 225

acc cac ccc ggc atc gtg aag gcc tac aac ttc atc gac gac ccc cgc   835
Thr His Pro Gly Ile Val Lys Ala Tyr Asn Phe Ile Asp Asp Pro Arg
230                 235                 240                 245

gtc ccc ggc gga ttc atc gtc atg gaa tac gtc aac ggc ccc tcc ctg   883
Val Pro Gly Gly Phe Ile Val Met Glu Tyr Val Asn Gly Pro Ser Leu
                250                 255                 260

aaa gac cgc tgc aaa gcc caa ccc gac ggc gtg ctc cgc gtc gac ctc   931
Lys Asp Arg Cys Lys Ala Gln Pro Asp Gly Val Leu Arg Val Asp Leu
            265                 270                 275

gcc atc ggc tac atc ctc gaa ctc ctc ccc gcc atg gac tac ctg cac   979
Ala Ile Gly Tyr Ile Leu Glu Leu Leu Pro Ala Met Asp Tyr Leu His
        280                 285                 290

caa cgc ggc gta gtg tac aac gac ctc aaa ccc gaa aac gtc atc gcc   1027
Gln Arg Gly Val Val Tyr Asn Asp Leu Lys Pro Glu Asn Val Ile Ala
    295                 300                 305

acc gaa gac caa gtt aaa ctc atc gac ctc ggc gcg gtt acc ggc atc   1075
Thr Glu Asp Gln Val Lys Leu Ile Asp Leu Gly Ala Val Thr Gly Ile
```

```
310                 315                 320                 325

ggc gca ttc ggc tac att tac ggc acc aaa gga ttc caa gca ccc gaa   1123
Gly Ala Phe Gly Tyr Ile Tyr Gly Thr Lys Gly Phe Gln Ala Pro Glu
                330                 335                 340

gta gcc acc cat ggc ccc tca atc tcc tcc gat att ttc acc atc gga   1171
Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp Ile Phe Thr Ile Gly
            345                 350                 355

cgc acc ctc gca gca ctc acc atg ccc ctc ccc gtt gaa gac ggt gtc   1219
Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro Val Glu Asp Gly Val
        360                 365                 370

ctc gca ccg ggc atc ccc tcg ccc aaa aat tca cct ctt ctg cgc agg   1267
Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser Pro Leu Leu Arg Arg
    375                 380                 385

cat ttg tcg ttc tac cgc ctc ctg caa cgc gcc acc gcc gac gac ccc   1315
His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala Thr Ala Asp Asp Pro
390                 395                 400                 405

caa cac cga ttc cgc aac gtc agc gaa cta cgc acc caa ctc tac ggc   1363
Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg Thr Gln Leu Tyr Gly
                410                 415                 420

gta ctg cgt gaa att ttg gca gtc cgc gac ggc aaa caa tac ccg cca   1411
Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly Lys Gln Tyr Pro Pro
            425                 430                 435

cag cac tca cta ttc tcc cca cag cga agc acc ttt ggc acc aaa cac   1459
Gln His Ser Leu Phe Ser Pro Gln Arg Ser Thr Phe Gly Thr Lys His
        440                 445                 450

ctc gtg ttc cgc acc gac cgc atc atc gac ggc atc gaa cga caa gca   1507
Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly Ile Glu Arg Gln Ala
    455                 460                 465

cgc atc aca gca cca gaa att gtc tcc gcg ctg cct gtc cca ctc atc   1555
Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu Pro Val Pro Leu Ile
470                 475                 480                 485

gac cgc acc gac ccc ggc gcc cgt atg ctc tcc gga tcc tcc tat gca   1603
Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser Gly Ser Ser Tyr Ala
                490                 495                 500

gaa ccc tcc gaa acc ctg gaa act ctg cgc aac tcc atg gaa gac gag   1651
Glu Pro Ser Glu Thr Leu Glu Thr Leu Arg Asn Ser Met Glu Asp Glu
            505                 510                 515

caa tac cgc caa tca atc gag atc ccc ctc ggt                      1684
Gln Tyr Arg Gln Ser Ile Glu Ile Pro Leu Gly
        520                 525
```

<210> 92
<211> 528
<212> PRT
<213> Corynebacterium glutamicum

<400> 92

```
Met Lys Asp Asn Glu Asp Phe Asp Pro Asp Ser Pro Ala Thr Glu Ala
  1               5                  10                  15

Val Ala Phe Asn Pro Phe Asp Asp Asp Asp Glu Asp Asp Ser Pro Ala
             20                  25                  30

Thr Ser Ala Val Ala Phe Asn Pro Phe Glu Asp Asp Asp Asp Asp Asp
         35                  40                  45

Glu Phe Gln Gly Glu Gly Leu Glu Phe Leu Leu Arg Asp Leu Asp Asn
     50                  55                  60

Leu Arg Ala Thr Gln Gly Gln Met Val Val Glu Gln Pro Ala Val Glu
 65                  70                  75                  80

Asp Ser Leu Gly Ser Ala Ser Ala His Thr Glu Thr Thr Ala Ala Ser
                 85                  90                  95

Leu Arg Pro Arg Pro Glu Val Asp Pro Ser Glu Arg Ser Arg Arg Gln
            100                 105                 110

Ala Ile Ser Leu Phe Arg Glu Arg Arg Arg Val Arg Arg Gln Ser Arg
        115                 120                 125

Pro Val Ala Asp Gly Met Val Glu Leu Pro Phe Ile Thr Pro Lys Pro
    130                 135                 140

Glu Asp Glu Leu Leu Ile Asp Pro Glu Lys Lys Arg Lys Pro Gly Val
145                 150                 155                 160

Ala Ala Pro Gln Leu Val Ala Gly Asp Ile Val Ala Glu Gln Tyr Glu
                165                 170                 175

Val Leu Gly Val Ile Ala His Gly Gly Met Gly Trp Ile Tyr Leu Ala
            180                 185                 190

Asn Asp Arg Asn Val Ser Gly Arg Ile Val Val Leu Lys Gly Met Met
        195                 200                 205

Ala Gln Ser Ser Val Gln Asp Gln Gly Thr Ala Glu Ala Glu Arg Glu
    210                 215                 220

Phe Leu Ala Asp Ile Thr His Pro Gly Ile Val Lys Ala Tyr Asn Phe
225                 230                 235                 240

Ile Asp Asp Pro Arg Val Pro Gly Gly Phe Ile Val Met Glu Tyr Val
                245                 250                 255

Asn Gly Pro Ser Leu Lys Asp Arg Cys Lys Ala Gln Pro Asp Gly Val
            260                 265                 270

Leu Arg Val Asp Leu Ala Ile Gly Tyr Ile Leu Glu Leu Leu Pro Ala
        275                 280                 285

Met Asp Tyr Leu His Gln Arg Gly Val Val Tyr Asn Asp Leu Lys Pro
    290                 295                 300

Glu Asn Val Ile Ala Thr Glu Asp Gln Val Lys Leu Ile Asp Leu Gly
305                 310                 315                 320

Ala Val Thr Gly Ile Gly Ala Phe Gly Tyr Ile Tyr Gly Thr Lys Gly
```

```
                325                 330                 335

Phe Gln Ala Pro Glu Val Ala Thr His Gly Pro Ser Ile Ser Ser Asp
            340                 345                 350

Ile Phe Thr Ile Gly Arg Thr Leu Ala Ala Leu Thr Met Pro Leu Pro
        355                 360                 365

Val Glu Asp Gly Val Leu Ala Pro Gly Ile Pro Ser Pro Lys Asn Ser
    370                 375                 380

Pro Leu Leu Arg Arg His Leu Ser Phe Tyr Arg Leu Leu Gln Arg Ala
385                 390                 395                 400

Thr Ala Asp Asp Pro Gln His Arg Phe Arg Asn Val Ser Glu Leu Arg
                405                 410                 415

Thr Gln Leu Tyr Gly Val Leu Arg Glu Ile Leu Ala Val Arg Asp Gly
            420                 425                 430

Lys Gln Tyr Pro Pro Gln His Ser Leu Phe Ser Pro Gln Arg Ser Thr
        435                 440                 445

Phe Gly Thr Lys His Leu Val Phe Arg Thr Asp Arg Ile Ile Asp Gly
    450                 455                 460

Ile Glu Arg Gln Ala Arg Ile Thr Ala Pro Glu Ile Val Ser Ala Leu
465                 470                 475                 480

Pro Val Pro Leu Ile Asp Arg Thr Asp Pro Gly Ala Arg Met Leu Ser
                485                 490                 495

Gly Ser Ser Tyr Ala Glu Pro Ser Glu Thr Leu Glu Thr Leu Arg Asn
            500                 505                 510

Ser Met Glu Asp Glu Gln Tyr Arg Gln Ser Ile Glu Ile Pro Leu Gly
        515                 520                 525
```

<210> 93
<211> 1313
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1290)
<223> RXA00857

<400> 93

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gca gtc ggt att gag gtg cca aac tct gac cgt gag atg gtt cgc ctg   48
Ala Val Gly Ile Glu Val Pro Asn Ser Asp Arg Glu Met Val Arg Leu
  1               5                  10                  15

ggt gat gtg ctc aat gcg cgt gcc acc gtg gaa aac aaa gac tcc atg   96
Gly Asp Val Leu Asn Ala Arg Ala Thr Val Glu Asn Lys Asp Ser Met
             20                  25                  30
```

```
ctc att ggt ttg ggt aag gat att gaa ggc gac ttc gtg tcc tac tcc   144
Leu Ile Gly Leu Gly Lys Asp Ile Glu Gly Asp Phe Val Ser Tyr Ser
         35                  40                  45

gtg cag aaa atg cct cac ctt ctt gtg gct ggt tcc acc ggt tct ggt   192
Val Gln Lys Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly
     50                  55                  60

aag tcg gcg ttc gtg aac tcg ctg ctg gtg tca ctg ctc acg cgt gca   240
Lys Ser Ala Phe Val Asn Ser Leu Leu Val Ser Leu Leu Thr Arg Ala
 65                  70                  75                  80

aag cca gaa gaa gtc cgt ctg att ctg gtg gac cca aag atg gtg gaa   288
Lys Pro Glu Glu Val Arg Leu Ile Leu Val Asp Pro Lys Met Val Glu
                 85                  90                  95

ctc aca cca tac gag ggc att cca cac ctg att acg ccg atc att acc   336
Leu Thr Pro Tyr Glu Gly Ile Pro His Leu Ile Thr Pro Ile Ile Thr
            100                 105                 110

caa cca aag aag gcc gcg gca gca ctg cag tgg ctg gtt gag gaa atg   384
Gln Pro Lys Lys Ala Ala Ala Ala Leu Gln Trp Leu Val Glu Glu Met
        115                 120                 125

gaa cag cgc tac atg gac atg aaa caa acc cgt gtg cgc cac atc aag   432
Glu Gln Arg Tyr Met Asp Met Lys Gln Thr Arg Val Arg His Ile Lys
    130                 135                 140

gac ttc aac cgc aag att aaa tct ggc gaa att gag acc cct cca gga   480
Asp Phe Asn Arg Lys Ile Lys Ser Gly Glu Ile Glu Thr Pro Pro Gly
145                 150                 155                 160

tcc aag cgc gaa tac cgt gcg tac cca tac atc gtg tgt gtg gtc gac   528
Ser Lys Arg Glu Tyr Arg Ala Tyr Pro Tyr Ile Val Cys Val Val Asp
                165                 170                 175

gag ctc gct gac ctg atg atg acc gca ccg aag gaa atc gaa gag tcc   576
Glu Leu Ala Asp Leu Met Met Thr Ala Pro Lys Glu Ile Glu Glu Ser
            180                 185                 190

atc gtg cgc atc acc cag aag gca cgt gcc gcc ggt atc cac ctc gtg   624
Ile Val Arg Ile Thr Gln Lys Ala Arg Ala Ala Gly Ile His Leu Val
        195                 200                 205

ctg gca acg cag cgc cca tcc gtg gac gtt gtg acc ggt ctg atc aag   672
Leu Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys
    210                 215                 220

acc aac gtt cct tca cgt ttg gct ttc gca acc tca tcg cta act gac   720
Thr Asn Val Pro Ser Arg Leu Ala Phe Ala Thr Ser Ser Leu Thr Asp
225                 230                 235                 240

tcc cgc gtt att ttg gac cag ggt ggc gct gaa aag ctg atc ggc atg   768
Ser Arg Val Ile Leu Asp Gln Gly Gly Ala Glu Lys Leu Ile Gly Met
                245                 250                 255

ggc gac gcg ctg ttc atc cca cag ggt gcc ggc aag cca caa cgt atc   816
Gly Asp Ala Leu Phe Ile Pro Gln Gly Ala Gly Lys Pro Gln Arg Ile
            260                 265                 270

cag ggt gcc ttt gtc acc gat gaa gaa atc caa gcg gtc gtg gac atg   864
```

```
Gln Gly Ala Phe Val Thr Asp Glu Glu Ile Gln Ala Val Val Asp Met
        275                 280                 285

gcc aag gct cag cgc cag cct gaa tac acc gac ggt gtc acc gaa gat   912
Ala Lys Ala Gln Arg Gln Pro Glu Tyr Thr Asp Gly Val Thr Glu Asp
    290                 295                 300

aag gct tcc gaa gct aag aag atc gat gcc gat atc gga aac gat ctg   960
Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
305                 310                 315                 320

gaa gat ctc ctc gaa gca gtc gaa ctc gtg gtg acc tca caa atg gga   1008
Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
                325                 330                 335

tcc acc tcc atg ctg cag cgc aaa ctg cgc atc ggt ttt gcc aag gcc   1056
Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
            340                 345                 350

gga cgc ctc atg gac ctc atg gaa acc cgc ggt gtg gtg ggc cca tcc   1104
Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
        355                 360                 365

gaa ggc tct aag gct cgt gaa gtt ttg gtc aag cca gaa gag ctg gaa   1152
Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
    370                 375                 380

acc att ttg tgg atg ctt aaa ggt gca gac ccc gcc gac gca ccg aag   1200
Thr Ile Leu Trp Met Leu Lys Gly Ala Asp Pro Ala Asp Ala Pro Lys
385                 390                 395                 400

gaa gag acc tgg gat gac gag gtg gca gcg gaa gct gaa gaa gcg gct   1248
Glu Glu Thr Trp Asp Asp Glu Val Ala Ala Glu Ala Glu Glu Ala Ala
                405                 410                 415

aac acc acc gtc gtg cag gct gat cct tcc aag gga gtg tgt           1290
Asn Thr Thr Val Val Gln Ala Asp Pro Ser Lys Gly Val Cys
            420                 425                 430

taaggcttta ggagcctagt ggc                                        1313


<210> 94
<211> 430
<212> PRT
<213> Corynebacterium glutamicum

<400> 94
Ala Val Gly Ile Glu Val Pro Asn Ser Asp Arg Glu Met Val Arg Leu
  1               5                  10                  15

Gly Asp Val Leu Asn Ala Arg Ala Thr Val Glu Asn Lys Asp Ser Met
             20                  25                  30

Leu Ile Gly Leu Gly Lys Asp Ile Glu Gly Asp Phe Val Ser Tyr Ser
         35                  40                  45

Val Gln Lys Met Pro His Leu Leu Val Ala Gly Ser Thr Gly Ser Gly
     50                  55                  60

Lys Ser Ala Phe Val Asn Ser Leu Leu Val Ser Leu Leu Thr Arg Ala
```

```
 65                  70                  75                  80

Lys Pro Glu Glu Val Arg Leu Ile Leu Val Asp Pro Lys Met Val Glu
                 85                  90                  95

Leu Thr Pro Tyr Glu Gly Ile Pro His Leu Ile Thr Pro Ile Ile Thr
            100                 105                 110

Gln Pro Lys Lys Ala Ala Ala Ala Leu Gln Trp Leu Val Glu Glu Met
        115                 120                 125

Glu Gln Arg Tyr Met Asp Met Lys Gln Thr Arg Val Arg His Ile Lys
    130                 135                 140

Asp Phe Asn Arg Lys Ile Lys Ser Gly Glu Ile Glu Thr Pro Pro Gly
145                 150                 155                 160

Ser Lys Arg Glu Tyr Arg Ala Tyr Pro Tyr Ile Val Cys Val Val Asp
                165                 170                 175

Glu Leu Ala Asp Leu Met Met Thr Ala Pro Lys Glu Ile Glu Glu Ser
            180                 185                 190

Ile Val Arg Ile Thr Gln Lys Ala Arg Ala Ala Gly Ile His Leu Val
        195                 200                 205

Leu Ala Thr Gln Arg Pro Ser Val Asp Val Val Thr Gly Leu Ile Lys
    210                 215                 220

Thr Asn Val Pro Ser Arg Leu Ala Phe Ala Thr Ser Ser Leu Thr Asp
225                 230                 235                 240

Ser Arg Val Ile Leu Asp Gln Gly Gly Ala Glu Lys Leu Ile Gly Met
                245                 250                 255

Gly Asp Ala Leu Phe Ile Pro Gln Gly Ala Gly Lys Pro Gln Arg Ile
            260                 265                 270

Gln Gly Ala Phe Val Thr Asp Glu Glu Ile Gln Ala Val Val Asp Met
        275                 280                 285

Ala Lys Ala Gln Arg Gln Pro Glu Tyr Thr Asp Gly Val Thr Glu Asp
    290                 295                 300

Lys Ala Ser Glu Ala Lys Lys Ile Asp Ala Asp Ile Gly Asn Asp Leu
305                 310                 315                 320

Glu Asp Leu Leu Glu Ala Val Glu Leu Val Val Thr Ser Gln Met Gly
                325                 330                 335

Ser Thr Ser Met Leu Gln Arg Lys Leu Arg Ile Gly Phe Ala Lys Ala
            340                 345                 350

Gly Arg Leu Met Asp Leu Met Glu Thr Arg Gly Val Val Gly Pro Ser
        355                 360                 365

Glu Gly Ser Lys Ala Arg Glu Val Leu Val Lys Pro Glu Glu Leu Glu
    370                 375                 380

Thr Ile Leu Trp Met Leu Lys Gly Ala Asp Pro Ala Asp Ala Pro Lys
385                 390                 395                 400
```

```
Glu Glu Thr Trp Asp Asp Glu Val Ala Ala Glu Ala Glu Glu Ala Ala
                405                 410                 415

Asn Thr Thr Val Val Gln Ala Asp Pro Ser Lys Gly Val Cys
            420                 425                 430


<210> 95
<211> 893
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(870)
<223> RXA01435

<400> 95
cct ctt gac cta ggc ttt acc acc gaa gca cgc caa tgg ctc gaa acc   48
Pro Leu Asp Leu Gly Phe Thr Thr Glu Ala Arg Gln Trp Leu Glu Thr
  1               5                  10                  15

cta gag gga cgc atc ggc gac gac tgg cga cac aaa tgg ttc tcc gga   96
Leu Glu Gly Arg Ile Gly Asp Asp Trp Arg His Lys Trp Phe Ser Gly
             20                  25                  30

atc acc tac ctc ctc ctc gac gac tac gcc acc gcc caa gta ttc ttc  144
Ile Thr Tyr Leu Leu Leu Asp Asp Tyr Ala Thr Ala Gln Val Phe Phe
         35                  40                  45

aac cac gtc ctg acc atc ctg ccc ggc gaa gcc gct cct aaa cta gcc  192
Asn His Val Leu Thr Ile Leu Pro Gly Glu Ala Ala Pro Lys Leu Ala
     50                  55                  60

ctc gca gct gtt gac gaa ctc atc ctc caa caa atc ggc gcc gaa tcc  240
Leu Ala Ala Val Asp Glu Leu Ile Leu Gln Gln Ile Gly Ala Glu Ser
 65                  70                  75                  80

acc gcc tat ctc acc cca gac atc gtc tct gca acc gcg acc ctc agc  288
Thr Ala Tyr Leu Thr Pro Asp Ile Val Ser Ala Thr Ala Thr Leu Ser
                 85                  90                  95

aaa gat ttc gaa gac ctc gac gcc tcc gcc ttc gaa tca ctc agc gac  336
Lys Asp Phe Glu Asp Leu Asp Ala Ser Ala Phe Glu Ser Leu Ser Asp
            100                 105                 110

acc tgg tcc cac atc tcc agc gac cca cac gta gtc cgc ttc cat tca  384
Thr Trp Ser His Ile Ser Ser Asp Pro His Val Val Arg Phe His Ser
        115                 120                 125

ctg cgc ctc tac gca ctt gtc tgg gca acc aac ccc acc acc gtg tcc  432
Leu Arg Leu Tyr Ala Leu Val Trp Ala Thr Asn Pro Thr Thr Val Ser
    130                 135                 140

tcc gcg ttc ggg ctc gcc cgc caa ctc atg gcc gaa aac caa atc gaa  480
Ser Ala Phe Gly Leu Ala Arg Gln Leu Met Ala Glu Asn Gln Ile Glu
145                 150                 155                 160

ctc gca gtc caa gcc cta gac aaa ctc ccc caa tca tcc acc cac tac  528
Leu Ala Val Gln Ala Leu Asp Lys Leu Pro Gln Ser Ser Thr His Tyr
```

```
                165                 170                 175

cga atg gcc acc ctc acc acc atc ttg ttg ctg gtc agc tcc aat ttg   576
Arg Met Ala Thr Leu Thr Thr Ile Leu Leu Leu Val Ser Ser Asn Leu
            180                 185                 190

agt gaa tcc cgc atc cga cgg gct gcc cgc cga ctc acc gaa atc ccc   624
Ser Glu Ser Arg Ile Arg Arg Ala Ala Arg Arg Leu Thr Glu Ile Pro
        195                 200                 205

aca aac gaa ccc cgc ttc aac caa atc aaa att gcc atc atg tcg gca   672
Thr Asn Glu Pro Arg Phe Asn Gln Ile Lys Ile Ala Ile Met Ser Ala
    210                 215                 220

ggc ctc agc tgg ctt cga gag cga aaa ctc aaa gct tcc gcc tcc gcg   720
Gly Leu Ser Trp Leu Arg Glu Arg Lys Leu Lys Ala Ser Ala Ser Ala
225                 230                 235                 240

aac cct ttg ttt gaa tac ccg ttc tcc caa aaa ggc ctg cgc acc ggc   768
Asn Pro Leu Phe Glu Tyr Pro Phe Ser Gln Lys Gly Leu Arg Thr Gly
                245                 250                 255

atc tcc gag gca ctc cgc att cag gca cgt tct gca ccg ttc ccg cac   816
Ile Ser Glu Ala Leu Arg Ile Gln Ala Arg Ser Ala Pro Phe Pro His
            260                 265                 270

cac cgt tac gca ctt gtg gat atg gcg aat gcc gtg cgg cca ctg agt   864
His Arg Tyr Ala Leu Val Asp Met Ala Asn Ala Val Arg Pro Leu Ser
        275                 280                 285

tgg ttc tagctgtttt gacttggggc tat                                893
Trp Phe
    290
```

Sequence Listing

<210> 96
<211> 290
<212> PRT
<213> Corynebacterium glutamicum

<400> 96

```
Pro Leu Asp Leu Gly Phe Thr Thr Glu Ala Arg Gln Trp Leu Glu Thr
  1               5                  10                  15

Leu Glu Gly Arg Ile Gly Asp Asp Trp Arg His Lys Trp Phe Ser Gly
             20                  25                  30

Ile Thr Tyr Leu Leu Leu Asp Asp Tyr Ala Thr Ala Gln Val Phe Phe
         35                  40                  45

Asn His Val Leu Thr Ile Leu Pro Gly Glu Ala Ala Pro Lys Leu Ala
     50                  55                  60

Leu Ala Ala Val Asp Glu Leu Ile Leu Gln Gln Ile Gly Ala Glu Ser
 65                  70                  75                  80

Thr Ala Tyr Leu Thr Pro Asp Ile Val Ser Ala Thr Ala Thr Leu Ser
                 85                  90                  95

Lys Asp Phe Glu Asp Leu Asp Ala Ser Ala Phe Glu Ser Leu Ser Asp
            100                 105                 110
```

```
Thr Trp Ser His Ile Ser Ser Asp Pro His Val Val Arg Phe His Ser
        115                 120                 125

Leu Arg Leu Tyr Ala Leu Val Trp Ala Thr Asn Pro Thr Thr Val Ser
    130                 135                 140

Ser Ala Phe Gly Leu Ala Arg Gln Leu Met Ala Glu Asn Gln Ile Glu
145                 150                 155                 160

Leu Ala Val Gln Ala Leu Asp Lys Leu Pro Gln Ser Ser Thr His Tyr
                165                 170                 175

Arg Met Ala Thr Leu Thr Thr Ile Leu Leu Leu Val Ser Ser Asn Leu
            180                 185                 190

Ser Glu Ser Arg Ile Arg Arg Ala Ala Arg Arg Leu Thr Glu Ile Pro
        195                 200                 205

Thr Asn Glu Pro Arg Phe Asn Gln Ile Lys Ile Ala Ile Met Ser Ala
    210                 215                 220

Gly Leu Ser Trp Leu Arg Glu Arg Lys Leu Lys Ala Ser Ala Ser Ala
225                 230                 235                 240

Asn Pro Leu Phe Glu Tyr Pro Phe Ser Gln Lys Gly Leu Arg Thr Gly
                245                 250                 255

Ile Ser Glu Ala Leu Arg Ile Gln Ala Arg Ser Ala Pro Phe Pro His
            260                 265                 270

His Arg Tyr Ala Leu Val Asp Met Ala Asn Ala Val Arg Pro Leu Ser
        275                 280                 285

Trp Phe
    290


<210> 97
<211> 1065
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1042)
<223> RXA01511

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gggcgtgtgt ttacctttgc ttttgtgtct aatggttccg cgattgtgcc ggcgcgtgag 60

gctttggatg agatggcgtc gattctgagg gactttaag gtg gca tcc ctc atc   115
                                        Val Ala Ser Leu Ile
                                          1               5

ggg aat ctt gag ctg cct agg gta agc cct aat ttc ttg gaa tta cgc   163
Gly Asn Leu Glu Leu Pro Arg Val Ser Pro Asn Phe Leu Glu Leu Arg
                  10                  15                  20

aag gcg gtg cgc cct tac ctg aaa gag cat gtg cac att ggg ttg tcg   211
Lys Ala Val Arg Pro Tyr Leu Lys Glu His Val His Ile Gly Leu Ser
```

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                25                  30                  35

ggc ggg ccg gat tca ttg gcg ctg gtg gct gct gtg ctc gcg gag aaa   259
Gly Gly Pro Asp Ser Leu Ala Leu Val Ala Ala Val Leu Ala Glu Lys
         40                  45                  50

tcc cag gta acg gcg att tgt atc gat cat aat ctg cag acc ggt tct   307
Ser Gln Val Thr Ala Ile Cys Ile Asp His Asn Leu Gln Thr Gly Ser
     55                  60                  65

gct gaa gtc acg cac aac gct gct gcg atg gcg cgc cac atg ggc gca   355
Ala Glu Val Thr His Asn Ala Ala Ala Met Ala Arg His Met Gly Ala
 70                  75                  80                  85

cag gcg atc gtg aag agc atc gag gtc gcg ccg ggg gag ggg atg gag   403
Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro Gly Glu Gly Met Glu
                 90                  95                 100

gcc gcc gcc agg gag gct cgg tac gcg gct ttt gcg cag ctc acc gat   451
Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe Ala Gln Leu Thr Asp
            105                 110                 115

gag att tgg gtg gcg cac acc atg gat gat caa gcc gag acc tat ctc   499
Glu Ile Trp Val Ala His Thr Met Asp Asp Gln Ala Glu Thr Tyr Leu
        120                 125                 130

ctt ggc ggt ttg cgg ggg aat ccc gcg ggc atg aaa gat gct tct cga   547
Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met Lys Asp Ala Ser Arg
    135                 140                 145

cgc ccc gag cta tcc att att cga ccc ctt ctg ggg gct cgg cgt gcg   595
Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu Gly Ala Arg Arg Ala
150                 155                 160                 165

cac acg cac ggg gcg tgc gtg gag ttg ggg ttg aaa ccg tgg cac gat   643
His Thr His Gly Ala Cys Val Glu Leu Gly Leu Lys Pro Trp His Asp
                170                 175                 180

ccg caa aat ttt gac gat gcc ttt cgg cgg gta gcc atc cga aac cag   691
Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val Ala Ile Arg Asn Gln
            185                 190                 195

gtg att cct ctt ctt gcg cag gtg cac ggg gga gac cct gta cct ggt   739
Val Ile Pro Leu Leu Ala Gln Val His Gly Gly Asp Pro Val Pro Gly
        200                 205                 210

ttg gca ctt gcg gcg cga cgc gct gtg gag gat gcc gaa gtg gtg gag   787
Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp Ala Glu Val Val Glu
    215                 220                 225

ggc gac gtc gag aag cgg cgt tta gag tgg cag gac ggt ttt cct gtg   835
Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln Asp Gly Phe Pro Val
230                 235                 240                 245

acg ttg gcc ggg gaa cct acg ggc ctt agg cga cgc atg ttg gcg gat   883
Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg Arg Met Leu Ala Asp
                250                 255                 260

ttt ttg cgt ggg gaa ggc atc gct gtg acc tcg agg aaa ctc gac gcc   931
Phe Leu Arg Gly Glu Gly Ile Ala Val Thr Ser Arg Lys Leu Asp Ala
            265                 270                 275
```

```
att gac cga ttg ctc acc gat tgg cgc gga cag ggt ggc gta gcc gtg   979
Ile Asp Arg Leu Leu Thr Asp Trp Arg Gly Gln Gly Gly Val Ala Val
        280                 285                 290

ggt aaa agc gat aat gga agg ttg gaa gtg gtg cgg caa agt ggc aag   1027
Gly Lys Ser Asp Asn Gly Arg Leu Glu Val Val Arg Gln Ser Gly Lys
    295                 300                 305

ctt aag atc act gat tgacacctga atctacaaca caa                    1065
Leu Lys Ile Thr Asp
310
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<210> 98
<211> 314
<212> PRT
<213> Corynebacterium glutamicum

<400> 98

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Val Ala Ser Leu Ile Gly Asn Leu Glu Leu Pro Arg Val Ser Pro Asn
  1               5                  10                  15

Phe Leu Glu Leu Arg Lys Ala Val Arg Pro Tyr Leu Lys Glu His Val
             20                  25                  30

His Ile Gly Leu Ser Gly Gly Pro Asp Ser Leu Ala Leu Val Ala Ala
         35                  40                  45

Val Leu Ala Glu Lys Ser Gln Val Thr Ala Ile Cys Ile Asp His Asn
     50                  55                  60

Leu Gln Thr Gly Ser Ala Glu Val Thr His Asn Ala Ala Ala Met Ala
 65                  70                  75                  80

Arg His Met Gly Ala Gln Ala Ile Val Lys Ser Ile Glu Val Ala Pro
                 85                  90                  95

Gly Glu Gly Met Glu Ala Ala Ala Arg Glu Ala Arg Tyr Ala Ala Phe
            100                 105                 110

Ala Gln Leu Thr Asp Glu Ile Trp Val Ala His Thr Met Asp Asp Gln
        115                 120                 125

Ala Glu Thr Tyr Leu Leu Gly Gly Leu Arg Gly Asn Pro Ala Gly Met
    130                 135                 140

Lys Asp Ala Ser Arg Arg Pro Glu Leu Ser Ile Ile Arg Pro Leu Leu
145                 150                 155                 160

Gly Ala Arg Arg Ala His Thr His Gly Ala Cys Val Glu Leu Gly Leu
                165                 170                 175

Lys Pro Trp His Asp Pro Gln Asn Phe Asp Asp Ala Phe Arg Arg Val
            180                 185                 190

Ala Ile Arg Asn Gln Val Ile Pro Leu Leu Ala Gln Val His Gly Gly
        195                 200                 205

Asp Pro Val Pro Gly Leu Ala Leu Ala Ala Arg Arg Ala Val Glu Asp
    210                 215                 220
```

```
Ala Glu Val Val Glu Gly Asp Val Glu Lys Arg Arg Leu Glu Trp Gln
225                 230                 235                 240

Asp Gly Phe Pro Val Thr Leu Ala Gly Glu Pro Thr Gly Leu Arg Arg
                245                 250                 255

Arg Met Leu Ala Asp Phe Leu Arg Gly Glu Gly Ile Ala Val Thr Ser
            260                 265                 270

Arg Lys Leu Asp Ala Ile Asp Arg Leu Leu Thr Asp Trp Arg Gly Gln
        275                 280                 285

Gly Gly Val Ala Val Gly Lys Ser Asp Asn Gly Arg Leu Glu Val Val
    290                 295                 300

Arg Gln Ser Gly Lys Leu Lys Ile Thr Asp
305                 310


<210> 99
<211> 2682
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2659)
<223> RXA01513

<400> 99
ccctcaactt cgtttgatta gttgtctagt agatcccttt tattcgattc cgagaaaggc 60

acgggcaaaa cggccttagt tgagccggtt gccactgcgt atg aaa aac aag aaa   115
                                            Met Lys Asn Lys Lys
                                              1               5

tac ctg cag ttc ggc ggt atc gca gcc gta atc ctc atc gtt ctg ttc   163
Tyr Leu Gln Phe Gly Gly Ile Ala Ala Val Ile Leu Ile Val Leu Phe
                 10                  15                  20

ttg gtg tcc ctg ttt agc agt gac acc agg aac ttc cag gag gtc gat   211
Leu Val Ser Leu Phe Ser Ser Asp Thr Arg Asn Phe Gln Glu Val Asp
             25                  30                  35

acc tct gtt gcg atg gca cag ctt gac gcc gga aac gtc gcc gaa gct   259
Thr Ser Val Ala Met Ala Gln Leu Asp Ala Gly Asn Val Ala Glu Ala
         40                  45                  50

caa atc gat gac agg gaa cag cgc gtc cga ctg acc ttg cgt gaa ccc   307
Gln Ile Asp Asp Arg Glu Gln Arg Val Arg Leu Thr Leu Arg Glu Pro
     55                  60                  65

atc acg gtg gat gaa cgc gaa ggc gtt gaa gag atc ctc gcg cag tac   355
Ile Thr Val Asp Glu Arg Glu Gly Val Glu Glu Ile Leu Ala Gln Tyr
 70                  75                  80                  85

cca gct cgt acc gcg cca gcg atc ttt gag aag gtg gaa gca tcc aac   403
Pro Ala Arg Thr Ala Pro Ala Ile Phe Glu Lys Val Glu Ala Ser Asn
                 90                  95                 100
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act gat tcc tat acc acc aat gtg acg cag gag agc ttc ctg atg tcc   451
Thr Asp Ser Tyr Thr Thr Asn Val Thr Gln Glu Ser Phe Leu Met Ser
            105                 110                 115

atg ctg agc ttc atc ctg ccg atg gtg atc atc ttc ggt ttg ctg atg   499
Met Leu Ser Phe Ile Leu Pro Met Val Ile Ile Phe Gly Leu Leu Met
        120                 125                 130

ttc ttc ctc acc cgc atg cag ggt ggt ggc atg ttt ggc atc ggt gga   547
Phe Phe Leu Thr Arg Met Gln Gly Gly Gly Met Phe Gly Ile Gly Gly
    135                 140                 145

tcc aag gcc aag cag ctg acc aag gat atg ccc acc aac acc ttc gcg   595
Ser Lys Ala Lys Gln Leu Thr Lys Asp Met Pro Thr Asn Thr Phe Ala
150                 155                 160                 165

gat gtt gct ggc gct gaa gaa gca gtg gat gaa ctc cat gag atc aag   643
Asp Val Ala Gly Ala Glu Glu Ala Val Asp Glu Leu His Glu Ile Lys
                170                 175                 180

gac ttc ctg gaa gac ccc acc cgc tac gaa gcc ctc gga gcg aaa atc   691
Asp Phe Leu Glu Asp Pro Thr Arg Tyr Glu Ala Leu Gly Ala Lys Ile
            185                 190                 195

cct cgt ggt gtg ctg ctt tac ggc cct ccc ggt act ggt aaa acc ctg   739
Pro Arg Gly Val Leu Leu Tyr Gly Pro Pro Gly Thr Gly Lys Thr Leu
        200                 205                 210

ctg gct cgt gcc gta gct ggt gag gct ggc gtg ccg ttc tac tca att   787
Leu Ala Arg Ala Val Ala Gly Glu Ala Gly Val Pro Phe Tyr Ser Ile
    215                 220                 225

tcc ggt tct gac ttt gtg gaa atg ttc gtc ggt gtt ggt gcc tcg cgt   835
Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly Val Gly Ala Ser Arg
230                 235                 240                 245

gtg cgt gat ctg ttt aag cag gcc aag gaa aac agt ccc tgc atc atc   883
Val Arg Asp Leu Phe Lys Gln Ala Lys Glu Asn Ser Pro Cys Ile Ile
                250                 255                 260

ttc gtc gat gag atc gat gcg gtt ggt cgc gcc cgt ggc tca gga atg   931
Phe Val Asp Glu Ile Asp Ala Val Gly Arg Ala Arg Gly Ser Gly Met
            265                 270                 275

ggt ggc gga cac gat gag cgt gaa cag acc ctg aac cag ttg ctc gtt   979
Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu Asn Gln Leu Leu Val
        280                 285                 290

gag atg gat ggc ttt ggt gat cgt caa ggc gtc att ctg atg gct gct  1027
Glu Met Asp Gly Phe Gly Asp Arg Gln Gly Val Ile Leu Met Ala Ala
    295                 300                 305

acc aac cgc cca gat gtt ctt gac cca gcg ctg ctg cgt cct ggc cgt  1075
Thr Asn Arg Pro Asp Val Leu Asp Pro Ala Leu Leu Arg Pro Gly Arg
310                 315                 320                 325

ttc gac cgc cag atc cca gtc acc aac cct gac cta cgc ggc cgt gaa  1123
Phe Asp Arg Gln Ile Pro Val Thr Asn Pro Asp Leu Arg Gly Arg Glu
                330                 335                 340

cag atc ctg gaa gtt cac gcc aag ggt aag cct ttc gca ccc gat gca  1171
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Gln Ile Leu Glu Val His Ala Lys Gly Lys Pro Phe Ala Pro Asp Ala
            345                 350                 355

gat atc aag gca ttg gca aag cgc acc gcc ggc atg tcc ggc gct gac   1219
Asp Ile Lys Ala Leu Ala Lys Arg Thr Ala Gly Met Ser Gly Ala Asp
        360                 365                 370

ctg gca aac gtg ctt aac gaa gcc gcg ctg cta acc gcc cgc gtg ggt   1267
Leu Ala Asn Val Leu Asn Glu Ala Ala Leu Leu Thr Ala Arg Val Gly
    375                 380                 385

ggc aac gtg atc acc gcc gac gct ctg gaa gaa gca acc gac cgc gtt   1315
Gly Asn Val Ile Thr Ala Asp Ala Leu Glu Glu Ala Thr Asp Arg Val
390                 395                 400                 405

gtc ggt gga cca cgt cgc tcc ggc aag gtg att tcc gag aag gaa aag   1363
Val Gly Gly Pro Arg Arg Ser Gly Lys Val Ile Ser Glu Lys Glu Lys
                410                 415                 420

aag gtc acc gcc tac cac gaa ggt gga cac acc ctg tcc gca tgg gcg   1411
Lys Val Thr Ala Tyr His Glu Gly Gly His Thr Leu Ser Ala Trp Ala
            425                 430                 435

ttg gaa gac atc gag cgc gtc tac aag gtc acc atc ttg gcc cgc ggt   1459
Leu Glu Asp Ile Glu Arg Val Tyr Lys Val Thr Ile Leu Ala Arg Gly
        440                 445                 450

cgc acc ggc ggt cac gcc atg act gcc caa gaa gat gac aag ggc atg   1507
Arg Thr Gly Gly His Ala Met Thr Ala Gln Glu Asp Asp Lys Gly Met
    455                 460                 465

tac aac cgc aac gaa ttg ttc gcc cgc ctg gtc ttt gcc atg ggt gga   1555
Tyr Asn Arg Asn Glu Leu Phe Ala Arg Leu Val Phe Ala Met Gly Gly
470                 475                 480                 485

cgc tcc gcg gaa gaa cta gtc ttc ggc gaa ccc acc acc ggc gcc tcc   1603
Arg Ser Ala Glu Glu Leu Val Phe Gly Glu Pro Thr Thr Gly Ala Ser
                490                 495                 500

gcc gat att gaa atg gcc acc aag atc gcc cga tcc atg gtg acc gaa   1651
Ala Asp Ile Glu Met Ala Thr Lys Ile Ala Arg Ser Met Val Thr Glu
            505                 510                 515

tat ggc atg tcc cca gct gtc ggc atg gtg aaa tac ggc caa gaa cag   1699
Tyr Gly Met Ser Pro Ala Val Gly Met Val Lys Tyr Gly Gln Glu Gln
        520                 525                 530

ggc gac cca ttc tcc gga cgc ggt ggc ggt gga aac ttg gac cac tcc   1747
Gly Asp Pro Phe Ser Gly Arg Gly Gly Gly Gly Asn Leu Asp His Ser
    535                 540                 545

caa gaa gtc gca gca acc atc gac acc gaa gtc cag ttc ctc ctg gac   1795
Gln Glu Val Ala Ala Thr Ile Asp Thr Glu Val Gln Phe Leu Leu Asp
550                 555                 560                 565

aaa gcc cat gaa gtg tcc tac tcc atc ctg gct gaa tac cgc gac cac   1843
Lys Ala His Glu Val Ser Tyr Ser Ile Leu Ala Glu Tyr Arg Asp His
                570                 575                 580

ctg gac cgc ctc gcg gaa aaa ctc ctg gaa aag gaa acc ctg cga cgc   1891
Leu Asp Arg Leu Ala Glu Lys Leu Leu Glu Lys Glu Thr Leu Arg Arg
```

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                585                 590                 595

cca gac ctc gaa gcg ctt ttc gac gac atc gtc cca cgc aag gtc gcc   1939
Pro Asp Leu Glu Ala Leu Phe Asp Asp Ile Val Pro Arg Lys Val Ala
        600                 605                 610

gaa gtc ttc ccc gac gag tcc aca cga ttc cct cgc caa gaa aac cgc   1987
Glu Val Phe Pro Asp Glu Ser Thr Arg Phe Pro Arg Gln Glu Asn Arg
    615                 620                 625

gaa cca gta aaa acc cca gtg gag ctc gca ctg gaa cgt ggc gaa gaa   2035
Glu Pro Val Lys Thr Pro Val Glu Leu Ala Leu Glu Arg Gly Glu Glu
630                 635                 640                 645

cca cca aag aag ttc tcc att ctt gag gcc tcc cgc gca acc cgc gaa   2083
Pro Pro Lys Lys Phe Ser Ile Leu Glu Ala Ser Arg Ala Thr Arg Glu
                650                 655                 660

cgc cgt cgc aag gaa ttg gaa gct cag ggt aag ttg ccg gtg cag cct   2131
Arg Arg Arg Lys Glu Leu Glu Ala Gln Gly Lys Leu Pro Val Gln Pro
            665                 670                 675

gcg tct tct gcc ggc gtg gca cct gcg gcc gga gca gct gcc gga tcc   2179
Ala Ser Ser Ala Gly Val Ala Pro Ala Ala Gly Ala Ala Ala Gly Ser
        680                 685                 690

tat ggc acc cca cct cca gct gat tgg agc gtg ccc ggt tcc gct gga   2227
Tyr Gly Thr Pro Pro Pro Ala Asp Trp Ser Val Pro Gly Ser Ala Gly
    695                 700                 705

aag cac cgc tca cgt gca gaa gaa cag cca gct gag cag ggc ttc ccg   2275
Lys His Arg Ser Arg Ala Glu Glu Gln Pro Ala Glu Gln Gly Phe Pro
710                 715                 720                 725

gct cag acc ccg gca caa gct cct gag cag tcc cct gat tca agt ggc   2323
Ala Gln Thr Pro Ala Gln Ala Pro Glu Gln Ser Pro Asp Ser Ser Gly
                730                 735                 740

ggc cgc ccc aac cct tac gcg act cca acc gca tcc ggt gag cac cct   2371
Gly Arg Pro Asn Pro Tyr Ala Thr Pro Thr Ala Ser Gly Glu His Pro
            745                 750                 755

ggt atg aag gcc tat ggc ttc ggc gat tcc gaa ctc atg gac caa tca   2419
Gly Met Lys Ala Tyr Gly Phe Gly Asp Ser Glu Leu Met Asp Gln Ser
        760                 765                 770

aca ggt gcg gaa cat acc cca ggt aac gtt tca cag gaa tcc cca acc   2467
Thr Gly Ala Glu His Thr Pro Gly Asn Val Ser Gln Glu Ser Pro Thr
    775                 780                 785

gaa atg atc ggg ttc cgt ttg ccg gat cat gaa cgt tcg gac tac cca   2515
Glu Met Ile Gly Phe Arg Leu Pro Asp His Glu Arg Ser Asp Tyr Pro
790                 795                 800                 805

gaa aag gcg caa aaa gag tcg gtg ctg gat gct tct gaa acc aca gaa   2563
Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala Ser Glu Thr Thr Glu
                810                 815                 820

atg cct gtc gtt cca gat cag ccc atc gat ggt gat tcc ggg aag tcc   2611
Met Pro Val Val Pro Asp Gln Pro Ile Asp Gly Asp Ser Gly Lys Ser
            825                 830                 835
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gct gag ggc aca cag gag aat ccg gaa aat gaa gga gac aac cgt gga   2659
Ala Glu Gly Thr Gln Glu Asn Pro Glu Asn Glu Gly Asp Asn Arg Gly
        840                 845                 850

taaccacgct gcagttcgcg agt                                       2682


<210> 100
<211> 853
<212> PRT
<213> Corynebacterium glutamicum

<400> 100
Met Lys Asn Lys Lys Tyr Leu Gln Phe Gly Gly Ile Ala Ala Val Ile
  1               5                  10                  15

Leu Ile Val Leu Phe Leu Val Ser Leu Phe Ser Ser Asp Thr Arg Asn
             20                  25                  30

Phe Gln Glu Val Asp Thr Ser Val Ala Met Ala Gln Leu Asp Ala Gly
         35                  40                  45

Asn Val Ala Glu Ala Gln Ile Asp Asp Arg Glu Gln Arg Val Arg Leu
     50                  55                  60

Thr Leu Arg Glu Pro Ile Thr Val Asp Glu Arg Glu Gly Val Glu Glu
 65                  70                  75                  80

Ile Leu Ala Gln Tyr Pro Ala Arg Thr Ala Pro Ala Ile Phe Glu Lys
                 85                  90                  95

Val Glu Ala Ser Asn Thr Asp Ser Tyr Thr Thr Asn Val Thr Gln Glu
            100                 105                 110

Ser Phe Leu Met Ser Met Leu Ser Phe Ile Leu Pro Met Val Ile Ile
        115                 120                 125

Phe Gly Leu Leu Met Phe Phe Leu Thr Arg Met Gln Gly Gly Gly Met
    130                 135                 140

Phe Gly Ile Gly Gly Ser Lys Ala Lys Gln Leu Thr Lys Asp Met Pro
145                 150                 155                 160

Thr Asn Thr Phe Ala Asp Val Ala Gly Ala Glu Glu Ala Val Asp Glu
                165                 170                 175

Leu His Glu Ile Lys Asp Phe Leu Glu Asp Pro Thr Arg Tyr Glu Ala
            180                 185                 190

Leu Gly Ala Lys Ile Pro Arg Gly Val Leu Leu Tyr Gly Pro Pro Gly
        195                 200                 205

Thr Gly Lys Thr Leu Leu Ala Arg Ala Val Ala Gly Glu Ala Gly Val
    210                 215                 220

Pro Phe Tyr Ser Ile Ser Gly Ser Asp Phe Val Glu Met Phe Val Gly
225                 230                 235                 240

Val Gly Ala Ser Arg Val Arg Asp Leu Phe Lys Gln Ala Lys Glu Asn
                245                 250                 255
```

```
Ser Pro Cys Ile Ile Phe Val Asp Glu Ile Asp Ala Val Gly Arg Ala
            260                 265                 270

Arg Gly Ser Gly Met Gly Gly Gly His Asp Glu Arg Glu Gln Thr Leu
        275                 280                 285

Asn Gln Leu Leu Val Glu Met Asp Gly Phe Gly Asp Arg Gln Gly Val
    290                 295                 300

Ile Leu Met Ala Ala Thr Asn Arg Pro Asp Val Leu Asp Pro Ala Leu
305                 310                 315                 320

Leu Arg Pro Gly Arg Phe Asp Arg Gln Ile Pro Val Thr Asn Pro Asp
                325                 330                 335

Leu Arg Gly Arg Glu Gln Ile Leu Glu Val His Ala Lys Gly Lys Pro
            340                 345                 350

Phe Ala Pro Asp Ala Asp Ile Lys Ala Leu Ala Lys Arg Thr Ala Gly
        355                 360                 365

Met Ser Gly Ala Asp Leu Ala Asn Val Leu Asn Glu Ala Ala Leu Leu
    370                 375                 380

Thr Ala Arg Val Gly Gly Asn Val Ile Thr Ala Asp Ala Leu Glu Glu
385                 390                 395                 400

Ala Thr Asp Arg Val Val Gly Gly Pro Arg Arg Ser Gly Lys Val Ile
                405                 410                 415

Ser Glu Lys Glu Lys Lys Val Thr Ala Tyr His Glu Gly Gly His Thr
            420                 425                 430

Leu Ser Ala Trp Ala Leu Glu Asp Ile Glu Arg Val Tyr Lys Val Thr
        435                 440                 445

Ile Leu Ala Arg Gly Arg Thr Gly Gly His Ala Met Thr Ala Gln Glu
    450                 455                 460

Asp Asp Lys Gly Met Tyr Asn Arg Asn Glu Leu Phe Ala Arg Leu Val
465                 470                 475                 480

Phe Ala Met Gly Gly Arg Ser Ala Glu Glu Leu Val Phe Gly Glu Pro
                485                 490                 495

Thr Thr Gly Ala Ser Ala Asp Ile Glu Met Ala Thr Lys Ile Ala Arg
            500                 505                 510

Ser Met Val Thr Glu Tyr Gly Met Ser Pro Ala Val Gly Met Val Lys
        515                 520                 525

Tyr Gly Gln Glu Gln Gly Asp Pro Phe Ser Gly Arg Gly Gly Gly Gly
    530                 535                 540

Asn Leu Asp His Ser Gln Glu Val Ala Ala Thr Ile Asp Thr Glu Val
545                 550                 555                 560

Gln Phe Leu Leu Asp Lys Ala His Glu Val Ser Tyr Ser Ile Leu Ala
                565                 570                 575
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Glu Tyr Arg Asp His Leu Asp Arg Leu Ala Glu Lys Leu Leu Glu Lys
            580                 585                 590

Glu Thr Leu Arg Arg Pro Asp Leu Glu Ala Leu Phe Asp Asp Ile Val
        595                 600                 605

Pro Arg Lys Val Ala Glu Val Phe Pro Asp Glu Ser Thr Arg Phe Pro
    610                 615                 620

Arg Gln Glu Asn Arg Glu Pro Val Lys Thr Pro Val Glu Leu Ala Leu
625                 630                 635                 640

Glu Arg Gly Glu Glu Pro Pro Lys Lys Phe Ser Ile Leu Glu Ala Ser
                645                 650                 655

Arg Ala Thr Arg Glu Arg Arg Arg Lys Glu Leu Glu Ala Gln Gly Lys
            660                 665                 670

Leu Pro Val Gln Pro Ala Ser Ser Ala Gly Val Ala Pro Ala Ala Gly
        675                 680                 685

Ala Ala Ala Gly Ser Tyr Gly Thr Pro Pro Pro Ala Asp Trp Ser Val
    690                 695                 700

Pro Gly Ser Ala Gly Lys His Arg Ser Arg Ala Glu Glu Gln Pro Ala
705                 710                 715                 720

Glu Gln Gly Phe Pro Ala Gln Thr Pro Ala Gln Ala Pro Glu Gln Ser
                725                 730                 735

Pro Asp Ser Ser Gly Gly Arg Pro Asn Pro Tyr Ala Thr Pro Thr Ala
            740                 745                 750

Ser Gly Glu His Pro Gly Met Lys Ala Tyr Gly Phe Gly Asp Ser Glu
        755                 760                 765

Leu Met Asp Gln Ser Thr Gly Ala Glu His Thr Pro Gly Asn Val Ser
    770                 775                 780

Gln Glu Ser Pro Thr Glu Met Ile Gly Phe Arg Leu Pro Asp His Glu
785                 790                 795                 800

Arg Ser Asp Tyr Pro Glu Lys Ala Gln Lys Glu Ser Val Leu Asp Ala
                805                 810                 815

Ser Glu Thr Thr Glu Met Pro Val Val Pro Asp Gln Pro Ile Asp Gly
            820                 825                 830

Asp Ser Gly Lys Ser Ala Glu Gly Thr Gln Glu Asn Pro Glu Asn Glu
        835                 840                 845

Gly Asp Asn Arg Gly
    850
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<210> 101
<211> 1869
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1846)
<223> RXA02098

<400> 101
ccccatttcg gcgacctcga ctccatgaaa gcaagagttt caccacattt aacgtggggt 60

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acctgtgtgc atcggggtca aacctgccac tatagagggt atg gat gcg act ttt   115
                                            Met Asp Ala Thr Phe
                                              1               5

tgg atc att gga cta gta gtc ctc gtg gtt ctc gcg atc atc att gta   163
Trp Ile Ile Gly Leu Val Val Leu Val Val Leu Ala Ile Ile Ile Val
                  10                  15                  20

ttg atc gta gga aat cag cga ggt aaa tca aag acc gtt agt ttt gaa   211
Leu Ile Val Gly Asn Gln Arg Gly Lys Ser Lys Thr Val Ser Phe Glu
             25                  30                  35

aaa cct gaa gag aat aaa aaa gaa cta acc cag caa gag aag tct gga   259
Lys Pro Glu Glu Asn Lys Lys Glu Leu Thr Gln Gln Glu Lys Ser Gly
         40                  45                  50

aat tac caa gcc caa ggt gga ttc aac ttc gcc cca gct aaa caa aca   307
Asn Tyr Gln Ala Gln Gly Gly Phe Asn Phe Ala Pro Ala Lys Gln Thr
     55                  60                  65

gaa gag cca gtg ctg cgt gaa ggc caa gat ctt ggc gca cca aag gct   355
Glu Glu Pro Val Leu Arg Glu Gly Gln Asp Leu Gly Ala Pro Lys Ala
 70                  75                  80                  85

gaa aca aca ccg att gtt cca cca gta gtt att ccg ccg gca gct cct   403
Glu Thr Thr Pro Ile Val Pro Pro Val Val Ile Pro Pro Ala Ala Pro
                 90                  95                 100

gaa gag gaa aag gcg ccg gag caa tcg act gaa act ttc gca gct caa   451
Glu Glu Glu Lys Ala Pro Glu Gln Ser Thr Glu Thr Phe Ala Ala Gln
            105                 110                 115

aag cct gct gaa gaa gca cct gca act cct gaa cca gaa acc tct gat   499
Lys Pro Ala Glu Glu Ala Pro Ala Thr Pro Glu Pro Glu Thr Ser Asp
        120                 125                 130

gat gtt gtc gag gaa cca gaa gtt aag gag cct gag gtt aaa gaa gtt   547
Asp Val Val Glu Glu Pro Glu Val Lys Glu Pro Glu Val Lys Glu Val
    135                 140                 145

gtc gct gtt gag cca gag gtc gaa act gaa gag cca gca gtt gtt gaa   595
Val Ala Val Glu Pro Glu Val Glu Thr Glu Glu Pro Ala Val Val Glu
150                 155                 160                 165

gaa cct gca gta gca gag gaa cca gca att gtt gag gaa cct gca gta   643
Glu Pro Ala Val Ala Glu Glu Pro Ala Ile Val Glu Glu Pro Ala Val
                170                 175                 180

gca gag gaa cct gca gta gca gag gaa cct gca gta gca gag gaa cca   691
Ala Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Ala Glu Glu Pro
            185                 190                 195

gca att gtt gag gaa cct gca gta gca gag gaa cct gca gtt gtt gag   739
Ala Ile Val Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Val Glu
```

```
        200                 205                 210

gaa cct gca gta gcg gaa gtt ccc gaa aca atc gaa gaa cct gca gtt   787
Glu Pro Ala Val Ala Glu Val Pro Glu Thr Ile Glu Glu Pro Ala Val
    215                 220                 225

gaa gaa ctt gcg gca gtt gct gag gtc acc gag gct gca gag gct gct   835
Glu Glu Leu Ala Ala Val Ala Glu Val Thr Glu Ala Ala Glu Ala Ala
230                 235                 240                 245

cag gtt gct gtg gaa tct gcg gaa gct gcg ctg gag gaa act cca gtt   883
Gln Val Ala Val Glu Ser Ala Glu Ala Ala Leu Glu Glu Thr Pro Val
                250                 255                 260

cca gat gtg gag ccg gag cca gct gcg gag cct att gat gag atc gtg   931
Pro Asp Val Glu Pro Glu Pro Ala Ala Glu Pro Ile Asp Glu Ile Val
            265                 270                 275

ccg gcg gcg ggt cgt atc ggt aag ctg cgt ggt cgt ctt tct cgg tca   979
Pro Ala Ala Gly Arg Ile Gly Lys Leu Arg Gly Arg Leu Ser Arg Ser
        280                 285                 290

cag agt gtt ttc ggt aag tca gtg ttg ggc att ttg tct gcg ggt gac   1027
Gln Ser Val Phe Gly Lys Ser Val Leu Gly Ile Leu Ser Ala Gly Asp
    295                 300                 305

ttg gat gaa gac gca tgg gaa gac atc gaa gcg atg ttg atc aag gcg   1075
Leu Asp Glu Asp Ala Trp Glu Asp Ile Glu Ala Met Leu Ile Lys Ala
310                 315                 320                 325

gat ttg ggc gcc aag atc act gcg cgt gtg gtg gat gag ctg cgt gac   1123
Asp Leu Gly Ala Lys Ile Thr Ala Arg Val Val Asp Glu Leu Arg Asp
                330                 335                 340

aag atc gca gag cat ggt gtt ggt agt gag gca gag gcg cgt gcg atg   1171
Lys Ile Ala Glu His Gly Val Gly Ser Glu Ala Glu Ala Arg Ala Met
            345                 350                 355

ctg cgt gct tcg ctg att gat gct tgc cgt cct gac ctt gat cgc tcc   1219
Leu Arg Ala Ser Leu Ile Asp Ala Cys Arg Pro Asp Leu Asp Arg Ser
        360                 365                 370

att aag gct atg ccg tat gag ggt aag cca ccg gtg gtg ttg gtt gtt   1267
Ile Lys Ala Met Pro Tyr Glu Gly Lys Pro Pro Val Val Leu Val Val
    375                 380                 385

ggt gtg aac ggt acc ggt aag acg acg act act ggc aag ctt gct cgt   1315
Gly Val Asn Gly Thr Gly Lys Thr Thr Thr Thr Gly Lys Leu Ala Arg
390                 395                 400                 405

gtg ttg gtg tcc atg ggt cat aag gtg att ctt ggt gct gcg gat acg   1363
Val Leu Val Ser Met Gly His Lys Val Ile Leu Gly Ala Ala Asp Thr
                410                 415                 420

ttc cgt gcg gcg gct gcg gat cag ttg gag acg tgg ggt cgc cgt gtg   1411
Phe Arg Ala Ala Ala Ala Asp Gln Leu Glu Thr Trp Gly Arg Arg Val
            425                 430                 435

ggt gcg gag act gtt cgt ggc gct gag ggc gcg gat cct gca tct att   1459
Gly Ala Glu Thr Val Arg Gly Ala Glu Gly Ala Asp Pro Ala Ser Ile
        440                 445                 450
```

Sequence Listing

```
gcg ttt gat gct gtg gct aag ggt gtt gag cgt cag gcg gat gtc gtt   1507
Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg Gln Ala Asp Val Val
    455                 460                 465

ttg gtt gac act gcg ggt cgt ttg cac acg tcg act ggt ttg atg gat   1555
Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser Thr Gly Leu Met Asp
470                 475                 480                 485

cag ttg ggc aag gtt aag cgc gtg gtg gag aag aag gca gtg gtg gat   1603
Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys Lys Ala Val Val Asp
                490                 495                 500

gaa gtg ctg ctg gtt ttg gat gcc acg gtt ggt cag aac ggt atg cag   1651
Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly Gln Asn Gly Met Gln
            505                 510                 515

cag gct cgt att ttc cgt gaa gtt gtg gat att acg ggt gtg gtg ttg   1699
Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile Thr Gly Val Val Leu
        520                 525                 530

acc aag ctg gat ggt act gcg aag ggc gga atc gtg ttc cag gtg cag   1747
Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile Val Phe Gln Val Gln
    535                 540                 545

gaa gag ttg ggt gtt cct gtg aag ctt gtt ggt ctt ggt gaa ggt gcg   1795
Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly Leu Gly Glu Gly Ala
550                 555                 560                 565

gat gat ttg gca ccg ttt gag gtt gag ggc ttc gtg gac gct ttg ctg   1843
Asp Asp Leu Ala Pro Phe Glu Val Glu Gly Phe Val Asp Ala Leu Leu
                570                 575                 580

ggc tagaaacccg ataagcgaga acc                                    1869
Gly
```

Sequence Listing

<210> 102
<211> 582
<212> PRT
<213> Corynebacterium glutamicum

<400> 102

```
Met Asp Ala Thr Phe Trp Ile Ile Gly Leu Val Val Leu Val Val Leu
  1               5                  10                  15

Ala Ile Ile Ile Val Leu Ile Val Gly Asn Gln Arg Gly Lys Ser Lys
             20                  25                  30

Thr Val Ser Phe Glu Lys Pro Glu Glu Asn Lys Lys Glu Leu Thr Gln
         35                  40                  45

Gln Glu Lys Ser Gly Asn Tyr Gln Ala Gln Gly Gly Phe Asn Phe Ala
     50                  55                  60

Pro Ala Lys Gln Thr Glu Glu Pro Val Leu Arg Glu Gly Gln Asp Leu
 65                  70                  75                  80

Gly Ala Pro Lys Ala Glu Thr Thr Pro Ile Val Pro Pro Val Val Ile
                 85                  90                  95
```

```
Pro Pro Ala Ala Pro Glu Glu Glu Lys Ala Pro Glu Gln Ser Thr Glu
            100                 105                 110

Thr Phe Ala Ala Gln Lys Pro Ala Glu Glu Ala Pro Ala Thr Pro Glu
        115                 120                 125

Pro Glu Thr Ser Asp Asp Val Val Glu Glu Pro Glu Val Lys Glu Pro
    130                 135                 140

Glu Val Lys Glu Val Val Ala Val Glu Pro Glu Val Glu Thr Glu Glu
145                 150                 155                 160

Pro Ala Val Val Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Ile Val
                165                 170                 175

Glu Glu Pro Ala Val Ala Glu Glu Pro Ala Val Ala Glu Glu Pro Ala
            180                 185                 190

Val Ala Glu Glu Pro Ala Ile Val Glu Glu Pro Ala Val Ala Glu Glu
        195                 200                 205

Pro Ala Val Val Glu Glu Pro Ala Val Ala Glu Val Pro Glu Thr Ile
    210                 215                 220

Glu Glu Pro Ala Val Glu Glu Leu Ala Ala Val Ala Glu Val Thr Glu
225                 230                 235                 240

Ala Ala Glu Ala Ala Gln Val Ala Val Glu Ser Ala Glu Ala Ala Leu
                245                 250                 255

Glu Glu Thr Pro Val Pro Asp Val Glu Pro Glu Pro Ala Ala Glu Pro
            260                 265                 270

Ile Asp Glu Ile Val Pro Ala Ala Gly Arg Ile Gly Lys Leu Arg Gly
        275                 280                 285

Arg Leu Ser Arg Ser Gln Ser Val Phe Gly Lys Ser Val Leu Gly Ile
    290                 295                 300

Leu Ser Ala Gly Asp Leu Asp Glu Asp Ala Trp Glu Asp Ile Glu Ala
305                 310                 315                 320

Met Leu Ile Lys Ala Asp Leu Gly Ala Lys Ile Thr Ala Arg Val Val
                325                 330                 335

Asp Glu Leu Arg Asp Lys Ile Ala Glu His Gly Val Gly Ser Glu Ala
            340                 345                 350

Glu Ala Arg Ala Met Leu Arg Ala Ser Leu Ile Asp Ala Cys Arg Pro
        355                 360                 365

Asp Leu Asp Arg Ser Ile Lys Ala Met Pro Tyr Glu Gly Lys Pro Pro
    370                 375                 380

Val Val Leu Val Val Gly Val Asn Gly Thr Gly Lys Thr Thr Thr Thr
385                 390                 395                 400

Gly Lys Leu Ala Arg Val Leu Val Ser Met Gly His Lys Val Ile Leu
                405                 410                 415
```

```
Gly Ala Ala Asp Thr Phe Arg Ala Ala Ala Ala Asp Gln Leu Glu Thr
            420                 425                 430

Trp Gly Arg Arg Val Gly Ala Glu Thr Val Arg Gly Ala Glu Gly Ala
        435                 440                 445

Asp Pro Ala Ser Ile Ala Phe Asp Ala Val Ala Lys Gly Val Glu Arg
    450                 455                 460

Gln Ala Asp Val Val Leu Val Asp Thr Ala Gly Arg Leu His Thr Ser
465                 470                 475                 480

Thr Gly Leu Met Asp Gln Leu Gly Lys Val Lys Arg Val Val Glu Lys
                485                 490                 495

Lys Ala Val Val Asp Glu Val Leu Leu Val Leu Asp Ala Thr Val Gly
            500                 505                 510

Gln Asn Gly Met Gln Gln Ala Arg Ile Phe Arg Glu Val Val Asp Ile
        515                 520                 525

Thr Gly Val Val Leu Thr Lys Leu Asp Gly Thr Ala Lys Gly Gly Ile
    530                 535                 540

Val Phe Gln Val Gln Glu Glu Leu Gly Val Pro Val Lys Leu Val Gly
545                 550                 555                 560

Leu Gly Glu Gly Ala Asp Asp Leu Ala Pro Phe Glu Val Glu Gly Phe
                565                 570                 575

Val Asp Ala Leu Leu Gly
            580
```

<210> 103
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXA02713

<400> 103

```
tgatatgtgg ctatgacatt gtcgcgcagt ttttttatcc acaaacataa gtacaagaca 60

ttggacatct aggccggcag gaaaaggggg gaacacgcac atg gaa gat ttt tcc   115
                                            Met Glu Asp Phe Ser
                                              1               5

ttg gat ggc aac cac gga cac gtt ccc gta atg cgt gat cgt atg gcg   163
Leu Asp Gly Asn His Gly His Val Pro Val Met Arg Asp Arg Met Ala
                  10                  15                  20

gct ttg atc gcc gaa cac gtg gaa gca ttg gga gaa aac gct gtc att   211
Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly Glu Asn Ala Val Ile
              25                  30                  35

gtt gac gca acc ctt ggc gca ggc ggg cat gcg gag ttc ttc ctg aac   259
Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala Glu Phe Phe Leu Asn
```

```
         40                  45                  50

acg ttc ccc aaa gcg cgc ctg att ggc ctt gat cgt gac caa aat gcg   307
Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp Arg Asp Gln Asn Ala
     55                  60                  65

ttg cgg gat gct cgc gcg cga ctt gct cct ttc ggg gag cgg ttc att   355
Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe Gly Glu Arg Phe Ile
 70                  75                  80                  85

ggc gtc cag acg cgt ttc gac gga ctc cgc gag gtg ttg gaa tct gtc   403
Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu Val Leu Glu Ser Val
                 90                  95                 100

gag ggc gac atc att gat tta gct cgc gag cac ggt atc gct ggc gct   451
Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His Gly Ile Ala Gly Ala
            105                 110                 115

ctg ttt gat ctg ggt gtc tcc tcg atg cag ctt gat cag gtg gag cgt   499
Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu Asp Gln Val Glu Arg
        120                 125                 130

ggc ttt gcc tac cgc acg gac gcg cct ctg gac atg cgc atg gat gca   547
Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp Met Arg Met Asp Ala
    135                 140                 145

act cag ggt att acg gct gca gat atc ctc aac act tat tcg cat ggt   595
Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn Thr Tyr Ser His Gly
150                 155                 160                 165

gac atc gct cga atc ttg aag act tac ggc gat gaa cgc ttc gcc ggc   643
Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp Glu Arg Phe Ala Gly
                170                 175                 180

aag att gct tct gcg gtg ctg aaa gaa cgt gaa aaa gag ccg ttc act   691
Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu Lys Glu Pro Phe Thr
            185                 190                 195

acc tct gct cgt ttg gtg gag ctt ctg tac gac gcc atc cct gca gcg   739
Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp Ala Ile Pro Ala Ala
        200                 205                 210

acc cgc cga acc ggt gga cac ccc gcg aaa cgt act ttc cag gcg ttg   787
Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg Thr Phe Gln Ala Leu
    215                 220                 225

cgc gtt gag gtg aac aac gag ctt gat tcc ctg aag aat gtg ctt cct   835
Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu Lys Asn Val Leu Pro
230                 235                 240                 245

caa atc act gac gcc ctc aat gtt ggg gga cgt gca gtg ttt atg agc   883
Gln Ile Thr Asp Ala Leu Asn Val Gly Gly Arg Ala Val Phe Met Ser
                250                 255                 260

tac cag tct cat gag gac aag ctg gtg aag aag ttc ttc acg gat ctg   931
Tyr Gln Ser His Glu Asp Lys Leu Val Lys Lys Phe Phe Thr Asp Leu
            265                 270                 275

acc acc tct aag acc cct ccg ggc ttg cct gtt gat ctt cct gga act   979
Thr Thr Ser Lys Thr Pro Pro Gly Leu Pro Val Asp Leu Pro Gly Thr
        280                 285                 290
```

```
gca cca cag ttt aag cag gtt act cgc ggt gct gaa acg gct tcg gaa   1027
Ala Pro Gln Phe Lys Gln Val Thr Arg Gly Ala Glu Thr Ala Ser Glu
    295                 300                 305

gct gaa att gaa gaa aac cca cgt gcc gca cct gtg aag gtg cgc gca   1075
Ala Glu Ile Glu Glu Asn Pro Arg Ala Ala Pro Val Lys Val Arg Ala
310                 315                 320                 325

atc gaa aga atc ggc aac aac tca gga gac ctc tca tgaccatgac       1121
Ile Glu Arg Ile Gly Asn Asn Ser Gly Asp Leu Ser
                330                 335

aaatggctcc cgc                                                  1134
```

<210> 104
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 104

```
Met Glu Asp Phe Ser Leu Asp Gly Asn His Gly His Val Pro Val Met
  1               5                  10                  15

Arg Asp Arg Met Ala Ala Leu Ile Ala Glu His Val Glu Ala Leu Gly
            20                  25                  30

Glu Asn Ala Val Ile Val Asp Ala Thr Leu Gly Ala Gly Gly His Ala
        35                  40                  45

Glu Phe Phe Leu Asn Thr Phe Pro Lys Ala Arg Leu Ile Gly Leu Asp
    50                  55                  60

Arg Asp Gln Asn Ala Leu Arg Asp Ala Arg Ala Arg Leu Ala Pro Phe
65                  70                  75                  80

Gly Glu Arg Phe Ile Gly Val Gln Thr Arg Phe Asp Gly Leu Arg Glu
                85                  90                  95

Val Leu Glu Ser Val Glu Gly Asp Ile Ile Asp Leu Ala Arg Glu His
            100                 105                 110

Gly Ile Ala Gly Ala Leu Phe Asp Leu Gly Val Ser Ser Met Gln Leu
        115                 120                 125

Asp Gln Val Glu Arg Gly Phe Ala Tyr Arg Thr Asp Ala Pro Leu Asp
    130                 135                 140

Met Arg Met Asp Ala Thr Gln Gly Ile Thr Ala Ala Asp Ile Leu Asn
145                 150                 155                 160

Thr Tyr Ser His Gly Asp Ile Ala Arg Ile Leu Lys Thr Tyr Gly Asp
                165                 170                 175

Glu Arg Phe Ala Gly Lys Ile Ala Ser Ala Val Leu Lys Glu Arg Glu
            180                 185                 190

Lys Glu Pro Phe Thr Thr Ser Ala Arg Leu Val Glu Leu Leu Tyr Asp
        195                 200                 205
```

```
Ala Ile Pro Ala Ala Thr Arg Arg Thr Gly Gly His Pro Ala Lys Arg
    210                 215                 220

Thr Phe Gln Ala Leu Arg Val Glu Val Asn Asn Glu Leu Asp Ser Leu
225                 230                 235                 240

Lys Asn Val Leu Pro Gln Ile Thr Asp Ala Leu Asn Val Gly Gly Arg
                245                 250                 255

Ala Val Phe Met Ser Tyr Gln Ser His Glu Asp Lys Leu Val Lys Lys
            260                 265                 270

Phe Phe Thr Asp Leu Thr Thr Ser Lys Thr Pro Pro Gly Leu Pro Val
        275                 280                 285

Asp Leu Pro Gly Thr Ala Pro Gln Phe Lys Gln Val Thr Arg Gly Ala
    290                 295                 300

Glu Thr Ala Ser Glu Ala Glu Ile Glu Glu Asn Pro Arg Ala Ala Pro
305                 310                 315                 320

Val Lys Val Arg Ala Ile Glu Arg Ile Gly Asn Asn Ser Gly Asp Leu
                325                 330                 335

Ser
```

Replacement Sheet

<210> 105
<211> 789
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN02723

<400> 105
cgtgctcacc atgggtgcag gttccgtgac catgcttgct ccagaaatcc tggatcagct 60

```
gcaaaacaat taggacgtaa gtgaacaagg caggactagc gtg aac aaa aaa gtc   115
                                            Val Asn Lys Lys Val
                                              1               5

atc gcc att gtt gtg ggt gtg gtt gtt gtc ctc gtg gca atc ctg ggc   163
Ile Ala Ile Val Val Gly Val Val Val Val Leu Val Ala Ile Leu Gly
                  10                  15                  20

gtt gtt gcc tgg ttc gtt ccc atc ctc aag gtg gga aac att gaa gta   211
Val Val Ala Trp Phe Val Pro Ile Leu Lys Val Gly Asn Ile Glu Val
              25                  30                  35

acc ggt gca acg cgc aca tat ccg gat caa gta ctg gaa gtc tcc ggg   259
Thr Gly Ala Thr Arg Thr Tyr Pro Asp Gln Val Leu Glu Val Ser Gly
          40                  45                  50

att gtt gag ggc aaa aac ctc ttc cgc gtc gat gcg act gca gca ggg   307
Ile Val Glu Gly Lys Asn Leu Phe Arg Val Asp Ala Thr Ala Ala Gly
      55                  60                  65
```

```
caa aac att gtg gaa ttg ccc tgg gtg aaa tcg gtg acc gtt aac cgt   355
Gln Asn Ile Val Glu Leu Pro Trp Val Lys Ser Val Thr Val Asn Arg
 70                  75                  80                  85

gcc ctg cca agc acc atc acc gtg gag ctg aca gag cgt gag cct gca   403
Ala Leu Pro Ser Thr Ile Thr Val Glu Leu Thr Glu Arg Glu Pro Ala
                90                  95                 100

gtg ttc atc aag cgt gct gat ggt gac cat gtc att gac acc gag ggt   451
Val Phe Ile Lys Arg Ala Asp Gly Asp His Val Ile Asp Thr Glu Gly
            105                 110                 115

aaa gaa att atc att gga aca ccc ccg gtg gga aca gta gaa gtt tct   499
Lys Glu Ile Ile Ile Gly Thr Pro Pro Val Gly Thr Val Glu Val Ser
        120                 125                 130

ggc gcg gat gaa gga aac tca gaa gtg ctt cct gcg gtt att gct gta   547
Gly Ala Asp Glu Gly Asn Ser Glu Val Leu Pro Ala Val Ile Ala Val
    135                 140                 145

atc aac gca att aaa gcg caa gat gcg cag atg aca gaa agt atc cag   595
Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln Met Thr Glu Ser Ile Gln
150                 155                 160                 165

gta gtg gaa gct ccg gat caa ttt gat atc ttg ctg aaa atg aat gat   643
Val Val Glu Ala Pro Asp Gln Phe Asp Ile Leu Leu Lys Met Asn Asp
                170                 175                 180

ggc cgg gaa atc tac tgg gga tcc tcg gaa aac aac cac gat aaa gcg   691
Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu Asn Asn His Asp Lys Ala
            185                 190                 195

gtg gca atg tcg act gtt ttg aag cgg gaa ggc caa cgt tgg aac att   739
Val Ala Met Ser Thr Val Leu Lys Arg Glu Gly Gln Arg Trp Asn Ile
        200                 205                 210

agc tca ccc tca atg gtg aca gtc cgc taaagtggct gggtagttcc         786
Ser Ser Pro Ser Met Val Thr Val Arg
    215                 220

ggt                                                              789
```

<210> 106
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 106

```
Val Asn Lys Lys Val Ile Ala Ile Val Val Gly Val Val Val Val Leu
  1               5                  10                  15

Val Ala Ile Leu Gly Val Val Ala Trp Phe Val Pro Ile Leu Lys Val
             20                  25                  30

Gly Asn Ile Glu Val Thr Gly Ala Thr Arg Thr Tyr Pro Asp Gln Val
         35                  40                  45

Leu Glu Val Ser Gly Ile Val Glu Gly Lys Asn Leu Phe Arg Val Asp
     50                  55                  60
```

```
Ala Thr Ala Ala Gly Gln Asn Ile Val Glu Leu Pro Trp Val Lys Ser
 65                  70                  75                  80

Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu Thr
                 85                  90                  95

Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His Val
            100                 105                 110

Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val Gly
        115                 120                 125

Thr Val Glu Val Ser Gly Ala Asp Glu Gly Asn Ser Glu Val Leu Pro
    130                 135                 140

Ala Val Ile Ala Val Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln Met
145                 150                 155                 160

Thr Glu Ser Ile Gln Val Val Glu Ala Pro Asp Gln Phe Asp Ile Leu
                165                 170                 175

Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu Asn
            180                 185                 190

Asn His Asp Lys Ala Val Ala Met Ser Thr Val Leu Lys Arg Glu Gly
        195                 200                 205

Gln Arg Trp Asn Ile Ser Ser Pro Ser Met Val Thr Val Arg
    210                 215                 220


<210> 107
<211> 500
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(477)
<223> FRXA02723

<400> 107
gat gcg act gca gca ggg caa aac att gtg gaa ttg ccc tgg gtg aaa   48
Asp Ala Thr Ala Ala Gly Gln Asn Ile Val Glu Leu Pro Trp Val Lys
  1               5                  10                  15

tcg gtg acc gtt aac cgt gcc ctg cca agc acc atc acc gtg gag ctg   96
Ser Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu
             20                  25                  30

aca gag cgt gag cct gca gtg ttc atc aag cgt gct gat ggt gac cat   144
Thr Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His
         35                  40                  45

gtc att gac acc gag ggt aaa gaa att atc att gga aca ccc ccg gtg   192
Val Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val
     50                  55                  60

gga aca gta gaa gtt tct ggc gcg gat gaa gga aac tca gaa gtg ctt   240
Gly Thr Val Glu Val Ser Gly Ala Asp Glu Gly Asn Ser Glu Val Leu
 65                  70                  75                  80
```

```
cct gcg gtt att gct gta atc aac gca att aaa gcg caa gat gcg cag   288
Pro Ala Val Ile Ala Val Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln
                 85                  90                  95

atg aca gaa agt atc cag gta gtg gaa gct ccg gat caa ttt gat atc   336
Met Thr Glu Ser Ile Gln Val Val Glu Ala Pro Asp Gln Phe Asp Ile
            100                 105                 110

ttg ctg aaa atg aat gat ggc cgg gaa atc tac tgg gga tcc tcg gaa   384
Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu
        115                 120                 125

aac aac cac gat aaa gcg gtg gca atg tcg act gtt ttg aag cgg gaa   432
Asn Asn His Asp Lys Ala Val Ala Met Ser Thr Val Leu Lys Arg Glu
    130                 135                 140

ggc caa cgt tgg aac att agc tca ccc tca atg gtg aca gtc cgc       477
Gly Gln Arg Trp Asn Ile Ser Ser Pro Ser Met Val Thr Val Arg
145                 150                 155

taaagtggct gggtagttcc ggt                                        500
```

<210> 108
<211> 159
<212> PRT
<213> Corynebacterium glutamicum

<400> 108

```
Asp Ala Thr Ala Ala Gly Gln Asn Ile Val Glu Leu Pro Trp Val Lys
  1               5                  10                  15

Ser Val Thr Val Asn Arg Ala Leu Pro Ser Thr Ile Thr Val Glu Leu
             20                  25                  30

Thr Glu Arg Glu Pro Ala Val Phe Ile Lys Arg Ala Asp Gly Asp His
         35                  40                  45

Val Ile Asp Thr Glu Gly Lys Glu Ile Ile Ile Gly Thr Pro Pro Val
     50                  55                  60

Gly Thr Val Glu Val Ser Gly Ala Asp Glu Gly Asn Ser Glu Val Leu
 65                  70                  75                  80

Pro Ala Val Ile Ala Val Ile Asn Ala Ile Lys Ala Gln Asp Ala Gln
                 85                  90                  95

Met Thr Glu Ser Ile Gln Val Val Glu Ala Pro Asp Gln Phe Asp Ile
            100                 105                 110

Leu Leu Lys Met Asn Asp Gly Arg Glu Ile Tyr Trp Gly Ser Ser Glu
        115                 120                 125

Asn Asn His Asp Lys Ala Val Ala Met Ser Thr Val Leu Lys Arg Glu
    130                 135                 140

Gly Gln Arg Trp Asn Ile Ser Ser Pro Ser Met Val Thr Val Arg
145                 150                 155
```

<210> 109
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXA01426

<400> 109
aaaaagcacc attcggcagc caacactcaa gcttcttaag ttgagtcgtt atagttgagt 60

gttgtaccgc tcgatatctt gcccgaaggg gacttttttc atg acc acg cct cca 115
Met Thr Thr Pro Pro
1 5

gca gcc gct gaa att ttc ggg gac aac ctc gaa aaa gcc att gca tat 163
Ala Ala Ala Glu Ile Phe Gly Asp Asn Leu Glu Lys Ala Ile Ala Tyr
10 15 20

cat gaa tct ttg gca aca gat gga tcc gtc cgc gga ttc atc ggc ccc 211
His Glu Ser Leu Ala Thr Asp Gly Ser Val Arg Gly Phe Ile Gly Pro
25 30 35

cgt gaa gtt ccc cgc ctg tgg gat cgc cac att cta aac tgt ggt gtc 259
Arg Glu Val Pro Arg Leu Trp Asp Arg His Ile Leu Asn Cys Gly Val
40 45 50

atc ggc gaa gct atg gat gag ggc atc tct gtt gca gat att ggt tct 307
Ile Gly Glu Ala Met Asp Glu Gly Ile Ser Val Ala Asp Ile Gly Ser
55 60 65

ggt gcg gga ctg cca gga att cct ctt gct atc gca cgc cca gat ctc 355
Gly Ala Gly Leu Pro Gly Ile Pro Leu Ala Ile Ala Arg Pro Asp Leu
70 75 80 85

aac atc act ctc att gag cca ttg ctc aag cgt tcg gtg tac ctc aac 403
Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg Ser Val Tyr Leu Asn
90 95 100

gag gta aaa gaa gcc ctg aac ttg gac aat gtc acc gtc gtt cgt ggt 451
Glu Val Lys Glu Ala Leu Asn Leu Asp Asn Val Thr Val Val Arg Gly
105 110 115

cgt gct gag gaa aaa gtg gtg cgc aag cag gtc gga ttg gtc gat att 499
Arg Ala Glu Glu Lys Val Val Arg Lys Gln Val Gly Leu Val Asp Ile
120 125 130

gtc acc tcc cga gct gtt gct cca ctg ggc aag cta gcg acc tgg tcg 547
Val Thr Ser Arg Ala Val Ala Pro Leu Gly Lys Leu Ala Thr Trp Ser
135 140 145

ttg ccg ctg gtg aaa atc ggt gga cgc atg gtg gcc atg aaa ggc tcc 595
Leu Pro Leu Val Lys Ile Gly Gly Arg Met Val Ala Met Lys Gly Ser
150 155 160 165

agc gtt gag gaa gaa att gag cgt gac gcc aag gaa atc cgc aag gct 643
Ser Val Glu Glu Glu Ile Glu Arg Asp Ala Lys Glu Ile Arg Lys Ala
170 175 180

```
ggc ggc act gac att aag gtt tat acc gtg ggt gag gcg ctg ttg agc   691
Gly Gly Thr Asp Ile Lys Val Tyr Thr Val Gly Glu Ala Leu Leu Ser
            185                 190                 195

gag ccc aca aca ctt att tca atc cgc agg gaa aag taaccatcca        737
Glu Pro Thr Thr Leu Ile Ser Ile Arg Arg Glu Lys
        200                 205

cttcggtgga atg                                                   750
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<210> 110
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 110

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Met Thr Thr Pro Pro Ala Ala Ala Glu Ile Phe Gly Asp Asn Leu Glu
  1               5                  10                  15

Lys Ala Ile Ala Tyr His Glu Ser Leu Ala Thr Asp Gly Ser Val Arg
             20                  25                  30

Gly Phe Ile Gly Pro Arg Glu Val Pro Arg Leu Trp Asp Arg His Ile
         35                  40                  45

Leu Asn Cys Gly Val Ile Gly Glu Ala Met Asp Glu Gly Ile Ser Val
     50                  55                  60

Ala Asp Ile Gly Ser Gly Ala Gly Leu Pro Gly Ile Pro Leu Ala Ile
 65                  70                  75                  80

Ala Arg Pro Asp Leu Asn Ile Thr Leu Ile Glu Pro Leu Leu Lys Arg
                 85                  90                  95

Ser Val Tyr Leu Asn Glu Val Lys Glu Ala Leu Asn Leu Asp Asn Val
            100                 105                 110

Thr Val Val Arg Gly Arg Ala Glu Glu Lys Val Val Arg Lys Gln Val
        115                 120                 125

Gly Leu Val Asp Ile Val Thr Ser Arg Ala Val Ala Pro Leu Gly Lys
    130                 135                 140

Leu Ala Thr Trp Ser Leu Pro Leu Val Lys Ile Gly Gly Arg Met Val
145                 150                 155                 160

Ala Met Lys Gly Ser Ser Val Glu Glu Glu Ile Glu Arg Asp Ala Lys
                165                 170                 175

Glu Ile Arg Lys Ala Gly Gly Thr Asp Ile Lys Val Tyr Thr Val Gly
            180                 185                 190

Glu Ala Leu Leu Ser Glu Pro Thr Thr Leu Ile Ser Ile Arg Arg Glu
        195                 200                 205

Lys
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<210> 111

<211> 1260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1237)
<223> RXA01428

<400> 111
gcgatgaatc cggtccgatc ggcctaaaac ctgcgaaata gcagtaaact tctttgaata 60

cgttaattgt tgtgctgtac gaaaggtgcg tctaagagcg atg gct cag aac aag 115
Met Ala Gln Asn Lys
1 5

ggt tcc gac aag tcc cag acg gaa aag cgt aag ggc ggt ctg ggg cgc 163
Gly Ser Asp Lys Ser Gln Thr Glu Lys Arg Lys Gly Gly Leu Gly Arg
10 15 20

ggt ctg gcc gca ctt att ccc tca gga cca agt aat tcc cca ggt ctt 211
Gly Leu Ala Ala Leu Ile Pro Ser Gly Pro Ser Asn Ser Pro Gly Leu
25 30 35

ggt ggc ggt gcg gct gac atc att ttg ggc ggt acc gtg ggt gcg cgt 259
Gly Gly Gly Ala Ala Asp Ile Ile Leu Gly Gly Thr Val Gly Ala Arg
40 45 50

act gct gca gct ccc aag cgt gag tcc aca cca gca gct cct gca cct 307
Thr Ala Ala Ala Pro Lys Arg Glu Ser Thr Pro Ala Ala Pro Ala Pro
55 60 65

gag gct cct gcg cag gcc gct cca caa cac act gag gcc aca aag cca 355
Glu Ala Pro Ala Gln Ala Ala Pro Gln His Thr Glu Ala Thr Lys Pro
70 75 80 85

gag gta gtt cca gag cca gca gct cct gct cca acg cag tca gca cag 403
Glu Val Val Pro Glu Pro Ala Ala Pro Ala Pro Thr Gln Ser Ala Gln
90 95 100

cag gaa gcg ccg cag gca cag cca gca cag cag tct gag ttc ggc gca 451
Gln Glu Ala Pro Gln Ala Gln Pro Ala Gln Gln Ser Glu Phe Gly Ala
105 110 115

tcc tac ctt gag atc ccg atc gag cag atc cgc ccc aac ccg cag cag 499
Ser Tyr Leu Glu Ile Pro Ile Glu Gln Ile Arg Pro Asn Pro Gln Gln
120 125 130

cct cgc cat gag ttt gat ccg cag gca ctt gac gag ttg gtg cat tcg 547
Pro Arg His Glu Phe Asp Pro Gln Ala Leu Asp Glu Leu Val His Ser
135 140 145

atc agc gag ttc ggc ctc atg cag ccg atc gtg gtg cgc agg tcc gag 595
Ile Ser Glu Phe Gly Leu Met Gln Pro Ile Val Val Arg Arg Ser Glu
150 155 160 165

gat ggc tat gag ctc atc atg ggt gag cgt cgt tgg cgt gca tcc aag 643
Asp Gly Tyr Glu Leu Ile Met Gly Glu Arg Arg Trp Arg Ala Ser Lys
170 175 180

cga gct ggc ctt gag gtt atc ccg gcg att gtc cgt gaa act gaa gac 691

```
Arg Ala Gly Leu Glu Val Ile Pro Ala Ile Val Arg Glu Thr Glu Asp
            185                 190                 195

agc gcg atg ctg cgc gac gcc ctt ttg gaa aat atc cac agg gtg cag   739
Ser Ala Met Leu Arg Asp Ala Leu Leu Glu Asn Ile His Arg Val Gln
        200                 205                 210

ctg aat cct ttg gaa gag gca gcc gcc tac cag cag ttg ctg gag gag   787
Leu Asn Pro Leu Glu Glu Ala Ala Ala Tyr Gln Gln Leu Leu Glu Glu
    215                 220                 225

ttc ggt gtc acc cag gca gag ctg gcc gat aag ctg ggc cgt tcc cgt   835
Phe Gly Val Thr Gln Ala Glu Leu Ala Asp Lys Leu Gly Arg Ser Arg
230                 235                 240                 245

ccg gta atc acc aat atg att cgt ctg ctg ggc ctt cca gtc aac gtg   883
Pro Val Ile Thr Asn Met Ile Arg Leu Leu Gly Leu Pro Val Asn Val
                250                 255                 260

cag acc aag gtg gca gcc ggt gtg ctg tct gca ggc cat gca cgc gca   931
Gln Thr Lys Val Ala Ala Gly Val Leu Ser Ala Gly His Ala Arg Ala
            265                 270                 275

ttg ctg ggg ctc aag gcc ggc gag gat gct cag gac acc ctg gcg acc   979
Leu Leu Gly Leu Lys Ala Gly Glu Asp Ala Gln Asp Thr Leu Ala Thr
        280                 285                 290

cga atc atc gct gag ggc ctg tct gtg cgt gct act gag gaa ttg gtg  1027
Arg Ile Ile Ala Glu Gly Leu Ser Val Arg Ala Thr Glu Glu Leu Val
    295                 300                 305

ctg ctg cac aac cgt ggt gat cag gat gag gag aag aag cca cgc gaa  1075
Leu Leu His Asn Arg Gly Asp Gln Asp Glu Glu Lys Lys Pro Arg Glu
310                 315                 320                 325

aag gct gca act cct gag gtc ttt acc cgt gcg gct gag tcc ttg gcg  1123
Lys Ala Ala Thr Pro Glu Val Phe Thr Arg Ala Ala Glu Ser Leu Ala
                330                 335                 340

gat aat ttg gat acc aag gtc tcg gtg atg atg ggt aag aag aag ggc  1171
Asp Asn Leu Asp Thr Lys Val Ser Val Met Met Gly Lys Lys Lys Gly
            345                 350                 355

aag ctc gtg gtg gaa ttc ggc gac aag gat gat ttc gag cgc atc atg  1219
Lys Leu Val Val Glu Phe Gly Asp Lys Asp Asp Phe Glu Arg Ile Met
        360                 365                 370

tcc ttg atc cag ggc caa taattttaag tttggcgcca tgc                1260
Ser Leu Ile Gln Gly Gln
    375
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<210> 112
<211> 379
<212> PRT
<213> Corynebacterium glutamicum

<400> 112

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Met Ala Gln Asn Lys Gly Ser Asp Lys Ser Gln Thr Glu Lys Arg Lys
  1               5                  10                  15
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Gly Gly Leu Gly Arg Gly Leu Ala Ala Leu Ile Pro Ser Gly Pro Ser
20 25 30

Asn Ser Pro Gly Leu Gly Gly Gly Ala Ala Asp Ile Ile Leu Gly Gly
35 40 45

Thr Val Gly Ala Arg Thr Ala Ala Ala Pro Lys Arg Glu Ser Thr Pro
50 55 60

Ala Ala Pro Ala Pro Glu Ala Pro Ala Gln Ala Ala Pro Gln His Thr
65 70 75 80

Glu Ala Thr Lys Pro Glu Val Val Pro Glu Pro Ala Ala Pro Ala Pro
85 90 95

Thr Gln Ser Ala Gln Gln Glu Ala Pro Gln Ala Gln Pro Ala Gln Gln
100 105 110

Ser Glu Phe Gly Ala Ser Tyr Leu Glu Ile Pro Ile Glu Gln Ile Arg
115 120 125

Pro Asn Pro Gln Gln Pro Arg His Glu Phe Asp Pro Gln Ala Leu Asp
130 135 140

Glu Leu Val His Ser Ile Ser Glu Phe Gly Leu Met Gln Pro Ile Val
145 150 155 160

Val Arg Arg Ser Glu Asp Gly Tyr Glu Leu Ile Met Gly Glu Arg Arg
165 170 175

Trp Arg Ala Ser Lys Arg Ala Gly Leu Glu Val Ile Pro Ala Ile Val
180 185 190

Arg Glu Thr Glu Asp Ser Ala Met Leu Arg Asp Ala Leu Leu Glu Asn
195 200 205

Ile His Arg Val Gln Leu Asn Pro Leu Glu Glu Ala Ala Ala Tyr Gln
210 215 220

Gln Leu Leu Glu Glu Phe Gly Val Thr Gln Ala Glu Leu Ala Asp Lys
225 230 235 240

Leu Gly Arg Ser Arg Pro Val Ile Thr Asn Met Ile Arg Leu Leu Gly
245 250 255

Leu Pro Val Asn Val Gln Thr Lys Val Ala Ala Gly Val Leu Ser Ala
260 265 270

Gly His Ala Arg Ala Leu Leu Gly Leu Lys Ala Gly Glu Asp Ala Gln
275 280 285

Asp Thr Leu Ala Thr Arg Ile Ile Ala Glu Gly Leu Ser Val Arg Ala
290 295 300

Thr Glu Glu Leu Val Leu Leu His Asn Arg Gly Asp Gln Asp Glu Glu
305 310 315 320

Lys Lys Pro Arg Glu Lys Ala Ala Thr Pro Glu Val Phe Thr Arg Ala
325 330 335

Ala Glu Ser Leu Ala Asp Asn Leu Asp Thr Lys Val Ser Val Met Met

```
            340                 345                 350

Gly Lys Lys Lys Gly Lys Leu Val Val Glu Phe Gly Asp Lys Asp Asp
        355                 360                 365

Phe Glu Arg Ile Met Ser Leu Ile Gln Gly Gln
    370                 375


<210> 113
<211> 3441
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(3418)
<223> RXA01640

<400> 113
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cttgattttt ccaatgatga tgggtatgag cgtcctgatg atg ttc gcc cca cct   115
                                        Met Phe Ala Pro Pro
                                          1               5

gaa ggt gac gat act gat gag gtt cgg cgc acc tat tta cgt cac ctg   163
Glu Gly Asp Asp Thr Asp Glu Val Arg Arg Thr Tyr Leu Arg His Leu
                  10                  15                  20

ggt gca ttg cgg gcg aaa gcg aca gat cac gcg gcg atg cag cgc agg   211
Gly Ala Leu Arg Ala Lys Ala Thr Asp His Ala Ala Met Gln Arg Arg
              25                  30                  35

cat gaa tgg cac agg cat cct gat cca gca acc ttg tgg tcc acg ttg   259
His Glu Trp His Arg His Pro Asp Pro Ala Thr Leu Trp Ser Thr Leu
          40                  45                  50

ggg act cgg cgg atg tgg gag cgc acc caa gat gat caa gat tgt ttg   307
Gly Thr Arg Arg Met Trp Glu Arg Thr Gln Asp Asp Gln Asp Cys Leu
      55                  60                  65

gaa atc cgt ttt ggt ttg ggc gtg acc agg ctt gat ccg gct att aac   355
Glu Ile Arg Phe Gly Leu Gly Val Thr Arg Leu Asp Pro Ala Ile Asn
  70                  75                  80                  85

gtg agt gat tcg ggt gcg ccg gag gat ctt gat ccg gta tgt gcg gtg   403
Val Ser Asp Ser Gly Ala Pro Glu Asp Leu Asp Pro Val Cys Ala Val
                  90                  95                 100

tcg ttg cgt cac acc att cgg gat gtg ggg tcg gtg cag agc atg ccg   451
Ser Leu Arg His Thr Ile Arg Asp Val Gly Ser Val Gln Ser Met Pro
              105                 110                 115

gtg tcg gtt cag ttg cag gcg ttt cga ttc att ggg ctc aac ggt gcg   499
Val Ser Val Gln Leu Gln Ala Phe Arg Phe Ile Gly Leu Asn Gly Ala
          120                 125                 130

ggc gca cat gat ctg gcg cgg gcg ctg gtt gtg cag ttg ttg tac cac   547
Gly Ala His Asp Leu Ala Arg Ala Leu Val Val Gln Leu Leu Tyr His
      135                 140                 145
```

```
cac gga ccg gag gtg gtg ggt atc aaa gcg atc ggg gag tcg ggt tgg   595
His Gly Pro Glu Val Val Gly Ile Lys Ala Ile Gly Glu Ser Gly Trp
150                 155                 160                 165

gag tgg ctg aaa tgg gta ccg cac acc cgc gat ccg gag aag gca gcc   643
Glu Trp Leu Lys Trp Val Pro His Thr Arg Asp Pro Glu Lys Ala Ala
                170                 175                 180

ttt cgg att ttg ctg gtg gat tcc gtg ttg acc aac ggc acc gaa agc   691
Phe Arg Ile Leu Leu Val Asp Ser Val Leu Thr Asn Gly Thr Glu Ser
            185                 190                 195

ttc att gat gac ccc caa tgg acc acg atc atc aac gtt ggc gcg cag   739
Phe Ile Asp Asp Pro Gln Trp Thr Thr Ile Ile Asn Val Gly Ala Gln
        200                 205                 210

acc agc acc gca ttg ggc cag ctg gca gag gat gaa ggg ctg ctg ttg   787
Thr Ser Thr Ala Leu Gly Gln Leu Ala Glu Asp Glu Gly Leu Leu Leu
    215                 220                 225

cac gtc gat aag cgt ctg cat gtg gct acc gcg cac ggc gcg gag gag   835
His Val Asp Lys Arg Leu His Val Ala Thr Ala His Gly Ala Glu Glu
230                 235                 240                 245

ctg ggc acg ccg gat gcg gtt agc gct gag ctt gcg gag gtt ttt ggc   883
Leu Gly Thr Pro Asp Ala Val Ser Ala Glu Leu Ala Glu Val Phe Gly
                250                 255                 260

cgc cgt ttg act gct ttt cga cgc aca acc aca gca cac gcg gcg agc   931
Arg Arg Leu Thr Ala Phe Arg Arg Thr Thr Thr Ala His Ala Ala Ser
            265                 270                 275

tct ggt gaa ttg ctg tcc ctt ttg ggg att gat gac gtg gag cat tta   979
Ser Gly Glu Leu Leu Ser Leu Leu Gly Ile Asp Asp Val Glu His Leu
        280                 285                 290

act cca gaa acc tta tgg atg aac aag cgc acg cag cct aaa act cgt   1027
Thr Pro Glu Thr Leu Trp Met Asn Lys Arg Thr Gln Pro Lys Thr Arg
    295                 300                 305

ttg gcg gtg ccc ttg ggt ttg aac gcg tcc ggt cgg ccg atg gta ctg   1075
Leu Ala Val Pro Leu Gly Leu Asn Ala Ser Gly Arg Pro Met Val Leu
310                 315                 320                 325

gat ctg aag gaa tcg gcg cac ggc gga atg gga cca cat ggg ctg tgc   1123
Asp Leu Lys Glu Ser Ala His Gly Gly Met Gly Pro His Gly Leu Cys
                330                 335                 340

atc ggc gct act ggc agc gga aaa tcc gaa ctt tta aga aca ctt gtt   1171
Ile Gly Ala Thr Gly Ser Gly Lys Ser Glu Leu Leu Arg Thr Leu Val
            345                 350                 355

cta ggt ttg acg atc acc cat tcg cct gag gaa ttg aat ctg gtg ttg   1219
Leu Gly Leu Thr Ile Thr His Ser Pro Glu Glu Leu Asn Leu Val Leu
        360                 365                 370

gtg gat ttt aaa ggt ggc gcc acc ttt ttg ggc ttc gag cag ctg cct   1267
Val Asp Phe Lys Gly Gly Ala Thr Phe Leu Gly Phe Glu Gln Leu Pro
    375                 380                 385
```

Sequence Listing

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cac acg tcc gcg gtg atc acc aac ttg gag gaa gag ccc gtg ctg gtg   1315
His Thr Ser Ala Val Ile Thr Asn Leu Glu Glu Glu Pro Val Leu Val
390                 395                 400                 405

gag cgc atg cat gat gcg att tcg ggt gag atg aac cgc agg caa gaa   1363
Glu Arg Met His Asp Ala Ile Ser Gly Glu Met Asn Arg Arg Gln Glu
                410                 415                 420

gcc ctt cgg cag gca ggt ggc tgc gcc aat gtg gat gaa tac aac cag   1411
Ala Leu Arg Gln Ala Gly Gly Cys Ala Asn Val Asp Glu Tyr Asn Gln
            425                 430                 435

cgt gat ggt gtg aaa ccg atg ccc gcg ctg ctc att gag agc gat gaa   1459
Arg Asp Gly Val Lys Pro Met Pro Ala Leu Leu Ile Glu Ser Asp Glu
        440                 445                 450

ttc tcg gag ttg ctt ggc caa cat ccc gat ttc gca gac cta ttc gtc   1507
Phe Ser Glu Leu Leu Gly Gln His Pro Asp Phe Ala Asp Leu Phe Val
    455                 460                 465

gcc gtc gga cgc ttg ggc cgt tcc tta cac atc cat ttg ttg ctc gct   1555
Ala Val Gly Arg Leu Gly Arg Ser Leu His Ile His Leu Leu Leu Ala
470                 475                 480                 485

agc caa cgt ctg gaa gag ggg cgg ttg cgc gga ttg gat tcc cac ttg   1603
Ser Gln Arg Leu Glu Glu Gly Arg Leu Arg Gly Leu Asp Ser His Leu
                490                 495                 500

tcc tac cgg atc ggc tta aaa acc ttt tcc gca tcc gaa tcg cgc cag   1651
Ser Tyr Arg Ile Gly Leu Lys Thr Phe Ser Ala Ser Glu Ser Arg Gln
            505                 510                 515

gta tta ggc atc act gac gca tat caa tta ccc agc caa ccc ggc gca   1699
Val Leu Gly Ile Thr Asp Ala Tyr Gln Leu Pro Ser Gln Pro Gly Ala
        520                 525                 530

ggt ttc ctc aaa tcc gac gtc gac acc gtc acc cgc ttc caa gca agt   1747
Gly Phe Leu Lys Ser Asp Val Asp Thr Val Thr Arg Phe Gln Ala Ser
    535                 540                 545

tat gta tcc ggc ccc atc atg cgt cgc cat cac ctc gca cca acg cag   1795
Tyr Val Ser Gly Pro Ile Met Arg Arg His His Leu Ala Pro Thr Gln
550                 555                 560                 565

tcc cgg gtg cgc ctt ttt acc agc tgg gag gaa ccc aaa gag gag gtg   1843
Ser Arg Val Arg Leu Phe Thr Ser Trp Glu Glu Pro Lys Glu Glu Val
                570                 575                 580

att gtc gag caa agc acc gag acg ctt atc gac gcc gtg gtt gcg cgc   1891
Ile Val Glu Gln Ser Thr Glu Thr Leu Ile Asp Ala Val Val Ala Arg
            585                 590                 595

gcc atc agc gcc gcg aag ttg cgg ggg tta agc gct cat cgc atc tgg   1939
Ala Ile Ser Ala Ala Lys Leu Arg Gly Leu Ser Ala His Arg Ile Trp
        600                 605                 610

ttg cca ccg ttg ccg gca gaa gtt tcg att ggt gct ttg gct gat gat   1987
Leu Pro Pro Leu Pro Ala Glu Val Ser Ile Gly Ala Leu Ala Asp Asp
    615                 620                 625

gtc ggt gag cta agc gcc gtg atc ggg atg atc gat aga ccc tat caa   2035
```

```
Val Gly Glu Leu Ser Ala Val Ile Gly Met Ile Asp Arg Pro Tyr Gln
630                 635                 640                 645

cag cga caa gat cca ttg ctg att gat ttt tct ctc acc ggt gga agc   2083
Gln Arg Gln Asp Pro Leu Leu Ile Asp Phe Ser Leu Thr Gly Gly Ser
                650                 655                 660

ggc cac tgg gct att tgt ggt ggg ccc caa acc gga aag tcc acg gca   2131
Gly His Trp Ala Ile Cys Gly Gly Pro Gln Thr Gly Lys Ser Thr Ala
            665                 670                 675

ttg cgc agc atc gtg atc tcc atg gca gca acg cat agc aca gaa aac   2179
Leu Arg Ser Ile Val Ile Ser Met Ala Ala Thr His Ser Thr Glu Asn
        680                 685                 690

atc cgc ttt tac gtg ctg gat tta tct gga acc tcc ctg gaa aat ctc   2227
Ile Arg Phe Tyr Val Leu Asp Leu Ser Gly Thr Ser Leu Glu Asn Leu
    695                 700                 705

tcc cgg ctg cct cat gtt gca ggc gtg gca gga cgc aaa gat cca gag   2275
Ser Arg Leu Pro His Val Ala Gly Val Ala Gly Arg Lys Asp Pro Glu
710                 715                 720                 725

aaa gtc cgc cga gtt gtc gat gaa gta cga ggc ctg atc aac cac cct   2323
Lys Val Arg Arg Val Val Asp Glu Val Arg Gly Leu Ile Asn His Pro
                730                 735                 740

gaa caa cgc cac acc ttc ctt att gtg gac ggc tgg cac acc atc acc   2371
Glu Gln Arg His Thr Phe Leu Ile Val Asp Gly Trp His Thr Ile Thr
            745                 750                 755

caa gaa ttc gac gag ctt ttc gac gcc ttc gta gac atc gcc gcc aac   2419
Gln Glu Phe Asp Glu Leu Phe Asp Ala Phe Val Asp Ile Ala Ala Asn
        760                 765                 770

ggc ctt gcc tcg cgg gtg cat tta gtt tta agc act caa cgc tgg agt   2467
Gly Leu Ala Ser Arg Val His Leu Val Leu Ser Thr Gln Arg Trp Ser
    775                 780                 785

tcc atc cgc ccc gcg gtc cgc gat ctg gtg act ggc aga atc gaa ttg   2515
Ser Ile Arg Pro Ala Val Arg Asp Leu Val Thr Gly Arg Ile Glu Leu
790                 795                 800                 805

aaa ctc ggc gaa gcc atg gat tcg gtg att gat cgt aaa gct cag ctt   2563
Lys Leu Gly Glu Ala Met Asp Ser Val Ile Asp Arg Lys Ala Gln Leu
                810                 815                 820

cgg atc ccg tcg aaa cct ggg cgt ggc ctc aac ctg gat aaa gaa cac   2611
Arg Ile Pro Ser Lys Pro Gly Arg Gly Leu Asn Leu Asp Lys Glu His
            825                 830                 835

atc ctt att gct cat gcg tct ggc caa gac atc gcc cag gta tgc gtc   2659
Ile Leu Ile Ala His Ala Ser Gly Gln Asp Ile Ala Gln Val Cys Val
        840                 845                 850

atg gcc gat ggg caa gga tgg cag cag gtc cca caa tta agc gtg ctg   2707
Met Ala Asp Gly Gln Gly Trp Gln Gln Val Pro Gln Leu Ser Val Leu
    855                 860                 865

cct gcg cat atc ctg ctt cac gag ctt gag ctt tct gcg aca cct ggc   2755
Pro Ala His Ile Leu Leu His Glu Leu Glu Leu Ser Ala Thr Pro Gly
```

```
870                 875                 880                 885

atc ccg att gca cgg gga ggt gct gaa cta tcc acg ctg acg tgg gat   2803
Ile Pro Ile Ala Arg Gly Gly Ala Glu Leu Ser Thr Leu Thr Trp Asp
                890                 895                 900

cca gaa tcc agc cgc cac ctt cta gct ttt ggt tct caa ggt tgt ggc   2851
Pro Glu Ser Ser Arg His Leu Leu Ala Phe Gly Ser Gln Gly Cys Gly
            905                 910                 915

aaa tcc tcg ctg atc cgc acg att gtc acg ggt ctg aca att gtg ggg   2899
Lys Ser Ser Leu Ile Arg Thr Ile Val Thr Gly Leu Thr Ile Val Gly
        920                 925                 930

cgg gag aaa gca cgc ttg gta ttt ttc gac ctt cga cgc acc cac cta   2947
Arg Glu Lys Ala Arg Leu Val Phe Phe Asp Leu Arg Arg Thr His Leu
    935                 940                 945

ggc ctg gtc ccc gaa gac atg ttg gct gct tat tgt gct act tcc aca   2995
Gly Leu Val Pro Glu Asp Met Leu Ala Ala Tyr Cys Ala Thr Ser Thr
950                 955                 960                 965

gca gtc cac aac acc atc aaa gac atg gtg gct acg cta tcc gcc aga   3043
Ala Val His Asn Thr Ile Lys Asp Met Val Ala Thr Leu Ser Ala Arg
                970                 975                 980

ctt cca gga cct gat atc acc gcc caa gaa ctc cgc gat cgt tcc tgg   3091
Leu Pro Gly Pro Asp Ile Thr Ala Gln Glu Leu Arg Asp Arg Ser Trp
            985                 990                 995

tgg cag ggg ccc gac att tat tta gtt atc gat gat tat gat ttg ctc   3139
Trp Gln Gly Pro Asp Ile Tyr Leu Val Ile Asp Asp Tyr Asp Leu Leu
        1000                1005                1010

ccc gcc ggc acc ctg cac ccg ctg cgc gag atc atc ccg cat gca aga   3187
Pro Ala Gly Thr Leu His Pro Leu Arg Glu Ile Ile Pro His Ala Arg
    1015                1020                1025

gac gta ggc ctg cac atc gtg ctc acc cgc aaa gcc ggt ggc gcc tcg   3235
Asp Val Gly Leu His Ile Val Leu Thr Arg Lys Ala Gly Gly Ala Ser
1030                1035                1040                1045

cgt gcg ctc tac gat ccg gtc atg tcc gag atc aag gac caa tca ccg   3283
Arg Ala Leu Tyr Asp Pro Val Met Ser Glu Ile Lys Asp Gln Ser Pro
                1050                1055                1060

cac gtc gtg ctt ttc gac gcc gac cgc gac gaa ggc gct atc cta ggc   3331
His Val Val Leu Phe Asp Ala Asp Arg Asp Glu Gly Ala Ile Leu Gly
            1065                1070                1075

atc aaa ccc aca gca caa cca cca gga cgt gcc acg atg tcc atc cgt   3379
Ile Lys Pro Thr Ala Gln Pro Pro Gly Arg Ala Thr Met Ser Ile Arg
        1080                1085                1090

ggt gaa aac atc ggt gtt gca cag atg gca ccg cat agg tgatgactca   3428
Gly Glu Asn Ile Gly Val Ala Gln Met Ala Pro His Arg
    1095                1100                1105

tgagcaccca aac                                                  3441
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<210> 114
<211> 1106
<212> PRT
<213> Corynebacterium glutamicum

<400> 114

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Met Phe Ala Pro Pro Glu Gly Asp Asp Thr Asp Glu Val Arg Arg Thr
  1               5                  10                  15

Tyr Leu Arg His Leu Gly Ala Leu Arg Ala Lys Ala Thr Asp His Ala
             20                  25                  30

Ala Met Gln Arg Arg His Glu Trp His Arg His Pro Asp Pro Ala Thr
         35                  40                  45

Leu Trp Ser Thr Leu Gly Thr Arg Arg Met Trp Glu Arg Thr Gln Asp
     50                  55                  60

Asp Gln Asp Cys Leu Glu Ile Arg Phe Gly Leu Gly Val Thr Arg Leu
 65                  70                  75                  80

Asp Pro Ala Ile Asn Val Ser Asp Ser Gly Ala Pro Glu Asp Leu Asp
                 85                  90                  95

Pro Val Cys Ala Val Ser Leu Arg His Thr Ile Arg Asp Val Gly Ser
            100                 105                 110

Val Gln Ser Met Pro Val Ser Val Gln Leu Gln Ala Phe Arg Phe Ile
        115                 120                 125

Gly Leu Asn Gly Ala Gly Ala His Asp Leu Ala Arg Ala Leu Val Val
    130                 135                 140

Gln Leu Leu Tyr His His Gly Pro Glu Val Val Gly Ile Lys Ala Ile
145                 150                 155                 160

Gly Glu Ser Gly Trp Glu Trp Leu Lys Trp Val Pro His Thr Arg Asp
                165                 170                 175

Pro Glu Lys Ala Ala Phe Arg Ile Leu Leu Val Asp Ser Val Leu Thr
            180                 185                 190

Asn Gly Thr Glu Ser Phe Ile Asp Asp Pro Gln Trp Thr Thr Ile Ile
        195                 200                 205

Asn Val Gly Ala Gln Thr Ser Thr Ala Leu Gly Gln Leu Ala Glu Asp
    210                 215                 220

Glu Gly Leu Leu Leu His Val Asp Lys Arg Leu His Val Ala Thr Ala
225                 230                 235                 240

His Gly Ala Glu Glu Leu Gly Thr Pro Asp Ala Val Ser Ala Glu Leu
                245                 250                 255

Ala Glu Val Phe Gly Arg Arg Leu Thr Ala Phe Arg Arg Thr Thr Thr
            260                 265                 270

Ala His Ala Ala Ser Ser Gly Glu Leu Leu Ser Leu Leu Gly Ile Asp
        275                 280                 285

Asp Val Glu His Leu Thr Pro Glu Thr Leu Trp Met Asn Lys Arg Thr
```

```
    290                 295                 300

Gln Pro Lys Thr Arg Leu Ala Val Pro Leu Gly Leu Asn Ala Ser Gly
305                 310                 315                 320

Arg Pro Met Val Leu Asp Leu Lys Glu Ser Ala His Gly Gly Met Gly
                325                 330                 335

Pro His Gly Leu Cys Ile Gly Ala Thr Gly Ser Gly Lys Ser Glu Leu
            340                 345                 350

Leu Arg Thr Leu Val Leu Gly Leu Thr Ile Thr His Ser Pro Glu Glu
        355                 360                 365

Leu Asn Leu Val Leu Val Asp Phe Lys Gly Gly Ala Thr Phe Leu Gly
    370                 375                 380

Phe Glu Gln Leu Pro His Thr Ser Ala Val Ile Thr Asn Leu Glu Glu
385                 390                 395                 400

Glu Pro Val Leu Val Glu Arg Met His Asp Ala Ile Ser Gly Glu Met
                405                 410                 415

Asn Arg Arg Gln Glu Ala Leu Arg Gln Ala Gly Gly Cys Ala Asn Val
            420                 425                 430

Asp Glu Tyr Asn Gln Arg Asp Gly Val Lys Pro Met Pro Ala Leu Leu
        435                 440                 445

Ile Glu Ser Asp Glu Phe Ser Glu Leu Leu Gly Gln His Pro Asp Phe
    450                 455                 460

Ala Asp Leu Phe Val Ala Val Gly Arg Leu Gly Arg Ser Leu His Ile
465                 470                 475                 480

His Leu Leu Leu Ala Ser Gln Arg Leu Glu Glu Gly Arg Leu Arg Gly
                485                 490                 495

Leu Asp Ser His Leu Ser Tyr Arg Ile Gly Leu Lys Thr Phe Ser Ala
            500                 505                 510

Ser Glu Ser Arg Gln Val Leu Gly Ile Thr Asp Ala Tyr Gln Leu Pro
        515                 520                 525

Ser Gln Pro Gly Ala Gly Phe Leu Lys Ser Asp Val Asp Thr Val Thr
    530                 535                 540

Arg Phe Gln Ala Ser Tyr Val Ser Gly Pro Ile Met Arg Arg His His
545                 550                 555                 560

Leu Ala Pro Thr Gln Ser Arg Val Arg Leu Phe Thr Ser Trp Glu Glu
                565                 570                 575

Pro Lys Glu Glu Val Ile Val Glu Gln Ser Thr Glu Thr Leu Ile Asp
            580                 585                 590

Ala Val Val Ala Arg Ala Ile Ser Ala Ala Lys Leu Arg Gly Leu Ser
        595                 600                 605

Ala His Arg Ile Trp Leu Pro Pro Leu Pro Ala Glu Val Ser Ile Gly
    610                 615                 620
```

```
Ala Leu Ala Asp Asp Val Gly Glu Leu Ser Ala Val Ile Gly Met Ile
625                 630                 635                 640

Asp Arg Pro Tyr Gln Gln Arg Gln Asp Pro Leu Leu Ile Asp Phe Ser
                645                 650                 655

Leu Thr Gly Gly Ser Gly His Trp Ala Ile Cys Gly Gly Pro Gln Thr
            660                 665                 670

Gly Lys Ser Thr Ala Leu Arg Ser Ile Val Ile Ser Met Ala Ala Thr
        675                 680                 685

His Ser Thr Glu Asn Ile Arg Phe Tyr Val Leu Asp Leu Ser Gly Thr
    690                 695                 700

Ser Leu Glu Asn Leu Ser Arg Leu Pro His Val Ala Gly Val Ala Gly
705                 710                 715                 720

Arg Lys Asp Pro Glu Lys Val Arg Arg Val Val Asp Glu Val Arg Gly
                725                 730                 735

Leu Ile Asn His Pro Glu Gln Arg His Thr Phe Leu Ile Val Asp Gly
            740                 745                 750

Trp His Thr Ile Thr Gln Glu Phe Asp Glu Leu Phe Asp Ala Phe Val
        755                 760                 765

Asp Ile Ala Ala Asn Gly Leu Ala Ser Arg Val His Leu Val Leu Ser
    770                 775                 780

Thr Gln Arg Trp Ser Ser Ile Arg Pro Ala Val Arg Asp Leu Val Thr
785                 790                 795                 800

Gly Arg Ile Glu Leu Lys Leu Gly Glu Ala Met Asp Ser Val Ile Asp
                805                 810                 815

Arg Lys Ala Gln Leu Arg Ile Pro Ser Lys Pro Gly Arg Gly Leu Asn
            820                 825                 830

Leu Asp Lys Glu His Ile Leu Ile Ala His Ala Ser Gly Gln Asp Ile
        835                 840                 845

Ala Gln Val Cys Val Met Ala Asp Gly Gln Gly Trp Gln Gln Val Pro
    850                 855                 860

Gln Leu Ser Val Leu Pro Ala His Ile Leu Leu His Glu Leu Glu Leu
865                 870                 875                 880

Ser Ala Thr Pro Gly Ile Pro Ile Ala Arg Gly Gly Ala Glu Leu Ser
                885                 890                 895

Thr Leu Thr Trp Asp Pro Glu Ser Ser Arg His Leu Leu Ala Phe Gly
            900                 905                 910

Ser Gln Gly Cys Gly Lys Ser Ser Leu Ile Arg Thr Ile Val Thr Gly
        915                 920                 925

Leu Thr Ile Val Gly Arg Glu Lys Ala Arg Leu Val Phe Phe Asp Leu
    930                 935                 940
```

```
Arg Arg Thr His Leu Gly Leu Val Pro Glu Asp Met Leu Ala Ala Tyr
945                 950                 955                 960

Cys Ala Thr Ser Thr Ala Val His Asn Thr Ile Lys Asp Met Val Ala
                965                 970                 975

Thr Leu Ser Ala Arg Leu Pro Gly Pro Asp Ile Thr Ala Gln Glu Leu
            980                 985                 990

Arg Asp Arg Ser Trp Trp Gln Gly Pro Asp Ile Tyr Leu Val Ile Asp
        995                 1000                1005

Asp Tyr Asp Leu Leu Pro Ala Gly Thr Leu His Pro Leu Arg Glu Ile
    1010                1015                1020

Ile Pro His Ala Arg Asp Val Gly Leu His Ile Val Leu Thr Arg Lys
1025                1030                1035                1040

Ala Gly Gly Ala Ser Arg Ala Leu Tyr Asp Pro Val Met Ser Glu Ile
                1045                1050                1055

Lys Asp Gln Ser Pro His Val Val Leu Phe Asp Ala Asp Arg Asp Glu
            1060                1065                1070

Gly Ala Ile Leu Gly Ile Lys Pro Thr Ala Gln Pro Pro Gly Arg Ala
        1075                1080                1085

Thr Met Ser Ile Arg Gly Glu Asn Ile Gly Val Ala Gln Met Ala Pro
    1090                1095                1100

His Arg
1105


<210> 115
<211> 1446
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1423)
<223> RXA01829

<400> 115
tgcaacggct ggctgctcaa gctttgccag tgtgcgtgaa cttagaagta acaaccggtg 60

gcgatagaaa cgaacccgga gtcaattgta gggaggtctc atg aac acg ctt gaa   115
                                            Met Asn Thr Leu Glu
                                              1               5

cga tta aag ctt cgt cgc acg gaa atg tgg ctg ctg ata ctt gcc aca   163
Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu Leu Ile Leu Ala Thr
                  10                  15                  20

ctc gtt gtg tcg atc atg ttc atc agc ctc gag ctg gcc atg ggc aat   211
Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu Leu Ala Met Gly Asn
              25                  30                  35

gag ttg ggt acc cat att ttg atg ctg atg ggc gga tat atc ggt atc   259
Glu Leu Gly Thr His Ile Leu Met Leu Met Gly Gly Tyr Ile Gly Ile
```

```
         40                  45                  50

ttc atc gtc gcg cac cta gcc atg gca tgg gtg gcg ccg ttt gct gat   307
Phe Ile Val Ala His Leu Ala Met Ala Trp Val Ala Pro Phe Ala Asp
     55                  60                  65

caa atc atg ctg cct gtg gtg gcg gtg ctc aat ggc att ggt ttg gtg   355
Gln Ile Met Leu Pro Val Val Ala Val Leu Asn Gly Ile Gly Leu Val
 70                  75                  80                  85

atg att tat cgc ctt gat gag gcc acg ggc tac agc acg gtc aat agc   403
Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr Ser Thr Val Asn Ser
                 90                  95                 100

caa ttg atg tgg acg gtt gtt ggc gtc acg ctg atg gtg gct gtg ttg   451
Gln Leu Met Trp Thr Val Val Gly Val Thr Leu Met Val Ala Val Leu
            105                 110                 115

ttg ctg ttg cgt gat tac aag tcg ctt tcg cgt tat tcc tac ctc ctc   499
Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg Tyr Ser Tyr Leu Leu
        120                 125                 130

ggt gtg gtg ggc atc gtg ctg ctg gcg ctg cct ctc gtg tgg ccg cag   547
Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro Leu Val Trp Pro Gln
    135                 140                 145

cca ggc ggc gtg gaa gcc cgc atc tgg att tgg ctt gga cct ttc tcc   595
Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp Leu Gly Pro Phe Ser
150                 155                 160                 165

atc cag cca ggt gag ttc tcc aag att ttg ctg ctg ctg ttc ttt gct   643
Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu Leu Leu Phe Phe Ala
                170                 175                 180

cag ctg cta gcc acc aag cgt gct ttg ttt act gtt gcg ggc tac cgt   691
Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr Val Ala Gly Tyr Arg
            185                 190                 195

ttc ctc ggc atg gat ttc cct cgt ttg cgt gac ctc gcg ccg att ctt   739
Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp Leu Ala Pro Ile Leu
        200                 205                 210

gtg gtg tgg gcg ttg gct att ttg atc atg gct ggc gcc aac gac ttc   787
Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala Gly Ala Asn Asp Phe
    215                 220                 225

ggt cct gca ctg ctg ctt ttc act acc gtt ttg gcc atg gtg tac ctg   835
Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu Ala Met Val Tyr Leu
230                 235                 240                 245

gct acc ggc cgt ggt tcc tgg ctg ttg att ggt gct gtg ttg gtg gct   883
Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly Ala Val Leu Val Ala
                250                 255                 260

gtc ggc gcg ttc acg gtg tac caa gtt tca agc aag att cag gaa cgc   931
Val Gly Ala Phe Thr Val Tyr Gln Val Ser Ser Lys Ile Gln Glu Arg
            265                 270                 275

gtg caa aac ttc gtg gat cct gtg gcc cac tat gac acc acc ggt tac   979
Val Gln Asn Phe Val Asp Pro Val Ala His Tyr Asp Thr Thr Gly Tyr
        280                 285                 290
```

```
cag ctg tcc cag tcc ttg ttt ggc atg agt tgg ggc gga atc acc ggc   1027
Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp Gly Gly Ile Thr Gly
    295                 300                 305

acc ggc att ggt cag ggt tac ccc aac atg atc cct gtc gtg cac tcg   1075
Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile Pro Val Val His Ser
310                 315                 320                 325

gac ttc att ctc gca gcc att ggt gag gag ctt ggt ctg att ggc ctg   1123
Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu Gly Leu Ile Gly Leu
                330                 335                 340

gcg gcc atc atc gtg ctg ttt ggt gtg ttt gtc acc cgc ggt atg cgc   1171
Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val Thr Arg Gly Met Arg
            345                 350                 355

acc gct acc ctg gct cgt gac agc tac gga aag ctc gtg gca tct ggt   1219
Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys Leu Val Ala Ser Gly
        360                 365                 370

ctg tcg atg acc atc atg atc cag att ttc gtc gtc gtg gca ggt att   1267
Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val Val Val Ala Gly Ile
    375                 380                 385

tct tca ctg atg ccc atg aca ggt ttg acc act ccg ttt atg tcc cag   1315
Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr Pro Phe Met Ser Gln
390                 395                 400                 405

ggt ggt tca tcc ctg atg gct aac tac att ctg atg gcc atc atc ttg   1363
Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu Met Ala Ile Ile Leu
                410                 415                 420

cgt att tct gac agt gcc cgc cga cct gtc atg tcc aag caa gca tcg   1411
Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met Ser Lys Gln Ala Ser
            425                 430                 435

gag gtg gct gcg tgaaccgctc gattcgaatc aca                        1446
Glu Val Ala Ala
        440
```

<210> 116
<211> 441
<212> PRT
<213> Corynebacterium glutamicum

<400> 116

```
Met Asn Thr Leu Glu Arg Leu Lys Leu Arg Arg Thr Glu Met Trp Leu
  1               5                  10                  15

Leu Ile Leu Ala Thr Leu Val Val Ser Ile Met Phe Ile Ser Leu Glu
             20                  25                  30

Leu Ala Met Gly Asn Glu Leu Gly Thr His Ile Leu Met Leu Met Gly
         35                  40                  45

Gly Tyr Ile Gly Ile Phe Ile Val Ala His Leu Ala Met Ala Trp Val
     50                  55                  60

Ala Pro Phe Ala Asp Gln Ile Met Leu Pro Val Val Ala Val Leu Asn
```

```
65                  70                  75                  80

Gly Ile Gly Leu Val Met Ile Tyr Arg Leu Asp Glu Ala Thr Gly Tyr
                85                  90                  95

Ser Thr Val Asn Ser Gln Leu Met Trp Thr Val Val Gly Val Thr Leu
            100                 105                 110

Met Val Ala Val Leu Leu Leu Leu Arg Asp Tyr Lys Ser Leu Ser Arg
        115                 120                 125

Tyr Ser Tyr Leu Leu Gly Val Val Gly Ile Val Leu Leu Ala Leu Pro
    130                 135                 140

Leu Val Trp Pro Gln Pro Gly Gly Val Glu Ala Arg Ile Trp Ile Trp
145                 150                 155                 160

Leu Gly Pro Phe Ser Ile Gln Pro Gly Glu Phe Ser Lys Ile Leu Leu
                165                 170                 175

Leu Leu Phe Phe Ala Gln Leu Leu Ala Thr Lys Arg Ala Leu Phe Thr
            180                 185                 190

Val Ala Gly Tyr Arg Phe Leu Gly Met Asp Phe Pro Arg Leu Arg Asp
        195                 200                 205

Leu Ala Pro Ile Leu Val Val Trp Ala Leu Ala Ile Leu Ile Met Ala
    210                 215                 220

Gly Ala Asn Asp Phe Gly Pro Ala Leu Leu Leu Phe Thr Thr Val Leu
225                 230                 235                 240

Ala Met Val Tyr Leu Ala Thr Gly Arg Gly Ser Trp Leu Leu Ile Gly
                245                 250                 255

Ala Val Leu Val Ala Val Gly Ala Phe Thr Val Tyr Gln Val Ser Ser
            260                 265                 270

Lys Ile Gln Glu Arg Val Gln Asn Phe Val Asp Pro Val Ala His Tyr
        275                 280                 285

Asp Thr Thr Gly Tyr Gln Leu Ser Gln Ser Leu Phe Gly Met Ser Trp
    290                 295                 300

Gly Gly Ile Thr Gly Thr Gly Ile Gly Gln Gly Tyr Pro Asn Met Ile
305                 310                 315                 320

Pro Val Val His Ser Asp Phe Ile Leu Ala Ala Ile Gly Glu Glu Leu
                325                 330                 335

Gly Leu Ile Gly Leu Ala Ala Ile Ile Val Leu Phe Gly Val Phe Val
            340                 345                 350

Thr Arg Gly Met Arg Thr Ala Thr Leu Ala Arg Asp Ser Tyr Gly Lys
        355                 360                 365

Leu Val Ala Ser Gly Leu Ser Met Thr Ile Met Ile Gln Ile Phe Val
    370                 375                 380

Val Val Ala Gly Ile Ser Ser Leu Met Pro Met Thr Gly Leu Thr Thr
385                 390                 395                 400
```

```
Pro Phe Met Ser Gln Gly Gly Ser Ser Leu Met Ala Asn Tyr Ile Leu
                405                 410                 415

Met Ala Ile Ile Leu Arg Ile Ser Asp Ser Ala Arg Arg Pro Val Met
            420                 425                 430

Ser Lys Gln Ala Ser Glu Val Ala Ala
        435                 440
```

<210> 117
<211> 1044
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1021)
<223> RXA01427

<400> 117

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cacttcggtg gaatgggtac agcgttaagc actaatgtgg aatcgatgac gtgtgcatga 60

agaattcgca tgcacaggaa gatagggatg gttgacgtcg atg gaa gac act act   115
                                          Met Glu Asp Thr Thr
                                            1               5

tgg gaa gac aca cca att gct gcg gcg gcg cgt cgt gca gct cag gtg   163
Trp Glu Asp Thr Pro Ile Ala Ala Ala Arg Arg Ala Ala Gln Val
                10                  15                  20

atg aca ccc aac tcc ctg acg ttg ccg aaa cct aaa gaa cca cgc cta   211
Met Thr Pro Asn Ser Leu Thr Leu Pro Lys Pro Lys Glu Pro Arg Leu
            25                  30                  35

att acc atc gcc aac caa aaa ggc ggc gtt ggt aaa acc acc tcc acg   259
Ile Thr Ile Ala Asn Gln Lys Gly Gly Val Gly Lys Thr Thr Ser Thr
        40                  45                  50

gtg aat ttg gct gcg tct tta gca att cat ggg ctt aaa gtt ctc gtc   307
Val Asn Leu Ala Ala Ser Leu Ala Ile His Gly Leu Lys Val Leu Val
    55                  60                  65

gtg gat ttg gat ccg cag gga aat gcg tcg aca gcg ttg ggt gtc gag   355
Val Asp Leu Asp Pro Gln Gly Asn Ala Ser Thr Ala Leu Gly Val Glu
70                  75                  80                  85

cac cgc tct gga acc ttg tca tct tat gaa cta ctg atc ggt gaa tgc   403
His Arg Ser Gly Thr Leu Ser Ser Tyr Glu Leu Leu Ile Gly Glu Cys
                90                  95                  100

act gct gat gaa gca atg cag cca tcc aca gct aac gaa aac ctc ttc   451
Thr Ala Asp Glu Ala Met Gln Pro Ser Thr Ala Asn Glu Asn Leu Phe
            105                 110                 115

tgc att cca gca acc ctg gat ctt gct ggc gca gaa att gaa ttg gtc   499
Cys Ile Pro Ala Thr Leu Asp Leu Ala Gly Ala Glu Ile Glu Leu Val
        120                 125                 130

agc ttg gtc cgc cgc gaa tac cgt ttg gcg gat gcg ttg ggc cgt gag   547
```

```
Ser Leu Val Arg Arg Glu Tyr Arg Leu Ala Asp Ala Leu Gly Arg Glu
    135                 140                 145

ttc att gac aag cac gat ttt gat tac atg atc att gac tgc cca ccg   595
Phe Ile Asp Lys His Asp Phe Asp Tyr Met Ile Ile Asp Cys Pro Pro
150                 155                 160                 165

tct ttg ggt ctg ctc acc att aac gcc atg acc gcg gtg aat gaa gtg   643
Ser Leu Gly Leu Leu Thr Ile Asn Ala Met Thr Ala Val Asn Glu Val
                170                 175                 180

ctc att ccg atc cag tgt gag tac tac gct ctg gag ggc gtg ggc cag   691
Leu Ile Pro Ile Gln Cys Glu Tyr Tyr Ala Leu Glu Gly Val Gly Gln
            185                 190                 195

cta ctg aac aac atc act atg ttg cgt cag cac ctg aac cgc cag ctg   739
Leu Leu Asn Asn Ile Thr Met Leu Arg Gln His Leu Asn Arg Gln Leu
        200                 205                 210

cat att tcc gcg atc ttg ctg acc atg tat gac gcc cgc acc aac ctc   787
His Ile Ser Ala Ile Leu Leu Thr Met Tyr Asp Ala Arg Thr Asn Leu
    215                 220                 225

gca gaa cag gtg gcc aca gag gtt aat gat cac ttc ggt gac gtg gtg   835
Ala Glu Gln Val Ala Thr Glu Val Asn Asp His Phe Gly Asp Val Val
230                 235                 240                 245

ttg ggt aac aag att cca cgt tca gtg aag gtg tct gaa gct cct ggc   883
Leu Gly Asn Lys Ile Pro Arg Ser Val Lys Val Ser Glu Ala Pro Gly
                250                 255                 260

tat ggg cag act gtc att gaa tat gat cca ggt tcc agg ggc gcc atg   931
Tyr Gly Gln Thr Val Ile Glu Tyr Asp Pro Gly Ser Arg Gly Ala Met
            265                 270                 275

gcg tat ttg gat gct gct aaa gaa ttg gcc act cgt ggc gat tac ttg   979
Ala Tyr Leu Asp Ala Ala Lys Glu Leu Ala Thr Arg Gly Asp Tyr Leu
        280                 285                 290

cct agc gat gaa tcc ggt ccg atc ggc cta aaa cct gcg aaa           1021
Pro Ser Asp Glu Ser Gly Pro Ile Gly Leu Lys Pro Ala Lys
    295                 300                 305

tagcagtaaa cttctttgaa tac                                        1044
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<210> 118
<211> 307
<212> PRT
<213> Corynebacterium glutamicum

<400> 118

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Met Glu Asp Thr Thr Trp Glu Asp Thr Pro Ile Ala Ala Ala Ala Arg
  1               5                  10                  15

Arg Ala Ala Gln Val Met Thr Pro Asn Ser Leu Thr Leu Pro Lys Pro
             20                  25                  30

Lys Glu Pro Arg Leu Ile Thr Ile Ala Asn Gln Lys Gly Gly Val Gly
         35                  40                  45
```

```
Lys Thr Thr Ser Thr Val Asn Leu Ala Ala Ser Leu Ala Ile His Gly
 50                  55                  60

Leu Lys Val Leu Val Val Asp Leu Asp Pro Gln Gly Asn Ala Ser Thr
65                  70                  75                  80

Ala Leu Gly Val Glu His Arg Ser Gly Thr Leu Ser Ser Tyr Glu Leu
                85                  90                  95

Leu Ile Gly Glu Cys Thr Ala Asp Glu Ala Met Gln Pro Ser Thr Ala
            100                 105                 110

Asn Glu Asn Leu Phe Cys Ile Pro Ala Thr Leu Asp Leu Ala Gly Ala
        115                 120                 125

Glu Ile Glu Leu Val Ser Leu Val Arg Arg Glu Tyr Arg Leu Ala Asp
    130                 135                 140

Ala Leu Gly Arg Glu Phe Ile Asp Lys His Asp Phe Asp Tyr Met Ile
145                 150                 155                 160

Ile Asp Cys Pro Pro Ser Leu Gly Leu Leu Thr Ile Asn Ala Met Thr
                165                 170                 175

Ala Val Asn Glu Val Leu Ile Pro Ile Gln Cys Glu Tyr Tyr Ala Leu
            180                 185                 190

Glu Gly Val Gly Gln Leu Leu Asn Asn Ile Thr Met Leu Arg Gln His
        195                 200                 205

Leu Asn Arg Gln Leu His Ile Ser Ala Ile Leu Leu Thr Met Tyr Asp
    210                 215                 220

Ala Arg Thr Asn Leu Ala Glu Gln Val Ala Thr Glu Val Asn Asp His
225                 230                 235                 240

Phe Gly Asp Val Val Leu Gly Asn Lys Ile Pro Arg Ser Val Lys Val
                245                 250                 255

Ser Glu Ala Pro Gly Tyr Gly Gln Thr Val Ile Glu Tyr Asp Pro Gly
            260                 265                 270

Ser Arg Gly Ala Met Ala Tyr Leu Asp Ala Ala Lys Glu Leu Ala Thr
        275                 280                 285

Arg Gly Asp Tyr Leu Pro Ser Asp Glu Ser Gly Pro Ile Gly Leu Lys
    290                 295                 300

Pro Ala Lys
305
```

<210> 119
<211> 754
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(754)
<223> RXN02973

<400> 119
gtcgagagct gtaaagtcaa ggctatatac ttctcaagtc gcgccgaaat ttgttaaatg 60

actataaaag gcagtcctag tcaaggaaga aggtttgact gtg agt gat gca ggg 115
Val Ser Asp Ala Gly
1 5

aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg 163
Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu Thr Gly Arg Pro Leu
10 15 20

cgc gag ttg cct gag cca tct cct ttg gaa aaa cat ggc cca gca acg 211
Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys His Gly Pro Ala Thr
25 30 35

atc att gcc atg gcg aat caa aaa ggt ggc gtt ggt aaa acc acg tcc 259
Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val Gly Lys Thr Thr Ser
40 45 50

acc atc aac ctc gga gca tgc ctt gca gag gcg gga cgt aaa gtc ctg 307
Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala Gly Arg Lys Val Leu
55 60 65

ctc gtt gac ttg gat ccg caa ggt gcg ttg act gct ggt ttg gga atc 355
Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr Ala Gly Leu Gly Ile
70 75 80 85

cac tac gac gac gtg gat atc acc gtg tat gac ctc atg gtg gac aac 403
His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp Leu Met Val Asp Asn
90 95 100

aat tcc acc att gat cag gcg atc cac cac act ggt ctt cct gat ctg 451
Asn Ser Thr Ile Asp Gln Ala Ile His His Thr Gly Leu Pro Asp Leu
105 110 115

gat gtc gtt cct gca aat att gac ttg tcc gct gca gaa att cag ctg 499
Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala Ala Glu Ile Gln Leu
120 125 130

gtc aat gaa gtt ggt cgt gaa caa aca ctt gcc agg gcg ctg cgt cct 547
Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala Arg Ala Leu Arg Pro
135 140 145

gtc atg aag gac tac gac ttc atc atc ctt gat tgt cag cca tca ctt 595
Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp Cys Gln Pro Ser Leu
150 155 160 165

ggt ctt ttg acg gtg aac gct ttg gcg tgc gcg cac ggg gtt atc atc 643
Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala His Gly Val Ile Ile
170 175 180

ccg atg gag tgc gag aac tta tca ctg cgc ggc ctc gca ttg ctc aca 691
Pro Met Glu Cys Glu Asn Leu Ser Leu Arg Gly Leu Ala Leu Leu Thr
185 190 195

gac acc gtg gaa aaa gtt gcc gat cgg ttg aac ttc gat ctg gaa atc 739
Asp Thr Val Glu Lys Val Ala Asp Arg Leu Asn Phe Asp Leu Glu Ile
200 205 210

ctc ggc atc ttg gtc 754

Leu Gly Ile Leu Val
215

<210> 120
<211> 218
<212> PRT
<213> Corynebacterium glutamicum

<400> 120
Val Ser Asp Ala Gly Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu
1 5 10 15

Thr Gly Arg Pro Leu Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys
20 25 30

His Gly Pro Ala Thr Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val
35 40 45

Gly Lys Thr Thr Ser Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala
50 55 60

Gly Arg Lys Val Leu Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr
65 70 75 80

Ala Gly Leu Gly Ile His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp
85 90 95

Leu Met Val Asp Asn Asn Ser Thr Ile Asp Gln Ala Ile His His Thr
100 105 110

Gly Leu Pro Asp Leu Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala
115 120 125

Ala Glu Ile Gln Leu Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala
130 135 140

Arg Ala Leu Arg Pro Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp
145 150 155 160

Cys Gln Pro Ser Leu Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala
165 170 175

His Gly Val Ile Ile Pro Met Glu Cys Glu Asn Leu Ser Leu Arg Gly
180 185 190

Leu Ala Leu Leu Thr Asp Thr Val Glu Lys Val Ala Asp Arg Leu Asn
195 200 205

Phe Asp Leu Glu Ile Leu Gly Ile Leu Val
210 215

<210> 121
<211> 721
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(721)

<223> FRXA01603

<400> 121

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gtcgagagct gtaaagtcaa ggctatatac ttctcaagtc gcgccgaaat ttgttaaatg 60

actataaaag gcagtcctag tcaaggaaga aggtttgact gtg agt gat gca ggg   115
                                           Val Ser Asp Ala Gly
                                             1               5

aag aag gac tct tcc aag gtg gag atc gga ctg acc ggt cga ccc ctg   163
Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu Thr Gly Arg Pro Leu
                 10                  15                  20

cgc gag ttg cct gag cca tct cct ttg gaa aaa cat ggc cca gca acg   211
Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys His Gly Pro Ala Thr
             25                  30                  35

atc att gcc atg gcg aat caa aaa ggt ggc gtt ggt aaa acc acg tcc   259
Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val Gly Lys Thr Thr Ser
         40                  45                  50

acc atc aac ctc gga gca tgc ctt gca gag gcg gga cgt aaa gtc ctg   307
Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala Gly Arg Lys Val Leu
     55                  60                  65

ctc gtt gac ttg gat ccg caa ggt gcg ttg act gct ggt ttg gga atc   355
Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr Ala Gly Leu Gly Ile
 70                  75                  80                  85

cac tac gac gac gtg gat atc acc gtg tat gac ctc atg gtg gac aac   403
His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp Leu Met Val Asp Asn
                 90                  95                 100

aat tcc acc att gat cag gcg atc cac cac act ggt ctt cct gat ctg   451
Asn Ser Thr Ile Asp Gln Ala Ile His His Thr Gly Leu Pro Asp Leu
            105                 110                 115

gat gtc gtt cct gca aat att gac ttg tcc gct gca gaa att cag ctg   499
Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala Ala Glu Ile Gln Leu
        120                 125                 130

gtc aat gaa gtt ggt cgt gaa caa aca ctt gcc agg gcg ctg cgt cct   547
Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala Arg Ala Leu Arg Pro
    135                 140                 145

gtc atg aag gac tac gac ttc atc atc ctt gat tgt cag cca tca ctt   595
Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp Cys Gln Pro Ser Leu
150                 155                 160                 165

ggt ctt ttg acg gtg aac gct ttg gcg tgc gcg cac ggg gtt atc atc   643
Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala His Gly Val Ile Ile
                170                 175                 180

ccg atg gag tgc gag tac ttc tca ctg cgt ggc ctc gca ttg ctc aca   691
Pro Met Glu Cys Glu Tyr Phe Ser Leu Arg Gly Leu Ala Leu Leu Thr
            185                 190                 195

gac acc gtg gaa aaa gtt gcc gat cgg ttg                          721
Asp Thr Val Glu Lys Val Ala Asp Arg Leu
        200                 205
```

<210> 122
<211> 207
<212> PRT
<213> Corynebacterium glutamicum

<400> 122

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Val Ser Asp Ala Gly Lys Lys Asp Ser Ser Lys Val Glu Ile Gly Leu
  1               5                  10                  15

Thr Gly Arg Pro Leu Arg Glu Leu Pro Glu Pro Ser Pro Leu Glu Lys
             20                  25                  30

His Gly Pro Ala Thr Ile Ile Ala Met Ala Asn Gln Lys Gly Gly Val
         35                  40                  45

Gly Lys Thr Thr Ser Thr Ile Asn Leu Gly Ala Cys Leu Ala Glu Ala
     50                  55                  60

Gly Arg Lys Val Leu Leu Val Asp Leu Asp Pro Gln Gly Ala Leu Thr
 65                  70                  75                  80

Ala Gly Leu Gly Ile His Tyr Asp Asp Val Asp Ile Thr Val Tyr Asp
                 85                  90                  95

Leu Met Val Asp Asn Asn Ser Thr Ile Asp Gln Ala Ile His His Thr
            100                 105                 110

Gly Leu Pro Asp Leu Asp Val Val Pro Ala Asn Ile Asp Leu Ser Ala
        115                 120                 125

Ala Glu Ile Gln Leu Val Asn Glu Val Gly Arg Glu Gln Thr Leu Ala
    130                 135                 140

Arg Ala Leu Arg Pro Val Met Lys Asp Tyr Asp Phe Ile Ile Leu Asp
145                 150                 155                 160

Cys Gln Pro Ser Leu Gly Leu Leu Thr Val Asn Ala Leu Ala Cys Ala
                165                 170                 175

His Gly Val Ile Ile Pro Met Glu Cys Glu Tyr Phe Ser Leu Arg Gly
            180                 185                 190

Leu Ala Leu Leu Thr Asp Thr Val Glu Lys Val Ala Asp Arg Leu
        195                 200                 205
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<210> 123
<211> 963
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(940)
<223> RXN00818

<400> 123

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ttcccaatgc gcaaccccag cacgtcactt caatctcatt ggtaacttta gtttctttct 60

cagtcttgga aagttgccaa aaagcgctaa actatgcggt gtg aag cac cca gat   115
```

```
                                                  Val Lys His Pro Asp
                                                    1               5

ccc gcc caa aaa gta gag ggc acc act gcg acc acc ccc aca aag gtg   163
Pro Ala Gln Lys Val Glu Gly Thr Thr Ala Thr Thr Pro Thr Lys Val
                  10                  15                  20

gct gct ttt ttc gat ctg gac aag acc atc atc gcc atg agt tcc acc   211
Ala Ala Phe Phe Asp Leu Asp Lys Thr Ile Ile Ala Met Ser Ser Thr
              25                  30                  35

tac gcc tac ggc cgt gag ttc atg aac agc ggg ctc atc tcc cct gtc   259
Tyr Ala Tyr Gly Arg Glu Phe Met Asn Ser Gly Leu Ile Ser Pro Val
          40                  45                  50

gaa gcc ctg caa tta agc ctc gcg caa gca acg tac atg ttc gcc ggc   307
Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr Tyr Met Phe Ala Gly
      55                  60                  65

cac acc agt gaa caa atg gac aac acc cgc gac caa ctc acc gcc atg   355
His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp Gln Leu Thr Ala Met
  70                  75                  80                  85

atc cgc ggc tgg gaa gtc caa cag gtg cgc tcg atc gcg gag gaa acc   403
Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser Ile Ala Glu Glu Thr
                  90                  95                 100

atg cat tcg gtg gtc act ccc acc atc tac gca gag gcc cgc gaa ctg   451
Met His Ser Val Val Thr Pro Thr Ile Tyr Ala Glu Ala Arg Glu Leu
              105                 110                 115

atc gag cac cac cag gag ctc ggc cac gat gtc atc atc att tcc gcc   499
Ile Glu His His Gln Glu Leu Gly His Asp Val Ile Ile Ile Ser Ala
          120                 125                 130

tct gtg aaa gaa ctg gtg gaa ccc atc gcc cgc gaa ctg ggt gta cat   547
Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg Glu Leu Gly Val His
      135                 140                 145

aaa act gtc acc acc gtg ctt gaa gcc cac gac ggt atg tac acc ggt   595
Lys Thr Val Thr Thr Val Leu Glu Ala His Asp Gly Met Tyr Thr Gly
150                 155                 160                 165

gaa gtg ctg ttt tac tgc aaa ggc gac gct aaa gcg cag tcc atc ctg   643
Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys Ala Gln Ser Ile Leu
                  170                 175                 180

gat ctc gcc gag gcg aac aat tac gac ctt tcc tta agc ttc gcc tac   691
Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser Leu Ser Phe Ala Tyr
              185                 190                 195

tcc gat tcc ttc acg gac ctg ccc atg ttg gaa gct gtc ggc aac ccg   739
Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu Ala Val Gly Asn Pro
          200                 205                 210

gcc gcc gtc aac ccc gac cgc gcg ctg aag aaa atc gcc ctt gaa cag   787
Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys Ile Ala Leu Glu Gln
      215                 220                 225

ggg tgg aaa atc tta agc ttc aaa aac cct gaa ccg ctg ttc caa atg   835
Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu Pro Leu Phe Gln Met
```

```
230                 235                 240                 245

ccc agc acc cgc gac gtc ggc atc gga acc gga gtt gtt gcc ggc atc   883
Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly Val Val Ala Gly Ile
                250                 255                 260

gca gct gtt aca gca ggt agt atc tgg tgg atg aaa cgc gca cgg cgc   931
Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met Lys Arg Ala Arg Arg
            265                 270                 275

gga tcg gcc tgagcctcac ctgacagcag tta                            963
Gly Ser Ala
        280


<210> 124
<211> 280
<212> PRT
<213> Corynebacterium glutamicum

<400> 124
Val Lys His Pro Asp Pro Ala Gln Lys Val Glu Gly Thr Thr Ala Thr
  1               5                  10                  15

Thr Pro Thr Lys Val Ala Ala Phe Phe Asp Leu Asp Lys Thr Ile Ile
             20                  25                  30

Ala Met Ser Ser Thr Tyr Ala Tyr Gly Arg Glu Phe Met Asn Ser Gly
         35                  40                  45

Leu Ile Ser Pro Val Glu Ala Leu Gln Leu Ser Leu Ala Gln Ala Thr
     50                  55                  60

Tyr Met Phe Ala Gly His Thr Ser Glu Gln Met Asp Asn Thr Arg Asp
 65                  70                  75                  80

Gln Leu Thr Ala Met Ile Arg Gly Trp Glu Val Gln Gln Val Arg Ser
                 85                  90                  95

Ile Ala Glu Glu Thr Met His Ser Val Val Thr Pro Thr Ile Tyr Ala
            100                 105                 110

Glu Ala Arg Glu Leu Ile Glu His His Gln Glu Leu Gly His Asp Val
        115                 120                 125

Ile Ile Ile Ser Ala Ser Val Lys Glu Leu Val Glu Pro Ile Ala Arg
    130                 135                 140

Glu Leu Gly Val His Lys Thr Val Thr Thr Val Leu Glu Ala His Asp
145                 150                 155                 160

Gly Met Tyr Thr Gly Glu Val Leu Phe Tyr Cys Lys Gly Asp Ala Lys
                165                 170                 175

Ala Gln Ser Ile Leu Asp Leu Ala Glu Ala Asn Asn Tyr Asp Leu Ser
            180                 185                 190

Leu Ser Phe Ala Tyr Ser Asp Ser Phe Thr Asp Leu Pro Met Leu Glu
        195                 200                 205

Ala Val Gly Asn Pro Ala Ala Val Asn Pro Asp Arg Ala Leu Lys Lys
```

```
    210                 215                 220

Ile Ala Leu Glu Gln Gly Trp Lys Ile Leu Ser Phe Lys Asn Pro Glu
225                 230                 235                 240

Pro Leu Phe Gln Met Pro Ser Thr Arg Asp Val Gly Ile Gly Thr Gly
                245                 250                 255

Val Val Ala Gly Ile Ala Ala Val Thr Ala Gly Ser Ile Trp Trp Met
            260                 265                 270

Lys Arg Ala Arg Arg Gly Ser Ala
        275                 280


<210> 125
<211> 2898
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2875)
<223> RXN03028

<400> 125
ctaattccaa gccgagctga aaaagtctgg aagttttgcc caataagggc gttaaagtgg 60

gtgaaagcga atttagaaat aaagaattaa ggggagagac atg ttc gag agg ttt   115
                                            Met Phe Glu Arg Phe
                                              1               5

acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc   163
Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
                  10                  15                  20

atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc   211
Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
              25                  30                  35

att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga   259
Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
          40                  45                  50

att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag   307
Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
      55                  60                  65

ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag   355
Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
  70                  75                  80                  85

aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag   403
Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
                  90                  95                 100

tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag   451
Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
              105                 110                 115

ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc   499
```

```
Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
        120                 125                 130

gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag   547
Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
    135                 140                 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct   595
Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
150                 155                 160                 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca   643
Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro
                170                 175                 180

ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc   691
Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu
            185                 190                 195

acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat   739
Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp
        200                 205                 210

aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac   787
Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn
    215                 220                 225

aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt   835
Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val
230                 235                 240                 245

gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc   883
Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu
                250                 255                 260

aag gac aag cag gtt tac tcc ctt gac tta ggt tcc ctg gtt gca ggt   931
Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly
            265                 270                 275

tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag   979
Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys
        280                 285                 290

gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac   1027
Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His
    295                 300                 305

acc ctc gtg ggt gca ggt gca gca gaa ggc gca atc gac gct gcc tcc   1075
Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala Ile Asp Ala Ala Ser
310                 315                 320                 325

ctg ctt aag cca aag ctt gcc cgc ggt gaa ctg cag acc att ggt gca   1123
Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu Gln Thr Ile Gly Ala
                330                 335                 340

acc acc ctg gat gag tac cgt aag cac att gaa aag gac gca gct ctt   1171
Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu
            345                 350                 355

gag cgt cgt ttc cag cca gtg cag gtt cca gag cct tcg gtt gat ctc   1219
Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu Pro Ser Val Asp Leu
```

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        360                 365                 370

acc gtt gag atc ttg aag ggt ctg cgc gac cgc tac gaa gct cac cac   1267
Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg Tyr Glu Ala His His
    375                 380                 385

cgc gta tcc atc acc gat ggt gct ctt act gca gca gct cag ctt gct   1315
Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala Ala Ala Gln Leu Ala
390                 395                 400                 405

gat cgc tac atc aac gac cgc ttc ttg cca gat aag gcc gtt gac ctc   1363
Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp Lys Ala Val Asp Leu
                410                 415                 420

atc gat gag gct ggc gcc cgc atg cgc atc aag cgc atg acc gca cct   1411
Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys Arg Met Thr Ala Pro
            425                 430                 435

tcc tcc ctc cgc gag gtt gat gag cgt atc gct gat gtt cgc cgt gag   1459
Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala Asp Val Arg Arg Glu
        440                 445                 450

aag gaa gca gcg atc gat gct cag gac ttt gag aag gca gca ggt ctt   1507
Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu Lys Ala Ala Gly Leu
    455                 460                 465

cgc gat aag gag cgc aag ctc ggc gaa gag cgt tca gag aag gaa aag   1555
Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg Ser Glu Lys Glu Lys
470                 475                 480                 485

cag tgg cgc tcc ggc gac ctc gag gac atc gct gag gtt ggc gaa gag   1603
Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala Glu Val Gly Glu Glu
                490                 495                 500

cag atc gca gaa gta ctg gcc aac tgg act ggt att cct gtc ttc aag   1651
Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly Ile Pro Val Phe Lys
            505                 510                 515

ctc acc gaa gct gaa tct tca cgc ctg ctc aac atg gaa gaa gag ttg   1699
Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu Asn Met Glu Glu Glu Leu
        520                 525                 530

cac aag cgc atc atc gga cag gat gaa gct gtc aag gct gtc tcc cgt   1747
His Lys Arg Ile Ile Gly Gln Asp Glu Ala Val Lys Ala Val Ser Arg
    535                 540                 545

gcg atc cgt cgt acc cgt gca ggt ctg aag gat cct aag cgt cct tcc   1795
Ala Ile Arg Arg Thr Arg Ala Gly Leu Lys Asp Pro Lys Arg Pro Ser
550                 555                 560                 565

ggc tcc ttc atc ttc gct ggt cca tcc ggc gtt ggt aag acc gag ctg   1843
Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val Gly Lys Thr Glu Leu
                570                 575                 580

tcc aag gct ctc gca gga ttc ctc ttc ggt gac gat gat tcc ctc atc   1891
Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly Asp Asp Ser Leu Ile
            585                 590                 595

caa atc gac atg ggt gag ttc cac gac cgc ttc acc gcg tcc cga ctt   1939
Gln Ile Asp Met Gly Glu Phe His Asp Arg Phe Thr Ala Ser Arg Leu
        600                 605                 610
```

```
ttc ggt gcc cct ccg gga tac gtt ggc tac gaa gaa ggt ggc cag ctg   1987
Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu
    615                 620                 625

acc gag aag gtt cgc cgt aag cca ttc tcc gtt gtg ctt ttc gac gaa   2035
Thr Glu Lys Val Arg Arg Lys Pro Phe Ser Val Val Leu Phe Asp Glu
630                 635                 640                 645

atc gag aag gcc cac aag gag atc tac aac acc ttg ctg cag gtg ttg   2083
Ile Glu Lys Ala His Lys Glu Ile Tyr Asn Thr Leu Leu Gln Val Leu
                650                 655                 660

gaa gat ggt cgc ctt acc gat ggt cag gga cgc atc gtg gac ttc aag   2131
Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg Ile Val Asp Phe Lys
            665                 670                 675

aac acc gtc ctg atc ttc acc tcc aac ctg ggc acc gct gac atc tcc   2179
Asn Thr Val Leu Ile Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser
        680                 685                 690

aag gct gtt ggc ctg ggc ttc tcc gga tcc tcc gag act gac agc gat   2227
Lys Ala Val Gly Leu Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp
    695                 700                 705

gct cag tac gac cgc atg aag aac aag gtc cac gac gag ctg aag aag   2275
Ala Gln Tyr Asp Arg Met Lys Asn Lys Val His Asp Glu Leu Lys Lys
710                 715                 720                 725

cac ttc cgc cct gag ttc ctg aac cgt att gat gag atc gtg gtc ttc   2323
His Phe Arg Pro Glu Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe
                730                 735                 740

cac cag ctc acc aag gat cag atc gtt cag atg gtc gac ctt ctt atc   2371
His Gln Leu Thr Lys Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile
            745                 750                 755

ggt cgc gtt tcc aac gca ctg gct gag aag gac atg agc atc gaa ctg   2419
Gly Arg Val Ser Asn Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu
        760                 765                 770

act gag aag gcc aag gac ctc ctg gct aac cga ggc ttc gat cca gtt   2467
Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val
    775                 780                 785

ctg ggt gca cga cca ttg cgt cgc acc atc cag cgc gaa att gaa gac   2515
Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp
790                 795                 800                 805

cag atg tcc gag aag atc ctc ttc ggt gaa atc ggc gca ggc gag atc   2563
Gln Met Ser Glu Lys Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile
                810                 815                 820

gtc acc gtt gac gtc gaa ggc tgg gac ggc gag tcc aag gac acc gac   2611
Val Thr Val Asp Val Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp
            825                 830                 835

cgt gcg aag ttc acc ttc aca cca cgt cca aag cca atg cca gaa ggt   2659
Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly
        840                 845                 850
```

```
aag ttc tct gag atc tct gtc gag gct gcg gaa gca att caa gat gta   2707
Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val
    855                 860                 865

gat tct gca gct gac ggc gat gtc cca gaa acc gat tca ctt tcc gac   2755
Asp Ser Ala Ala Asp Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp
870                 875                 880                 885

att gac ctt gaa acc ctt gaa aag ttt gag gaa gat gta gaa aac ggc   2803
Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu Asp Val Glu Asn Gly
                890                 895                 900

acc gac att gat cag gtg tcc ggt gac tac tac ggc acc gat gat cag   2851
Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln
            905                 910                 915

gga ggc act gct cca agc aag gag tagcaacctt ttgaaaaagg gcc         2898
Gly Gly Thr Ala Pro Ser Lys Glu
        920                 925
```

<210> 126
<211> 925
<212> PRT
<213> Corynebacterium glutamicum

<400> 126

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Met Phe Glu Arg Phe Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala
  1               5                  10                  15

Gln Glu Glu Ala Arg Met Leu Asn His Asn Tyr Ile Gly Thr Glu His
             20                  25                  30

Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala
         35                  40                  45

Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu
     50                  55                  60

Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
 65                  70                  75                  80

Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
                 85                  90                  95

Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
            100                 105                 110

Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
        115                 120                 125

Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly
    130                 135                 140

Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
145                 150                 155                 160

Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
                165                 170                 175

Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
```

```
            180                 185                 190

Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
        195                 200                 205

Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
    210                 215                 220

Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
225                 230                 235                 240

Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
                245                 250                 255

Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
            260                 265                 270

Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
        275                 280                 285

Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
    290                 295                 300

Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Glu Gly Ala
305                 310                 315                 320

Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu Leu
                325                 330                 335

Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile Glu
            340                 345                 350

Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro Glu
        355                 360                 365

Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp Arg
    370                 375                 380

Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr Ala
385                 390                 395                 400

Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro Asp
                405                 410                 415

Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile Lys
            420                 425                 430

Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile Ala
        435                 440                 445

Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe Glu
    450                 455                 460

Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu Arg
465                 470                 475                 480

Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile Ala
                485                 490                 495

Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr Gly
            500                 505                 510
```

Ile Pro Val Phe Lys Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu Asn
515 520 525

Met Glu Glu Glu Leu His Lys Arg Ile Ile Gly Gln Asp Glu Ala Val
530 535 540

Lys Ala Val Ser Arg Ala Ile Arg Arg Thr Arg Ala Gly Leu Lys Asp
545 550 555 560

Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly Val
565 570 575

Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly Asp
580 585 590

Asp Asp Ser Leu Ile Gln Ile Asp Met Gly Glu Phe His Asp Arg Phe
595 600 605

Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr Glu
610 615 620

Glu Gly Gly Gln Leu Thr Glu Lys Val Arg Arg Lys Pro Phe Ser Val
625 630 635 640

Val Leu Phe Asp Glu Ile Glu Lys Ala His Lys Glu Ile Tyr Asn Thr
645 650 655

Leu Leu Gln Val Leu Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly Arg
660 665 670

Ile Val Asp Phe Lys Asn Thr Val Leu Ile Phe Thr Ser Asn Leu Gly
675 680 685

Thr Ala Asp Ile Ser Lys Ala Val Gly Leu Gly Phe Ser Gly Ser Ser
690 695 700

Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg Met Lys Asn Lys Val His
705 710 715 720

Asp Glu Leu Lys Lys His Phe Arg Pro Glu Phe Leu Asn Arg Ile Asp
725 730 735

Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln Met
740 745 750

Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys Asp
755 760 765

Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn Arg
770 775 780

Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile Gln
785 790 795 800

Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu Ile
805 810 815

Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly Glu
820 825 830

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Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro Lys
        835                 840                 845

Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala Glu
    850                 855                 860

Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu Thr
865                 870                 875                 880

Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu Glu
                885                 890                 895

Asp Val Glu Asn Gly Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr Tyr
            900                 905                 910

Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro Ser Lys Glu
        915                 920                 925
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<210> 127
<211> 1104
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1081)
<223> FRXA02470

<400> 127

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ctaattccaa gccgagctga aaaagtctgg aagttttgcc caataagggc gttaaagtgg 60

gtgaaagcga atttagaaat aaagaattaa ggggagagac atg ttc gag agg ttt   115
                                          Met Phe Glu Arg Phe
                                            1               5

acc gat cgt gca cgc cgc gtg att gtg ctc gcg cag gaa gag gcg cgc   163
Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala Gln Glu Glu Ala Arg
                10                  15                  20

atg ctc aac cac aat tac atc ggc acg gag cac att ctc ctc ggc ctc   211
Met Leu Asn His Asn Tyr Ile Gly Thr Glu His Ile Leu Leu Gly Leu
            25                  30                  35

att cac gag ggc gag ggc gtt gca gcc aag gct ttg gaa tcc atg gga   259
Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala Leu Glu Ser Met Gly
        40                  45                  50

att tcc ctg gac gcc gtc cgc cag gaa gtc gaa gag att atc ggc cag   307
Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu Glu Ile Ile Gly Gln
    55                  60                  65

ggc tcc cag ccc acc acc ggc cac att cct ttt act cca cgt gcc aag   355
Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe Thr Pro Arg Ala Lys
70                  75                  80                  85

aag gtc ctg gag ctc agc ctc cgc gaa ggc cta caa atg gga cac aag   403
Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu Gln Met Gly His Lys
                90                  95                  100

tac atc ggt act gag ttc ctg ctt ctc ggt ttg atc cgt gag ggc gag   451
```

```
Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu Ile Arg Glu Gly Glu
            105                 110                 115

ggc gtt gct gcc cag gtc ctg gtc aag ctt ggt gct gat ctg cca cgc   499
Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly Ala Asp Leu Pro Arg
        120                 125                 130

gtg cgt cag caa gtt att cag ctt ctc tcc ggc tac gaa ggt ggc cag   547
Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly Tyr Glu Gly Gly Gln
    135                 140                 145

ggc gga tcc cca gag ggc ggc cag ggc gcc cct act ggc ggt gac gct   595
Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro Thr Gly Gly Asp Ala
150                 155                 160                 165

gtt ggt gca gga gct gct cct ggc ggt cgt cca tct tcg ggc agc cca   643
Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro Ser Ser Gly Ser Pro
                170                 175                 180

ggc gag cgt tct acc tct ttg gtc ctt gac cag ttc ggc cgc aac ctc   691
Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln Phe Gly Arg Asn Leu
            185                 190                 195

acc cag gct gca aag gac ggc aag ctg gat cca gtt gtt ggt cgc gat   739
Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro Val Val Gly Arg Asp
        200                 205                 210

aag gaa atc gag cgc atc atg cag gtg ctc tcc cgt cgt acc aag aac   787
Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser Arg Arg Thr Lys Asn
    215                 220                 225

aac cca gtt ctt att ggt gag cca ggt gtt ggt aag acc gca gtt gtt   835
Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys Thr Ala Val Val
230                 235                 240                 245

gaa ggt ctt gca cta gac att gtt aac ggc aag gtt cca gag acc ctc   883
Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys Val Pro Glu Thr Leu
                250                 255                 260

aag gac aag cag gtt tac tcc ctt gac tta ggt tcc ctg gtt gca ggt   931
Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly Ser Leu Val Ala Gly
            265                 270                 275

tcc cgt tac cgc ggt gac ttc gaa gag cga ctg aag aag gtc ctc aag   979
Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu Lys Lys Val Leu Lys
        280                 285                 290

gag att aac cag cgc ggc gac atc atc ctg ttt atc gat gag atc cac  1027
Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe Ile Asp Glu Ile His
    295                 300                 305

acc ctc gtg ggt gca ggt gca gca cga agg cgc aat cga cgc tgc ctc  1075
Thr Leu Val Gly Ala Gly Ala Ala Arg Arg Arg Asn Arg Arg Cys Leu
310                 315                 320                 325

cct gct taagccaaag cttgcccgcg gtg                               1104
Pro Ala
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<210> 128

<211> 327
<212> PRT
<213> Corynebacterium glutamicum

<400> 128

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Met Phe Glu Arg Phe Thr Asp Arg Ala Arg Arg Val Ile Val Leu Ala
  1               5                  10                  15

Gln Glu Glu Ala Arg Met Leu Asn His Asn Tyr Ile Gly Thr Glu His
             20                  25                  30

Ile Leu Leu Gly Leu Ile His Glu Gly Glu Gly Val Ala Ala Lys Ala
         35                  40                  45

Leu Glu Ser Met Gly Ile Ser Leu Asp Ala Val Arg Gln Glu Val Glu
     50                  55                  60

Glu Ile Ile Gly Gln Gly Ser Gln Pro Thr Thr Gly His Ile Pro Phe
 65                  70                  75                  80

Thr Pro Arg Ala Lys Lys Val Leu Glu Leu Ser Leu Arg Glu Gly Leu
                 85                  90                  95

Gln Met Gly His Lys Tyr Ile Gly Thr Glu Phe Leu Leu Leu Gly Leu
            100                 105                 110

Ile Arg Glu Gly Glu Gly Val Ala Ala Gln Val Leu Val Lys Leu Gly
        115                 120                 125

Ala Asp Leu Pro Arg Val Arg Gln Gln Val Ile Gln Leu Leu Ser Gly
    130                 135                 140

Tyr Glu Gly Gly Gln Gly Gly Ser Pro Glu Gly Gly Gln Gly Ala Pro
145                 150                 155                 160

Thr Gly Gly Asp Ala Val Gly Ala Gly Ala Ala Pro Gly Gly Arg Pro
                165                 170                 175

Ser Ser Gly Ser Pro Gly Glu Arg Ser Thr Ser Leu Val Leu Asp Gln
            180                 185                 190

Phe Gly Arg Asn Leu Thr Gln Ala Ala Lys Asp Gly Lys Leu Asp Pro
        195                 200                 205

Val Val Gly Arg Asp Lys Glu Ile Glu Arg Ile Met Gln Val Leu Ser
    210                 215                 220

Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly
225                 230                 235                 240

Lys Thr Ala Val Val Glu Gly Leu Ala Leu Asp Ile Val Asn Gly Lys
                245                 250                 255

Val Pro Glu Thr Leu Lys Asp Lys Gln Val Tyr Ser Leu Asp Leu Gly
            260                 265                 270

Ser Leu Val Ala Gly Ser Arg Tyr Arg Gly Asp Phe Glu Glu Arg Leu
        275                 280                 285

Lys Lys Val Leu Lys Glu Ile Asn Gln Arg Gly Asp Ile Ile Leu Phe
    290                 295                 300
```

```
Ile Asp Glu Ile His Thr Leu Val Gly Ala Gly Ala Ala Arg Arg Arg
305                 310                 315                 320

Asn Arg Arg Cys Leu Pro Ala
                325
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<210> 129
<211> 1956
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1933)
<223> FRXA02471

<400> 129

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ggtgacttcg aagagcgact gaagaaggtc ctcaaggaga ttaaccagcg cggcgacatc 60

atcctgttta tcgatgagat ccacaccctc gtgggtgcag gtg cag cac gaa ggc   115
                                            Val Gln His Glu Gly
                                              1               5

gca atc gac gct gcc tcc ctg ctt aag cca aag ctt gcc cgc ggt gaa   163
Ala Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys Leu Ala Arg Gly Glu
                 10                  15                  20

ctg cag acc att ggt gca acc acc ctg gat gag tac cgt aag cac att   211
Leu Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu Tyr Arg Lys His Ile
             25                  30                  35

gaa aag gac gca gct ctt gag cgt cgt ttc cag cca gtg cag gtt cca   259
Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Pro Val Gln Val Pro
         40                  45                  50

gag cct tcg gtt gat ctc acc gtt gag atc ttg aag ggt ctg cgc gac   307
Glu Pro Ser Val Asp Leu Thr Val Glu Ile Leu Lys Gly Leu Arg Asp
     55                  60                  65

cgc tac gaa gct cac cac cgc gta tcc atc acc gat ggt gct ctt act   355
Arg Tyr Glu Ala His His Arg Val Ser Ile Thr Asp Gly Ala Leu Thr
 70                  75                  80                  85

gca gca gct cag ctt gct gat cgc tac atc aac gac cgc ttc ttg cca   403
Ala Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn Asp Arg Phe Leu Pro
                 90                  95                 100

gat aag gcc gtt gac ctc atc gat gag gct ggc gcc cgc atg cgc atc   451
Asp Lys Ala Val Asp Leu Ile Asp Glu Ala Gly Ala Arg Met Arg Ile
            105                 110                 115

aag cgc atg acc gca cct tcc tcc ctc cgc gag gtt gat gag cgt atc   499
Lys Arg Met Thr Ala Pro Ser Ser Leu Arg Glu Val Asp Glu Arg Ile
        120                 125                 130

gct gat gtt cgc cgt gag aag gaa gca gcg atc gat gct cag gac ttt   547
Ala Asp Val Arg Arg Glu Lys Glu Ala Ala Ile Asp Ala Gln Asp Phe
    135                 140                 145
```

```
gag aag gca gca ggt ctt cgc gat aag gag cgc aag ctc ggc gaa gag   595
Glu Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg Lys Leu Gly Glu Glu
150                 155                 160                 165

cgt tca gag aag gaa aag cag tgg cgc tcc ggc gac ctc gag gac atc   643
Arg Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly Asp Leu Glu Asp Ile
                170                 175                 180

gct gag gtt ggc gaa gag cag atc gca gaa gta ctg gcc aac tgg act   691
Ala Glu Val Gly Glu Glu Gln Ile Ala Glu Val Leu Ala Asn Trp Thr
            185                 190                 195

ggt att cct gtc ttc aag ctc acc gaa gct gaa tct tca cgc ctg ctc   739
Gly Ile Pro Val Phe Lys Leu Thr Glu Ala Glu Ser Ser Arg Leu Leu
        200                 205                 210

aac atg gaa gaa gag ttg cac aag cgc atc atc gga cag gat gaa gct   787
Asn Met Glu Glu Glu Leu His Lys Arg Ile Ile Gly Gln Asp Glu Ala
    215                 220                 225

gtc aag gct gtc tcc cgt gcg atc cgt cgt acc cgt gca ggt ctg aag   835
Val Lys Ala Val Ser Arg Ala Ile Arg Arg Thr Arg Ala Gly Leu Lys
230                 235                 240                 245

gat cct aag cgt cct tcc ggc tcc ttc atc ttc gct ggt cca tcc ggc   883
Asp Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe Ala Gly Pro Ser Gly
                250                 255                 260

gtt ggt aag acc gag ctg tcc aag gct ctc gca gga ttc ctc ttc ggt   931
Val Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala Gly Phe Leu Phe Gly
            265                 270                 275

gac gat gat tcc ctc atc caa atc gac atg ggt gag ttc cac gac cgc   979
Asp Asp Asp Ser Leu Ile Gln Ile Asp Met Gly Glu Phe His Asp Arg
        280                 285                 290

ttc acc gcg tcc cga ctt ttc ggt gcc cct ccg gga tac gtt ggc tac   1027
Phe Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro Gly Tyr Val Gly Tyr
    295                 300                 305

gaa gaa ggt ggc cag ctg acc gag aag gtt cgc cgt aag cca ttc tcc   1075
Glu Glu Gly Gly Gln Leu Thr Glu Lys Val Arg Arg Lys Pro Phe Ser
310                 315                 320                 325

gtt gtg ctt ttc gac gaa atc gag aag gcc cac aag gag atc tac aac   1123
Val Val Leu Phe Asp Glu Ile Glu Lys Ala His Lys Glu Ile Tyr Asn
                330                 335                 340

acc ttg ctg cag gtg ttg gaa gat ggt cgc ctt acc gat ggt cag gga   1171
Thr Leu Leu Gln Val Leu Glu Asp Gly Arg Leu Thr Asp Gly Gln Gly
            345                 350                 355

cgc atc gtg gac ttc aag aac acc gtc ctg atc ttc acc tcc aac ctg   1219
Arg Ile Val Asp Phe Lys Asn Thr Val Leu Ile Phe Thr Ser Asn Leu
        360                 365                 370

ggc acc gct gac atc tcc aag gct gtt ggc ctg ggc ttc tcc gga tcc   1267
Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu Gly Phe Ser Gly Ser
    375                 380                 385

tcc gag act gac agc gat gct cag tac gac cgc atg aag aac aag gtc   1315
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Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg Met Lys Asn Lys Val
390                 395                 400                 405

cac gac gag ctg aag aag cac ttc cgc cct gag ttc ctg aac cgt att   1363
His Asp Glu Leu Lys Lys His Phe Arg Pro Glu Phe Leu Asn Arg Ile
                410                 415                 420

gat gag atc gtg gtc ttc cac cag ctc acc aag gat cag atc gtt cag   1411
Asp Glu Ile Val Val Phe His Gln Leu Thr Lys Asp Gln Ile Val Gln
            425                 430                 435

atg gtc gac ctt ctt atc ggt cgc gtt tcc aac gca ctg gct gag aag   1459
Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn Ala Leu Ala Glu Lys
        440                 445                 450

gac atg agc atc gaa ctg act gag aag gcc aag gac ctc ctg gct aac   1507
Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys Asp Leu Leu Ala Asn
    455                 460                 465

cga ggc ttc gat cca gtt ctg ggt gca cga cca ttg cgt cgc acc atc   1555
Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro Leu Arg Arg Thr Ile
470                 475                 480                 485

cag cgc gaa att gaa gac cag atg tcc gag aag atc ctc ttc ggt gaa   1603
Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys Ile Leu Phe Gly Glu
                490                 495                 500

atc ggc gca ggc gag atc gtc acc gtt gac gtc gaa ggc tgg gac ggc   1651
Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val Glu Gly Trp Asp Gly
            505                 510                 515

gag tcc aag gac acc gac cgt gcg aag ttc acc ttc aca cca cgt cca   1699
Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr Phe Thr Pro Arg Pro
        520                 525                 530

aag cca atg cca gaa ggt aag ttc tct gag atc tct gtc gag gct gcg   1747
Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile Ser Val Glu Ala Ala
    535                 540                 545

gaa gca att caa gat gta gat tct gca gct gac ggc gat gtc cca gaa   1795
Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp Gly Asp Val Pro Glu
550                 555                 560                 565

acc gat tca ctt tcc gac att gac ctt gaa acc ctt gaa aag ttt gag   1843
Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr Leu Glu Lys Phe Glu
                570                 575                 580

gaa gat gta gaa aac ggc acc gac att gat cag gtg tcc ggt gac tac   1891
Glu Asp Val Glu Asn Gly Thr Asp Ile Asp Gln Val Ser Gly Asp Tyr
            585                 590                 595

tac ggc acc gat gat cag gga ggc act gct cca agc aag gag           1933
Tyr Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro Ser Lys Glu
        600                 605                 610

tagcaacctt ttgaaaaagg gcc                                        1956


<210> 130
<211> 611
<212> PRT
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<213> Corynebacterium glutamicum

<400> 130

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Val Gln His Glu Gly Ala Ile Asp Ala Ala Ser Leu Leu Lys Pro Lys
  1               5                  10                  15

Leu Ala Arg Gly Glu Leu Gln Thr Ile Gly Ala Thr Thr Leu Asp Glu
             20                  25                  30

Tyr Arg Lys His Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln
         35                  40                  45

Pro Val Gln Val Pro Glu Pro Ser Val Asp Leu Thr Val Glu Ile Leu
     50                  55                  60

Lys Gly Leu Arg Asp Arg Tyr Glu Ala His His Arg Val Ser Ile Thr
 65                  70                  75                  80

Asp Gly Ala Leu Thr Ala Ala Ala Gln Leu Ala Asp Arg Tyr Ile Asn
                 85                  90                  95

Asp Arg Phe Leu Pro Asp Lys Ala Val Asp Leu Ile Asp Glu Ala Gly
            100                 105                 110

Ala Arg Met Arg Ile Lys Arg Met Thr Ala Pro Ser Ser Leu Arg Glu
        115                 120                 125

Val Asp Glu Arg Ile Ala Asp Val Arg Arg Glu Lys Glu Ala Ala Ile
    130                 135                 140

Asp Ala Gln Asp Phe Glu Lys Ala Ala Gly Leu Arg Asp Lys Glu Arg
145                 150                 155                 160

Lys Leu Gly Glu Glu Arg Ser Glu Lys Glu Lys Gln Trp Arg Ser Gly
                165                 170                 175

Asp Leu Glu Asp Ile Ala Glu Val Gly Glu Glu Gln Ile Ala Glu Val
            180                 185                 190

Leu Ala Asn Trp Thr Gly Ile Pro Val Phe Lys Leu Thr Glu Ala Glu
        195                 200                 205

Ser Ser Arg Leu Leu Asn Met Glu Glu Glu Leu His Lys Arg Ile Ile
    210                 215                 220

Gly Gln Asp Glu Ala Val Lys Ala Val Ser Arg Ala Ile Arg Arg Thr
225                 230                 235                 240

Arg Ala Gly Leu Lys Asp Pro Lys Arg Pro Ser Gly Ser Phe Ile Phe
                245                 250                 255

Ala Gly Pro Ser Gly Val Gly Lys Thr Glu Leu Ser Lys Ala Leu Ala
            260                 265                 270

Gly Phe Leu Phe Gly Asp Asp Asp Ser Leu Ile Gln Ile Asp Met Gly
        275                 280                 285

Glu Phe His Asp Arg Phe Thr Ala Ser Arg Leu Phe Gly Ala Pro Pro
    290                 295                 300

Gly Tyr Val Gly Tyr Glu Glu Gly Gly Gln Leu Thr Glu Lys Val Arg
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Sequence Page

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305                 310                 315                 320

Arg Lys Pro Phe Ser Val Val Leu Phe Asp Glu Ile Glu Lys Ala His
                325                 330                 335

Lys Glu Ile Tyr Asn Thr Leu Leu Gln Val Leu Glu Asp Gly Arg Leu
            340                 345                 350

Thr Asp Gly Gln Gly Arg Ile Val Asp Phe Lys Asn Thr Val Leu Ile
        355                 360                 365

Phe Thr Ser Asn Leu Gly Thr Ala Asp Ile Ser Lys Ala Val Gly Leu
    370                 375                 380

Gly Phe Ser Gly Ser Ser Glu Thr Asp Ser Asp Ala Gln Tyr Asp Arg
385                 390                 395                 400

Met Lys Asn Lys Val His Asp Glu Leu Lys Lys His Phe Arg Pro Glu
                405                 410                 415

Phe Leu Asn Arg Ile Asp Glu Ile Val Val Phe His Gln Leu Thr Lys
            420                 425                 430

Asp Gln Ile Val Gln Met Val Asp Leu Leu Ile Gly Arg Val Ser Asn
        435                 440                 445

Ala Leu Ala Glu Lys Asp Met Ser Ile Glu Leu Thr Glu Lys Ala Lys
    450                 455                 460

Asp Leu Leu Ala Asn Arg Gly Phe Asp Pro Val Leu Gly Ala Arg Pro
465                 470                 475                 480

Leu Arg Arg Thr Ile Gln Arg Glu Ile Glu Asp Gln Met Ser Glu Lys
                485                 490                 495

Ile Leu Phe Gly Glu Ile Gly Ala Gly Glu Ile Val Thr Val Asp Val
            500                 505                 510

Glu Gly Trp Asp Gly Glu Ser Lys Asp Thr Asp Arg Ala Lys Phe Thr
        515                 520                 525

Phe Thr Pro Arg Pro Lys Pro Met Pro Glu Gly Lys Phe Ser Glu Ile
    530                 535                 540

Ser Val Glu Ala Ala Glu Ala Ile Gln Asp Val Asp Ser Ala Ala Asp
545                 550                 555                 560

Gly Asp Val Pro Glu Thr Asp Ser Leu Ser Asp Ile Asp Leu Glu Thr
                565                 570                 575

Leu Glu Lys Phe Glu Glu Asp Val Glu Asn Gly Thr Asp Ile Asp Gln
            580                 585                 590

Val Ser Gly Asp Tyr Tyr Gly Thr Asp Asp Gln Gly Gly Thr Ala Pro
        595                 600                 605

Ser Lys Glu
    610
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<210> 131

<211> 1875
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1852)
<223> RXN03094

<400> 131
atagatatta gagagttaaa taatggcgct tgacctgcag gaaattgaga tcaacactga 60

ttgtgtaggt tggcgcccaa caaagaaagg gcgttgaaag atg agt tca ttc aat 115
Met Ser Ser Phe Asn
1 5

cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
10 15 20

tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211
Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
25 30 35

atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act 259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
40 45 50

ggt gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct 307
Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala
55 60 65

tct tac ccc aag gct tct ggc gcc aat atg gct aat cca aac ttc aac 355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn
70 75 80 85

cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag 403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu
90 95 100

ttg ggc gat gag tac gtc tca acc gaa gta ctt ctt gcc ggt atc gct 451
Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala
105 110 115

cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc 499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr
120 125 130

tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt 547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg
135 140 145

gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac 595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr
150 155 160 165

tcc act gac ctg acc aag ctt gct cgt gaa ggc aag att gat cct gtt 643
Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly Lys Ile Asp Pro Val
170 175 180

att ggc cgt gac cag gaa att cgt cgc gtc gtt cag gtg ctt agc cgt 691

```
Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg
            185                 190                 195

cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa   739
Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys
        200                 205                 210

acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt   787
Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val
    215                 220                 225

cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc   835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser
230                 235                 240                 245

atg gtt gcc ggc gct aag tat cgc ggt gaa ttc gag gag cga ctg aag   883
Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu Arg Leu Lys
                250                 255                 260

gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc   931
Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe
            265                 270                 275

atc gat gag ctg cac acc atc gtc ggc gct ggt gct tcg ggt gaa tcc   979
Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ser Gly Glu Ser
        280                 285                 290

gcc atg gat gcc gga aac atg att aag cca ctg ctt gcc cgc ggt gag   1027
Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu Leu Ala Arg Gly Glu
    295                 300                 305

ctg cgc ttg gtt ggt gcc acc acg ctg aat gag tac cgc aag tac atc   1075
Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu Tyr Arg Lys Tyr Ile
310                 315                 320                 325

gaa aag gac gct gcc ctg gag cgt agg ttc cag cag gtt tat gtc ggt   1123
Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Tyr Val Gly
                330                 335                 340

gag cca acg gta gaa gat gcc atc ggt att ctt cgt gga ttg aag gaa   1171
Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu Arg Gly Leu Lys Glu
            345                 350                 355

cgc tac gag gtc cat cac ggt gtc cgc atc cag gac tcc gca ctg gtc   1219
Arg Tyr Glu Val His His Gly Val Arg Ile Gln Asp Ser Ala Leu Val
        360                 365                 370

gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct   1267
Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro
    375                 380                 385

gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg   1315
Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met
390                 395                 400                 405

gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc   1363
Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val
                410                 415                 420

cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca   1411
Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala
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            425                 430                 435

gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa   1459
Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu
        440                 445                 450

cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act   1507
Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr
    455                 460                 465

gct att gac gat gtc cgg gag atg aaa gaa gag ctg gaa gcg ctg cgt   1555
Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu Leu Glu Ala Leu Arg
470                 475                 480                 485

tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca   1603
Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala
                490                 495                 500

aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat   1651
Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp
            505                 510                 515

gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag   1699
Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu
        520                 525                 530

gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att   1747
Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile
    535                 540                 545

cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg   1795
Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met
550                 555                 560                 565

gag cgc gtc ttg ggc aac cgt gtg gtc ggt cag cta gaa agc ggt aac   1843
Glu Arg Val Leu Gly Asn Arg Val Val Gly Gln Leu Glu Ser Gly Asn
                570                 575                 580

tgc agt gtc tgacgcggtg cgtcgttcac gcg                            1875
Cys Ser Val
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<210> 132
<211> 584
<212> PRT
<213> Corynebacterium glutamicum

<400> 132

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Ala Leu Gln Gln Ala Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala
             20                  25                  30

His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro
         35                  40                  45

Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala
     50                  55                  60
```

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Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala
 65                  70                  75                  80

Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln
                 85                  90                  95

Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu
            100                 105                 110

Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr
        115                 120                 125

Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val
    130                 135                 140

Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln
145                 150                 155                 160

Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly
                165                 170                 175

Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val
            180                 185                 190

Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu
        195                 200                 205

Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile
    210                 215                 220

Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser
225                 230                 235                 240

Leu Asp Leu Gly Ser Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe
                245                 250                 255

Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly
            260                 265                 270

Glu Val Val Thr Phe Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly
        275                 280                 285

Ala Ser Gly Glu Ser Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu
    290                 295                 300

Leu Ala Arg Gly Glu Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu
305                 310                 315                 320

Tyr Arg Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln
                325                 330                 335

Gln Val Tyr Val Gly Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu
            340                 345                 350

Arg Gly Leu Lys Glu Arg Tyr Glu Val His His Gly Val Arg Ile Gln
        355                 360                 365

Asp Ser Ala Leu Val Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr
    370                 375                 380

Ser Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala
```

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385                 390                 395                 400

Ser Arg Leu Arg Met Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu
                405                 410                 415

Leu Glu Arg Ile Val Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser
            420                 425                 430

Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
        435                 440                 445

Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
    450                 455                 460

Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
465                 470                 475                 480

Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
                485                 490                 495

Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
            500                 505                 510

Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
        515                 520                 525

Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
    530                 535                 540

Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
545                 550                 555                 560

Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Arg Val Val Gly Gln
                565                 570                 575

Leu Glu Ser Gly Asn Cys Ser Val
            580
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<210> 133
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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1816)
<223> FRXA01668

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ttgtgtaggt tggcgcccaa caaagaaagg gcgttgaaag atg agt tca ttc aat 115
                                                Met Ser Ser Phe Asn
                                                  1   5

cca act acc aaa acc aat gaa gcc atg cag gct gct ctt cag cag gca 163
Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala Ala Leu Gln Gln Ala
                  10   15   20

tcc tcg gct ggc aac cct gat att cgt cca gct cac ctg ttg gct gcc 211

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Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala His Leu Leu Ala Ala
             25                  30                  35

atc ttg gag caa act gat ggc gta gca gcg cca gtc ctc atg gct act   259
Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro Val Leu Met Ala Thr
         40                  45                  50

ggt gtg gat cct aag gag atc ctc gca gag gcc aag aag ttg gtt gct   307
Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala Lys Lys Leu Val Ala
     55                  60                  65

tct tac ccc aag gct tct ggc gcc aat atg gct aat cca aac ttc aac   355
Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala Asn Pro Asn Phe Asn
 70                  75                  80                  85

cgg gat gcc ctc aat gcg ttc act gca gct cag gag ctt gcc ggt gag   403
Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln Glu Leu Ala Gly Glu
                 90                  95                 100

ttg ggc gat gag tac gtc tca acc gaa gta ctt ctt gcc ggt atc gct   451
Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu Leu Ala Gly Ile Ala
            105                 110                 115

cgc gga aag tct gat gct gcg gat ctg ttg acc aac aag ggt gca acc   499
Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr Asn Lys Gly Ala Thr
        120                 125                 130

tat gac gcc atc aaa gag gct ttc cct tcg gtt cgt gga tct cag cgt   547
Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val Arg Gly Ser Gln Arg
    135                 140                 145

gtc acc act cag gat cca gag gga cag ttc cag gct ttg gaa aag tac   595
Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln Ala Leu Glu Lys Tyr
150                 155                 160                 165

tcc act gac ctg acc aag ctt gct cgt gaa ggc aag att gat cct gtt   643
Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly Lys Ile Asp Pro Val
                170                 175                 180

att ggc cgt gac cag gaa att cgt cgc gtc gtt cag gtg ctt agc cgt   691
Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val Gln Val Leu Ser Arg
            185                 190                 195

cgt acc aag aac aac cct gtt ctg atc ggt gag cca ggt gtc ggt aaa   739
Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu Pro Gly Val Gly Lys
        200                 205                 210

acc gcc atc gtg gaa ggc ctt gca cgc cgc atc gtt gct ggt gac gtt   787
Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile Val Ala Gly Asp Val
    215                 220                 225

cca gaa tcc ctc aag ggc aaa act ctg atc agt ctt gat ctt ggt tcc   835
Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser Leu Asp Leu Gly Ser
230                 235                 240                 245

atg gtt gcc ggc gct aag tat cgc ggt gaa ttc gag gag cga ctg aag   883
Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe Glu Glu Arg Leu Lys
                250                 255                 260

gct gtt ctg gat gag atc aag gga gct aac ggc gaa gtc gtt acc ttc   931
Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly Glu Val Val Thr Phe
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            265                 270                 275

atc gat gag ctg cac acc atc gtc ggc gct ggt gct tcg ggt gaa tcc   979
Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly Ala Ser Gly Glu Ser
        280                 285                 290

gcc atg gat gcc gga aac atg att aag cca ctg ctt gcc cgc ggt gag   1027
Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu Leu Ala Arg Gly Glu
    295                 300                 305

ctg cgc ttg gtt ggt gcc acc acg ctg aat gag tac cgc aag tac atc   1075
Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu Tyr Arg Lys Tyr Ile
310                 315                 320                 325

gaa aag gac gct gcc ctg gag cgt agg ttc cag cag gtt tat gtc ggt   1123
Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln Gln Val Tyr Val Gly
                330                 335                 340

gag cca acg gta gaa gat gcc atc ggt att ctt cgt gga ttg aag gaa   1171
Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu Arg Gly Leu Lys Glu
            345                 350                 355

cgc tac gag gtc cat cac ggt gtc cgc atc cag gac tcc gca ctg gtc   1219
Arg Tyr Glu Val His His Gly Val Arg Ile Gln Asp Ser Ala Leu Val
        360                 365                 370

gcc gca gct gaa ctc tca aac cgc tat atc acc agc cgt ttc ctt cct   1267
Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr Ser Arg Phe Leu Pro
    375                 380                 385

gat aag gct att gac tta gtt gat gag gca gca tca cgc ctg cgc atg   1315
Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala Ser Arg Leu Arg Met
390                 395                 400                 405

gag att gat tct tca cct cag gaa atc gat gag ctg gag cgt atc gtc   1363
Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu Leu Glu Arg Ile Val
                410                 415                 420

cgc cgc ctc gag atc gaa gag atg gcg ctg tcc aag gaa tcc gat gca   1411
Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser Lys Glu Ser Asp Ala
            425                 430                 435

gct tcc aag gaa cgt cta gaa aag ctg cgc tcg gaa ctt gct gat gaa   1459
Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser Glu Leu Ala Asp Glu
        440                 445                 450

cgc gaa aag ctc tct gag ttg aag gct cgt tgg cag aat gag aaa act   1507
Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp Gln Asn Glu Lys Thr
    455                 460                 465

gct att gac gat gtc cgg gag atg aaa gaa gag ctg gaa gcg ctg cgt   1555
Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu Leu Glu Ala Leu Arg
470                 475                 480                 485

tct gag tcg gat att gca aaa cgt gac ggc aat tat tgt cgt gtc gca   1603
Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn Tyr Cys Arg Val Ala
                490                 495                 500

aag ctt cgc tac ggc cga atc cct gag ctg gaa aag cag atc gag gat   1651
Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu Lys Gln Ile Glu Asp
            505                 510                 515
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gca gaa tcc aag gtc gag gtc aat gaa aat gcc atg ctc act gag gag   1699
Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala Met Leu Thr Glu Glu
        520                 525                 530

gtc acg cca gac acg atc gcc gat gtg gtt tcc gca tgg acg ggc att   1747
Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser Ala Trp Thr Gly Ile
    535                 540                 545

cct gca ggc aag atg atg cag ggt gag acc gag aag ctg ctc aac atg   1795
Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu Lys Leu Leu Asn Met
550                 555                 560                 565

gag cgc gtc ttg ggc aac ccg                                      1816
Glu Arg Val Leu Gly Asn Pro
                570
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<210> 134
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<400> 134

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Met Ser Ser Phe Asn Pro Thr Thr Lys Thr Asn Glu Ala Met Gln Ala
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Ala Leu Gln Gln Ala Ser Ser Ala Gly Asn Pro Asp Ile Arg Pro Ala
             20                  25                  30

His Leu Leu Ala Ala Ile Leu Glu Gln Thr Asp Gly Val Ala Ala Pro
         35                  40                  45

Val Leu Met Ala Thr Gly Val Asp Pro Lys Glu Ile Leu Ala Glu Ala
     50                  55                  60

Lys Lys Leu Val Ala Ser Tyr Pro Lys Ala Ser Gly Ala Asn Met Ala
 65                  70                  75                  80

Asn Pro Asn Phe Asn Arg Asp Ala Leu Asn Ala Phe Thr Ala Ala Gln
                 85                  90                  95

Glu Leu Ala Gly Glu Leu Gly Asp Glu Tyr Val Ser Thr Glu Val Leu
            100                 105                 110

Leu Ala Gly Ile Ala Arg Gly Lys Ser Asp Ala Ala Asp Leu Leu Thr
        115                 120                 125

Asn Lys Gly Ala Thr Tyr Asp Ala Ile Lys Glu Ala Phe Pro Ser Val
    130                 135                 140

Arg Gly Ser Gln Arg Val Thr Thr Gln Asp Pro Glu Gly Gln Phe Gln
145                 150                 155                 160

Ala Leu Glu Lys Tyr Ser Thr Asp Leu Thr Lys Leu Ala Arg Glu Gly
                165                 170                 175

Lys Ile Asp Pro Val Ile Gly Arg Asp Gln Glu Ile Arg Arg Val Val
            180                 185                 190

Gln Val Leu Ser Arg Arg Thr Lys Asn Asn Pro Val Leu Ile Gly Glu
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        195                 200                 205

Pro Gly Val Gly Lys Thr Ala Ile Val Glu Gly Leu Ala Arg Arg Ile
    210                 215                 220

Val Ala Gly Asp Val Pro Glu Ser Leu Lys Gly Lys Thr Leu Ile Ser
225                 230                 235                 240

Leu Asp Leu Gly Ser Met Val Ala Gly Ala Lys Tyr Arg Gly Glu Phe
                245                 250                 255

Glu Glu Arg Leu Lys Ala Val Leu Asp Glu Ile Lys Gly Ala Asn Gly
            260                 265                 270

Glu Val Val Thr Phe Ile Asp Glu Leu His Thr Ile Val Gly Ala Gly
        275                 280                 285

Ala Ser Gly Glu Ser Ala Met Asp Ala Gly Asn Met Ile Lys Pro Leu
    290                 295                 300

Leu Ala Arg Gly Glu Leu Arg Leu Val Gly Ala Thr Thr Leu Asn Glu
305                 310                 315                 320

Tyr Arg Lys Tyr Ile Glu Lys Asp Ala Ala Leu Glu Arg Arg Phe Gln
                325                 330                 335

Gln Val Tyr Val Gly Glu Pro Thr Val Glu Asp Ala Ile Gly Ile Leu
            340                 345                 350

Arg Gly Leu Lys Glu Arg Tyr Glu Val His His Gly Val Arg Ile Gln
        355                 360                 365

Asp Ser Ala Leu Val Ala Ala Ala Glu Leu Ser Asn Arg Tyr Ile Thr
    370                 375                 380

Ser Arg Phe Leu Pro Asp Lys Ala Ile Asp Leu Val Asp Glu Ala Ala
385                 390                 395                 400

Ser Arg Leu Arg Met Glu Ile Asp Ser Ser Pro Gln Glu Ile Asp Glu
                405                 410                 415

Leu Glu Arg Ile Val Arg Arg Leu Glu Ile Glu Glu Met Ala Leu Ser
            420                 425                 430

Lys Glu Ser Asp Ala Ala Ser Lys Glu Arg Leu Glu Lys Leu Arg Ser
        435                 440                 445

Glu Leu Ala Asp Glu Arg Glu Lys Leu Ser Glu Leu Lys Ala Arg Trp
    450                 455                 460

Gln Asn Glu Lys Thr Ala Ile Asp Asp Val Arg Glu Met Lys Glu Glu
465                 470                 475                 480

Leu Glu Ala Leu Arg Ser Glu Ser Asp Ile Ala Lys Arg Asp Gly Asn
                485                 490                 495

Tyr Cys Arg Val Ala Lys Leu Arg Tyr Gly Arg Ile Pro Glu Leu Glu
            500                 505                 510

Lys Gln Ile Glu Asp Ala Glu Ser Lys Val Glu Val Asn Glu Asn Ala
        515                 520                 525
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Met Leu Thr Glu Glu Val Thr Pro Asp Thr Ile Ala Asp Val Val Ser
530 535 540

Ala Trp Thr Gly Ile Pro Ala Gly Lys Met Met Gln Gly Glu Thr Glu
545 550 555 560

Lys Leu Leu Asn Met Glu Arg Val Leu Gly Asn Pro
565 570

<210> 135
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<213> Corynebacterium glutamicum

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<222> (101)..(502)
<223> RXN02937

<400> 135
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tcgaaacatc caacgcattg gtgacaccgg tgttgtcgcg gtg atc agc aat ggg 115
Val Ile Ser Asn Gly
1 5

gaa ggt ccg gtt gtt gcg ctt cgt ggc gac att gat gcg ttg ccc atg 163
Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile Asp Ala Leu Pro Met
10 15 20

gcg gag cga tcc ggc aaa gaa tac gca gca acc gga gtg aca cag gtg 211
Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr Gly Val Thr Gln Val
25 30 35

gat aac acc acc ggt caa gaa act ccg gtg gcg cat acc tgt ggc cac 259
Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala His Thr Cys Gly His
40 45 50

gat gtg cat att tca tca ctg ttg ggt gcg gtg cag gcg ttc aat tct 307
Asp Val His Ile Ser Ser Leu Leu Gly Ala Val Gln Ala Phe Asn Ser
55 60 65

cat cgg gaa ttg tgg aac gga acg ttg atg gcc gtt ttc cag cca gcg 355
His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala Val Phe Gln Pro Ala
70 75 80 85

gaa gag acg gca gct ggt gcg agg atg atg gcg gat cag gac aac gcg 403
Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala Asp Gln Asp Asn Ala
90 95 100

ccg gga aat cac tct cca gcg ttc gcg cca gat atg cag cca act ctt 451
Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp Met Gln Pro Thr Leu
105 110 115

gat cgt ggt gtg gaa gcg ctg gtt gta gct gct tct gcg tgg cta gta 499
Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala Ser Ala Trp Leu Val
120 125 130

aaa taattggcta atgaatcctt ttc 525

Lys

<210> 136
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<212> PRT
<213> Corynebacterium glutamicum

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Val Ile Ser Asn Gly Glu Gly Pro Val Val Ala Leu Arg Gly Asp Ile
1 5 10 15

Asp Ala Leu Pro Met Ala Glu Arg Ser Gly Lys Glu Tyr Ala Ala Thr
20 25 30

Gly Val Thr Gln Val Asp Asn Thr Thr Gly Gln Glu Thr Pro Val Ala
35 40 45

His Thr Cys Gly His Asp Val His Ile Ser Ser Leu Leu Gly Ala Val
50 55 60

Gln Ala Phe Asn Ser His Arg Glu Leu Trp Asn Gly Thr Leu Met Ala
65 70 75 80

Val Phe Gln Pro Ala Glu Glu Thr Ala Ala Gly Ala Arg Met Met Ala
85 90 95

Asp Gln Asp Asn Ala Pro Gly Asn His Ser Pro Ala Phe Ala Pro Asp
100 105 110

Met Gln Pro Thr Leu Asp Arg Gly Val Glu Ala Leu Val Val Ala Ala
115 120 125

Ser Ala Trp Leu Val Lys
130

<210> 137
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<212> DNA
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<222> (101)..(1285)
<223> RXN03077

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Val Met Glu Ile Gly
1 5

gtg cag gtt gcc tca tgg atg gac cgc cac cat gac gag gtc ata aag 163
Val Gln Val Ala Ser Trp Met Asp Arg His His Asp Glu Val Ile Lys
10 15 20

tgg cgc agg cat ttg cac agc cat cct gag ctc tcc cac atg gaa tac 211
Trp Arg Arg His Leu His Ser His Pro Glu Leu Ser His Met Glu Tyr

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                25                  30                  35

cgc acg act gag tat ttg gcc tcg gtt ctg aaa gat cac ggc atg gaa   259
Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys Asp His Gly Met Glu
         40                  45                  50

cca cac ctg ttc cca gga acc ggt ttg atg gtg gat atc gga cca gaa   307
Pro His Leu Phe Pro Gly Thr Gly Leu Met Val Asp Ile Gly Pro Glu
     55                  60                  65

ggg gac tcc cgc ctg gcg ttt cgc gct gat atc gat gcc ctt ccg ctg   355
Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile Asp Ala Leu Pro Leu
 70                  75                  80                  85

ctt gaa tca acc ggc tta gag ttc tct tcc aca gcc act ggc gtt gcg   403
Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr Ala Thr Gly Val Ala
                 90                  95                 100

cat gcc tgc gga cat gac gtg cac acg gtg atc gct ttg gca ctt gcc   451
His Ala Cys Gly His Asp Val His Thr Val Ile Ala Leu Ala Leu Ala
            105                 110                 115

tgt gca ctg aac acc atc gaa ctg ccc atc ggc att cgg gtg att ttc   499
Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly Ile Arg Val Ile Phe
        120                 125                 130

cag ccg gca gaa gaa gtc atg act ggt ggc gca acg gac gtc att gcc   547
Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala Thr Asp Val Ile Ala
    135                 140                 145

cac ggt ggc ctt gat ggt gtg gat gcg att tac gcc atc cac gtt gaa   595
His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr Ala Ile His Val Glu
150                 155                 160                 165

ccc aaa ttg aag gtc ggt cgc gtc ggt gta cgc gct ggc gcg att act   643
Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg Ala Gly Ala Ile Thr
                170                 175                 180

tct gcc tca gat gtg atc gaa atc aga gtc aag ggt gaa gga gga cat   691
Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys Gly Glu Gly Gly His
            185                 190                 195

agc gca cgt cca cac ctc tcc gct gat gtt gtt tac gcc ttg agc aaa   739
Ser Ala Arg Pro His Leu Ser Ala Asp Val Val Tyr Ala Leu Ser Lys
        200                 205                 210

ttg gtc gtt gat ctt ccc ggt ttg ctg tcc agg cgc gtc gat cca cgc   787
Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg Arg Val Asp Pro Arg
    215                 220                 225

acc ggc acc gtg ctt gtt ttc ggc acc atc aac gcc ggc tat gcg ccc   835
Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn Ala Gly Tyr Ala Pro
230                 235                 240                 245

aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc   883
Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
                250                 255                 260

gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg   931
Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
            265                 270                 275
```

```
gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat   979
Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
        280                 285                 290

ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg   1027
Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
    295                 300                 305

gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg   1075
Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
310                 315                 320                 325

cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca   1123
Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
                330                 335                 340

gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa   1171
Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
            345                 350                 355

gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt   1219
Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
        360                 365                 370

ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct   1267
Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
    375                 380                 385

gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct                1308
Glu Ala Phe Leu Asn Ser
390                 395
```

<210> 138
<211> 395
<212> PRT
<213> Corynebacterium glutamicum

<400> 138

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Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
  1               5                  10                  15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
             20                  25                  30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
         35                  40                  45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
     50                  55                  60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
 65                  70                  75                  80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
                 85                  90                  95

Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
            100                 105                 110
```

```
Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
        115                 120                 125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
    130                 135                 140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
145                 150                 155                 160

Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg
                165                 170                 175

Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys
            180                 185                 190

Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val
        195                 200                 205

Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg
    210                 215                 220

Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn
225                 230                 235                 240

Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly
                245                 250                 255

Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu
            260                 265                 270

Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His
        275                 280                 285

Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val
    290                 295                 300

Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser
305                 310                 315                 320

Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr
                325                 330                 335

Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly
            340                 345                 350

His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu
        355                 360                 365

Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln
    370                 375                 380

Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser
385                 390                 395
```

<210> 139
<211> 1308
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1285)
<223> FRXA02855

<400> 139
accccgatcc tttgttttcg tgggatcact attagactcg actctaccgc gctgcaggtt 60

ttcctgatac gcctgcggac aaaacagaaa ggtatttcac gtg atg gaa att ggt 115
Val Met Glu Ile Gly
1 5

gtg cag gtt gcc tca tgg atg gac cgc cac cat gac gag gtc ata aag 163
Val Gln Val Ala Ser Trp Met Asp Arg His His Asp Glu Val Ile Lys
10 15 20

tgg cgc agg cat ttg cac agc cat cct gag ctc tcc cac atg gaa tac 211
Trp Arg Arg His Leu His Ser His Pro Glu Leu Ser His Met Glu Tyr
25 30 35

cgc acg act gag tat ttg gcc tcg gtt ctg aaa gat cac ggc atg gaa 259
Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys Asp His Gly Met Glu
40 45 50

cca cac ctg ttc cca gga acc ggt ttg atg gtg gat atc gga cca gaa 307
Pro His Leu Phe Pro Gly Thr Gly Leu Met Val Asp Ile Gly Pro Glu
55 60 65

ggg gac tcc cgc ctg gcg ttt cgc gct gat atc gat gcc ctt ccg ctg 355
Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile Asp Ala Leu Pro Leu
70 75 80 85

ctt gaa tca acc ggc tta gag ttc tct tcc aca gcc act ggc gtt gcg 403
Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr Ala Thr Gly Val Ala
90 95 100

cat gcc tgc gga cat gac gtg cac acg gtg atc gct ttg gca ctt gcc 451
His Ala Cys Gly His Asp Val His Thr Val Ile Ala Leu Ala Leu Ala
105 110 115

tgt gca ctg aac acc atc gaa ctg ccc atc ggc att cgg gtg att ttc 499
Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly Ile Arg Val Ile Phe
120 125 130

cag ccg gca gaa gaa gtc atg act ggt ggc gca acg gac gtc att gcc 547
Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala Thr Asp Val Ile Ala
135 140 145

cac ggt ggc ctt gat ggt gtg gat gcg att tac gcc atc cac gtt gaa 595
His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr Ala Ile His Val Glu
150 155 160 165

ccc aaa ttg aag gtc ggt cgc gtc ggt gta cgc gct ggc gcg att act 643
Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg Ala Gly Ala Ile Thr
170 175 180

tct gcc tca gat gtg atc gaa atc aga gtc aag ggt gaa gga gga cat 691
Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys Gly Glu Gly Gly His
185 190 195

agc gca cgt cca cac ctc tcc gct gat gtt gtt tac gcc ttg agc aaa 739
Ser Ala Arg Pro His Leu Ser Ala Asp Val Val Tyr Ala Leu Ser Lys

```
        200                 205                 210

ttg gtc gtt gat ctt ccc ggt ttg ctg tcc agg cgc gtc gat cca cgc   787
Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg Arg Val Asp Pro Arg
    215                 220                 225

acc ggc acc gtg ctt gtt ttc ggc acc atc aac gcc ggc tat gcg ccc   835
Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn Ala Gly Tyr Ala Pro
230                 235                 240                 245

aac gcg atc cca gat tcc ggc atc gtg tca ggc acc ttg cgt aca gcc   883
Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly Thr Leu Arg Thr Ala
                250                 255                 260

gac atc tct acc tgg cgt gac atg cgt ccg ctt atc tct gag ctg gtg   931
Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu Ile Ser Glu Leu Val
            265                 270                 275

gaa cag gtg ctc gca ccc acc gga gtc acc cat gaa ctg atc tac aat   979
Glu Gln Val Leu Ala Pro Thr Gly Val Thr His Glu Leu Ile Tyr Asn
        280                 285                 290

ccg ggt gtt cca cca gtg ctt aac gac gat gtc gcc acc gct ttg ttg   1027
Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val Ala Thr Ala Leu Leu
    295                 300                 305

gca agc gca gca cgc gac atg gac aca caa tct gtt gtc caa gcg ccg   1075
Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser Val Val Gln Ala Pro
310                 315                 320                 325

cag tca tcc ggt gga gaa gac ttc tcg tgg tac ctt gaa cac gtc cca   1123
Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr Leu Glu His Val Pro
                330                 335                 340

gga tca atg gcc cgg ttg ggt tgc tgg ccg ggg cac gga ccc aag caa   1171
Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly His Gly Pro Lys Gln
            345                 350                 355

gac ctc cat caa agt gac ctg gtt gtg gat gag cga gcc atc gga gtt   1219
Asp Leu His Gln Ser Asp Leu Val Val Asp Glu Arg Ala Ile Gly Val
        360                 365                 370

ggc gtc agg ctc ttt ggc tcc ctt gtg cag cag tac agt agc cga tct   1267
Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln Tyr Ser Ser Arg Ser
    375                 380                 385

gaa gct ttc tta aat tcc taatgggggt agtgtgtagg gct                1308
Glu Ala Phe Leu Asn Ser
390                 395
```

<210> 140
<211> 395
<212> PRT
<213> Corynebacterium glutamicum

<400> 140

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Val Met Glu Ile Gly Val Gln Val Ala Ser Trp Met Asp Arg His His
  1               5                  10                  15

Asp Glu Val Ile Lys Trp Arg Arg His Leu His Ser His Pro Glu Leu
```

```
            20                  25                  30

Ser His Met Glu Tyr Arg Thr Thr Glu Tyr Leu Ala Ser Val Leu Lys
         35                  40                  45

Asp His Gly Met Glu Pro His Leu Phe Pro Gly Thr Gly Leu Met Val
     50                  55                  60

Asp Ile Gly Pro Glu Gly Asp Ser Arg Leu Ala Phe Arg Ala Asp Ile
 65                  70                  75                  80

Asp Ala Leu Pro Leu Leu Glu Ser Thr Gly Leu Glu Phe Ser Ser Thr
                 85                  90                  95

Ala Thr Gly Val Ala His Ala Cys Gly His Asp Val His Thr Val Ile
            100                 105                 110

Ala Leu Ala Leu Ala Cys Ala Leu Asn Thr Ile Glu Leu Pro Ile Gly
        115                 120                 125

Ile Arg Val Ile Phe Gln Pro Ala Glu Glu Val Met Thr Gly Gly Ala
    130                 135                 140

Thr Asp Val Ile Ala His Gly Gly Leu Asp Gly Val Asp Ala Ile Tyr
145                 150                 155                 160

Ala Ile His Val Glu Pro Lys Leu Lys Val Gly Arg Val Gly Val Arg
                165                 170                 175

Ala Gly Ala Ile Thr Ser Ala Ser Asp Val Ile Glu Ile Arg Val Lys
            180                 185                 190

Gly Glu Gly Gly His Ser Ala Arg Pro His Leu Ser Ala Asp Val Val
        195                 200                 205

Tyr Ala Leu Ser Lys Leu Val Val Asp Leu Pro Gly Leu Leu Ser Arg
    210                 215                 220

Arg Val Asp Pro Arg Thr Gly Thr Val Leu Val Phe Gly Thr Ile Asn
225                 230                 235                 240

Ala Gly Tyr Ala Pro Asn Ala Ile Pro Asp Ser Gly Ile Val Ser Gly
                245                 250                 255

Thr Leu Arg Thr Ala Asp Ile Ser Thr Trp Arg Asp Met Arg Pro Leu
            260                 265                 270

Ile Ser Glu Leu Val Glu Gln Val Leu Ala Pro Thr Gly Val Thr His
        275                 280                 285

Glu Leu Ile Tyr Asn Pro Gly Val Pro Pro Val Leu Asn Asp Asp Val
    290                 295                 300

Ala Thr Ala Leu Leu Ala Ser Ala Ala Arg Asp Met Asp Thr Gln Ser
305                 310                 315                 320

Val Val Gln Ala Pro Gln Ser Ser Gly Gly Glu Asp Phe Ser Trp Tyr
                325                 330                 335

Leu Glu His Val Pro Gly Ser Met Ala Arg Leu Gly Cys Trp Pro Gly
            340                 345                 350
```

```
His Gly Pro Lys Gln Asp Leu His Gln Ser Asp Leu Val Val Asp Glu
        355                 360                 365

Arg Ala Ile Gly Val Gly Val Arg Leu Phe Gly Ser Leu Val Gln Gln
    370                 375                 380

Tyr Ser Ser Arg Ser Glu Ala Phe Leu Asn Ser
385                 390                 395


<210> 141
<211> 1629
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1606)
<223> RXN00982

<400> 141
gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaaggg tagtagcagt 60

tcttgccgcc tcgactgcgc ttagcccctt tttggtatca atg ccc act gca gca   115
                                              Met Pro Thr Ala Ala
                                                1               5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att   163
Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
                10                  15                  20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat   211
Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
            25                  30                  35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa   259
Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
        40                  45                  50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc   307
Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
    55                  60                  65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc   355
Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
70                  75                  80                  85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc   403
Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
                90                  95                  100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc   451
Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
            105                 110                 115

ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag   499
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
        120                 125                 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc   547
```

```
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala
    135                 140                 145

aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc   595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser
150                 155                 160                 165

atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc   643
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr
                170                 175                 180

cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg   691
Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala
            185                 190                 195

ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac   739
Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr
        200                 205                 210

aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac   787
Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp
    215                 220                 225

acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca   835
Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser
230                 235                 240                 245

aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca   883
Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro
                250                 255                 260

cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa   931
Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln
            265                 270                 275

gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc   979
Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu
        280                 285                 290

cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg   1027
Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu
    295                 300                 305

agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc   1075
Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr
310                 315                 320                 325

tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc atc cct gac   1123
Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro Ile Pro Asp
                330                 335                 340

gta act gac acc ggc gac gac cca tac gtc atc gaa agc atc aac gcc   1171
Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile Glu Ser Ile Asn Ala
            345                 350                 355

agc gtc aac atg cag cgc atg gtc atg tgc aac gaa aac acc gtc gca   1219
Ser Val Asn Met Gln Arg Met Val Met Cys Asn Glu Asn Thr Val Ala
        360                 365                 370

cca gac cca gta gca atg gca cgc atg gcc tgg aca agc atg gtc acc   1267
Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp Thr Ser Met Val Thr
```

```
    375                 380                 385

ggc gac gtc ttt gac att tac tcc gtt aaa ttc agc tcc gga caa gcc   1315
Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe Ser Ser Gly Gln Ala
390                 395                 400                 405

tgc tcc ggc atc acc cca aca agc ggc cgc cag cca acc gac gga tct   1363
Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln Pro Thr Asp Gly Ser
                410                 415                 420

caa cta gca gtc caa cca cta ctc ctc cag gga acc agc gac cca caa   1411
Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro Gln
            425                 430                 435

acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc cac   1459
Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala His
        440                 445                 450

gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc acc   1507
Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly Thr
    455                 460                 465

aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga cac   1555
Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly His
470                 475                 480                 485

acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg gct   1603
Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr Ala
                490                 495                 500

ggc taattgcttt ccacttagta gat                                    1629
Gly
```

SEQUENCE LISTING

<210> 142
<211> 502
<212> PRT
<213> Corynebacterium glutamicum

<400> 142

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Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
  1               5                  10                  15

Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
             20                  25                  30

Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
         35                  40                  45

Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
     50                  55                  60

Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65                  70                  75                  80

Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
                 85                  90                  95

Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
            100                 105                 110
```

```
Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
        115                 120                 125

Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
    130                 135                 140

Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
145                 150                 155                 160

Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
                165                 170                 175

Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
            180                 185                 190

Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
        195                 200                 205

Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
    210                 215                 220

Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
225                 230                 235                 240

Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
                245                 250                 255

Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
            260                 265                 270

Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
        275                 280                 285

Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
    290                 295                 300

Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
305                 310                 315                 320

Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
                325                 330                 335

Thr Pro Ile Pro Asp Val Thr Asp Thr Gly Asp Asp Pro Tyr Val Ile
            340                 345                 350

Glu Ser Ile Asn Ala Ser Val Asn Met Gln Arg Met Val Met Cys Asn
        355                 360                 365

Glu Asn Thr Val Ala Pro Asp Pro Val Ala Met Ala Arg Met Ala Trp
    370                 375                 380

Thr Ser Met Val Thr Gly Asp Val Phe Asp Ile Tyr Ser Val Lys Phe
385                 390                 395                 400

Ser Ser Gly Gln Ala Cys Ser Gly Ile Thr Pro Thr Ser Gly Arg Gln
                405                 410                 415

Pro Thr Asp Gly Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly
            420                 425                 430
```

Sequence Listing

```
Thr Ser Asp Pro Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp
        435                 440                 445

Ala Met Asn Ala His Val Val Thr Val Asn Gly Pro Gly His Gly Gln
    450                 455                 460

Ser Ile Gly Gly Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr
465                 470                 475                 480

Leu Arg Thr Gly His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro
                485                 490                 495

Thr Pro Ile Thr Ala Gly
            500
```

<210> 143
<211> 1114
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> FRXA00977

<400> 143

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gaaaacaaac gtccttgaag ccgtaatgcc ccgttcgaca ataaaaaggg tagtagcagt 60

tcttgccgcc tcgactgcgc ttagcccctt tttggtatca atg ccc act gca gca   115
                                              Met Pro Thr Ala Ala
                                                1               5

gcg caa gaa aac atc cgc tgg gaa gaa tgc cca cct cag gta gat att   163
Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro Pro Gln Val Asp Ile
                  10                  15                  20

gcc tcc gct caa tgt ggc agc atc gac gtg ccc atg cac tat tct gat   211
Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro Met His Tyr Ser Asp
              25                  30                  35

ccc tca ctt ggc gat atc agc gtg ggc ttt gtc aag gtc cct gcc caa   259
Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val Lys Val Pro Ala Gln
          40                  45                  50

ggc gaa aag cac ggc acc atc ttc ggt aac tcc ggt ggc cct ggt ggc   307
Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser Gly Gly Pro Gly Gly
      55                  60                  65

gat gcc tat agc ttc ttc ggc agc caa tcc atg aac tgg cca gaa gcc   355
Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met Asn Trp Pro Glu Ala
  70                  75                  80                  85

atg tac caa aac tac gac ctc gtt gca gtg cag cct cgc gga atg gtc   403
Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln Pro Arg Gly Met Val
                  90                  95                 100

ggc tcc aca ccg gtt aac tgc gac aac atc gca cca gga tac gat ttc   451
Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala Pro Gly Tyr Asp Phe
              105                 110                 115
```

```
ctc tcg ctg ctc acc cgc gaa ggc gct ttc gtt aaa gaa tcc tgc gag   499
Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val Lys Glu Ser Cys Glu
        120                 125                 130

atc ggc acc ccc ggc tac acc tcc agc ctg acc acc gac aac acc gcc   547
Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr Thr Asp Asn Thr Ala
    135                 140                 145

aac gac tgg gag cgc gtc cgc caa gca ctt ggc gat gac aag atc tcc   595
Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly Asp Asp Lys Ile Ser
150                 155                 160                 165

atc ttc gga ctg tcc tac gga acc tac ctc gga tcg gtc tac gcc acc   643
Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly Ser Val Tyr Ala Thr
                170                 175                 180

cgc tac cca cag cac acc gac aag gtt gtc ctc gat tcc gca atg gcg   691
Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu Asp Ser Ala Met Ala
            185                 190                 195

ccc agc ctg gca tgg aac ggc atc atg gcc tcc caa gaa cag ggc tac   739
Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser Gln Glu Gln Gly Tyr
        200                 205                 210

aaa aac tcc ctc aac gac ttc ttc acc tgg gtt gca gaa aac aac gac   787
Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val Ala Glu Asn Asn Asp
    215                 220                 225

acg tat ggc ctc ggc act acc cca cta gcc gtg tac caa aac tgg tca   835
Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val Tyr Gln Asn Trp Ser
230                 235                 240                 245

aac aag atc gtc gcc gaa acc gga acc aac cca acc gtt gct cca cca   883
Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro Thr Val Ala Pro Pro
                250                 255                 260

cca gca caa gtt ggc gat gtc cca cca gca ttc gca tgg gcc ggc caa   931
Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe Ala Trp Ala Gly Gln
            265                 270                 275

gca ggc gca gac atg atg acc gcc acc aac cca acc tcc gtg caa ctc   979
Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro Thr Ser Val Gln Leu
        280                 285                 290

cag ggc ctt gcc acc cag ctc cta aac cct gga tcc aac cag tca ctg   1027
Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly Ser Asn Gln Ser Leu
    295                 300                 305

agc cct ctg ctc aac gtc acc cgc gcc tac att cca cag cca tca acc   1075
Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile Pro Gln Pro Ser Thr
310                 315                 320                 325

tgg ccc atg ctc gca ggc gcc atc tca ggg caa aca ccc              1114
Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln Thr Pro
                330                 335
```

<210> 144
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 144

```
Met Pro Thr Ala Ala Ala Gln Glu Asn Ile Arg Trp Glu Glu Cys Pro
  1               5                  10                  15

Pro Gln Val Asp Ile Ala Ser Ala Gln Cys Gly Ser Ile Asp Val Pro
             20                  25                  30

Met His Tyr Ser Asp Pro Ser Leu Gly Asp Ile Ser Val Gly Phe Val
         35                  40                  45

Lys Val Pro Ala Gln Gly Glu Lys His Gly Thr Ile Phe Gly Asn Ser
     50                  55                  60

Gly Gly Pro Gly Gly Asp Ala Tyr Ser Phe Phe Gly Ser Gln Ser Met
 65                  70                  75                  80

Asn Trp Pro Glu Ala Met Tyr Gln Asn Tyr Asp Leu Val Ala Val Gln
                 85                  90                  95

Pro Arg Gly Met Val Gly Ser Thr Pro Val Asn Cys Asp Asn Ile Ala
            100                 105                 110

Pro Gly Tyr Asp Phe Leu Ser Leu Leu Thr Arg Glu Gly Ala Phe Val
        115                 120                 125

Lys Glu Ser Cys Glu Ile Gly Thr Pro Gly Tyr Thr Ser Ser Leu Thr
    130                 135                 140

Thr Asp Asn Thr Ala Asn Asp Trp Glu Arg Val Arg Gln Ala Leu Gly
145                 150                 155                 160

Asp Asp Lys Ile Ser Ile Phe Gly Leu Ser Tyr Gly Thr Tyr Leu Gly
                165                 170                 175

Ser Val Tyr Ala Thr Arg Tyr Pro Gln His Thr Asp Lys Val Val Leu
            180                 185                 190

Asp Ser Ala Met Ala Pro Ser Leu Ala Trp Asn Gly Ile Met Ala Ser
        195                 200                 205

Gln Glu Gln Gly Tyr Lys Asn Ser Leu Asn Asp Phe Phe Thr Trp Val
    210                 215                 220

Ala Glu Asn Asn Asp Thr Tyr Gly Leu Gly Thr Thr Pro Leu Ala Val
225                 230                 235                 240

Tyr Gln Asn Trp Ser Asn Lys Ile Val Ala Glu Thr Gly Thr Asn Pro
                245                 250                 255

Thr Val Ala Pro Pro Pro Ala Gln Val Gly Asp Val Pro Pro Ala Phe
            260                 265                 270

Ala Trp Ala Gly Gln Ala Gly Ala Asp Met Met Thr Ala Thr Asn Pro
        275                 280                 285

Thr Ser Val Gln Leu Gln Gly Leu Ala Thr Gln Leu Leu Asn Pro Gly
    290                 295                 300

Ser Asn Gln Ser Leu Ser Pro Leu Leu Asn Val Thr Arg Ala Tyr Ile
305                 310                 315                 320
```

```
Pro Gln Pro Ser Thr Trp Pro Met Leu Ala Gly Ala Ile Ser Gly Gln
                325                 330                 335

Thr Pro
```

<210> 145
<211> 269
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(246)
<223> FRXA00982

<400> 145

```
tct caa cta gca gtc caa cca cta ctc ctc cag gga acc agc gac cca   48
Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro
  1               5                  10                  15

caa acc cca tac tgg acc cac aac gag ctt gcc gac gcc atg aac gcc   96
Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala
             20                  25                  30

cac gtg gtc acc gtc aac gga cca gga cac ggc caa tcc atc ggc ggc   144
His Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly
         35                  40                  45

acc aac caa gca atc aac gac att gtt gtg gac tac ctc cgc acc gga   192
Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly
     50                  55                  60

cac acc gac gcc acc tgg gtc gaa ggc aac aca ccc acc cca att acg   240
His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr
 65                  70                  75                  80

gct ggc taattgcttt ccacttagta gat                                269
Ala Gly
```

<210> 146
<211> 82
<212> PRT
<213> Corynebacterium glutamicum

<400> 146

```
Ser Gln Leu Ala Val Gln Pro Leu Leu Leu Gln Gly Thr Ser Asp Pro
  1               5                  10                  15

Gln Thr Pro Tyr Trp Thr His Asn Glu Leu Ala Asp Ala Met Asn Ala
             20                  25                  30

His Val Val Thr Val Asn Gly Pro Gly His Gly Gln Ser Ile Gly Gly
         35                  40                  45

Thr Asn Gln Ala Ile Asn Asp Ile Val Val Asp Tyr Leu Arg Thr Gly
     50                  55                  60
```

```
His Thr Asp Ala Thr Trp Val Glu Gly Asn Thr Pro Thr Pro Ile Thr
 65                  70                  75                  80

Ala Gly
```

<210> 147
<211> 980
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(957)
<223> RXN01181

<400> 147

```
tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg   48
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
  1               5                  10                  15

tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac   96
Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
             20                  25                  30

ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt   144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
         35                  40                  45

ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt   192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
     50                  55                  60

ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct   240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65                  70                  75                  80

ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag   288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
                 85                  90                  95

cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca   336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
            100                 105                 110

tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc   384
Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
        115                 120                 125

aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac   432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
    130                 135                 140

gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc   480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
145                 150                 155                 160

gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc   528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
```

```
                165                 170                 175

att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca   576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
            180                 185                 190

acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt   624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
        195                 200                 205

gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc   672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
    210                 215                 220

gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat   720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
225                 230                 235                 240

gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc   768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
                245                 250                 255

cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt   816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
            260                 265                 270

ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac   864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
        275                 280                 285

aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa   912
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
    290                 295                 300

cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc        957
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
305                 310                 315

taaacgctag ttaaagatca gga                                         980
```

<210> 148
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 148

```
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
  1               5                  10                  15

Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
             20                  25                  30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
         35                  40                  45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
     50                  55                  60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65                  70                  75                  80
```

```
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
                 85                  90                  95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
            100                 105                 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
        115                 120                 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
    130                 135                 140

Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
145                 150                 155                 160

Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
                165                 170                 175

Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
            180                 185                 190

Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
        195                 200                 205

Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
    210                 215                 220

Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
225                 230                 235                 240

Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
                245                 250                 255

Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
            260                 265                 270

Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
        275                 280                 285

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
    290                 295                 300

Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
305                 310                 315
```

<210> 149
<211> 980
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(957)
<223> FRXA01181

<400> 149

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tct gta ctg ctc gct cgc gac ttg gtg aac acc cct tca tca cac ctg   48
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
  1               5                  10                  15
```

```
tac cca gag tcc tac tca gta att gca tcc aac gaa gcg tcc aag cac   96
Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
            20                  25                  30

ggc ttg cag acc acc atc ctg gat gag aag cag ctt gct gat caa ggt  144
Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
        35                  40                  45

ttc ggc ggc atc ctc gca gtc ggt aac ggc tcc tcc cgc aag cct cgt  192
Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
    50                  55                  60

ctg ctg cgc atc gat tgg aag cca cgc aag gct aag aag tcg atc gct  240
Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
65                  70                  75                  80

ttg gtt ggc aag ggc atc acc ttt gac acc ggc gga att tcc atc aag  288
Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
                85                  90                  95

cct ggc gca agc atg gag aac atg atc tcc gac atg ggt gga tcc gca  336
Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
            100                 105                 110

tcc gta ttg gcc acc att atc gct gca gct cgt ttg aac ctg tcg atc  384
Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
        115                 120                 125

aac gtc ttc gcg ttc cta cca atg gct gag aac atg cca tcc ggt gac  432
Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
    130                 135                 140

gct ttc cgc ccc ggc gat gtc atc act cat ttc ggt ggt atc acc tcc  480
Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
145                 150                 155                 160

gaa atc ttg aac acc gac gct gaa ggc cgc ctc att ctg gca gat gcc  528
Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
                165                 170                 175

att gct tac gct tct gaa gat aag cct gac tac ctc att gat gcg gca  576
Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
            180                 185                 190

acc ctg act ggt gct caa tta gtc gct tta ggc ctg cgg act tca ggt  624
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
        195                 200                 205

gtc atg ggt acc gat gag ttc cgc gac agc gtt gcc aag act ggc cgc  672
Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
    210                 215                 220

gag gtt ggc gag caa gca tgg gca atg cct ctt cct gaa gag ctc gat  720
Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
225                 230                 235                 240

gag cag gtt aag tcc cct gtc gct gac ctg cgc aat gtc acc aat tcc  768
Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
                245                 250                 255
```

Sequence Listing

```
cgt ttc gca gga atg tct gct gcg ggt cgt tac ttg cag gaa ttc gtt   816
Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
            260                 265                 270

ggt gcc gac atc gag tgg gct cac gtc gat atc gct ggc cct gca tac   864
Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
        275                 280                 285

aac act gct ggt gaa ttc ggt tac acg cca aag cgc gca acc gga caa   912
Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
    290                 295                 300

cca gtg cgc acc ttc gtt cag gtt ctg aag gat ctg tcg gaa agc       957
Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
305                 310                 315

taaacgctag ttaaagatca gga                                        980
```

<210> 150
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 150
Ser Val Leu Leu Ala Arg Asp Leu Val Asn Thr Pro Ser Ser His Leu
  1               5                  10                  15

Tyr Pro Glu Ser Tyr Ser Val Ile Ala Ser Asn Glu Ala Ser Lys His
             20                  25                  30

Gly Leu Gln Thr Thr Ile Leu Asp Glu Lys Gln Leu Ala Asp Gln Gly
         35                  40                  45

Phe Gly Gly Ile Leu Ala Val Gly Asn Gly Ser Ser Arg Lys Pro Arg
     50                  55                  60

Leu Leu Arg Ile Asp Trp Lys Pro Arg Lys Ala Lys Lys Ser Ile Ala
 65                  70                  75                  80

Leu Val Gly Lys Gly Ile Thr Phe Asp Thr Gly Gly Ile Ser Ile Lys
                 85                  90                  95

Pro Gly Ala Ser Met Glu Asn Met Ile Ser Asp Met Gly Gly Ser Ala
            100                 105                 110

Ser Val Leu Ala Thr Ile Ile Ala Ala Ala Arg Leu Asn Leu Ser Ile
        115                 120                 125

Asn Val Phe Ala Phe Leu Pro Met Ala Glu Asn Met Pro Ser Gly Asp
    130                 135                 140

Ala Phe Arg Pro Gly Asp Val Ile Thr His Phe Gly Gly Ile Thr Ser
145                 150                 155                 160

Glu Ile Leu Asn Thr Asp Ala Glu Gly Arg Leu Ile Leu Ala Asp Ala
                165                 170                 175

Ile Ala Tyr Ala Ser Glu Asp Lys Pro Asp Tyr Leu Ile Asp Ala Ala
            180                 185                 190
```

```
Thr Leu Thr Gly Ala Gln Leu Val Ala Leu Gly Leu Arg Thr Ser Gly
        195                 200                 205

Val Met Gly Thr Asp Glu Phe Arg Asp Ser Val Ala Lys Thr Gly Arg
    210                 215                 220

Glu Val Gly Glu Gln Ala Trp Ala Met Pro Leu Pro Glu Glu Leu Asp
225                 230                 235                 240

Glu Gln Val Lys Ser Pro Val Ala Asp Leu Arg Asn Val Thr Asn Ser
                245                 250                 255

Arg Phe Ala Gly Met Ser Ala Ala Gly Arg Tyr Leu Gln Glu Phe Val
            260                 265                 270

Gly Ala Asp Ile Glu Trp Ala His Val Asp Ile Ala Gly Pro Ala Tyr
        275                 280                 285

Asn Thr Ala Gly Glu Phe Gly Tyr Thr Pro Lys Arg Ala Thr Gly Gln
    290                 295                 300

Pro Val Arg Thr Phe Val Gln Val Leu Lys Asp Leu Ser Glu Ser
305                 310                 315


<210> 151
<211> 2724
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2701)
<223> RXN01014

<400> 151
tcttaaagtt ttctagcaat ccacactagg cgcgaactat cgtggtgtca ttgcgcacct 60

tctaagggta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat   115
                                              Leu Thr Ser Thr Asn
                                                1               5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa   163
Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
            10                  15                  20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt   211
Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
        25                  30                  35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt   259
Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
    40                  45                  50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg   307
Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
 55                  60                  65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag   355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
70                  75                  80                  85
```

```
acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg   403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
                 90                  95                 100

cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac   451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His
            105                 110                 115

cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt   499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe
        120                 125                 130

gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac   547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp
    135                 140                 145

ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag   595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys
150                 155                 160                 165

atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac   643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr
                170                 175                 180

gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att   691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile
            185                 190                 195

gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt   739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly
        200                 205                 210

acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg   787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu
    215                 220                 225

act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt   835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu
230                 235                 240                 245

gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac   883
Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr
                250                 255                 260

cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc   931
His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile
            265                 270                 275

ttc gtc cct gaa ttt aat gct ggc gcg atg gag aac gcc ggc gct gtc   979
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu Asn Ala Gly Ala Val
        280                 285                 290

acc atc cgc gat gag tac gtt ttt gca tcc aag gca acc cgt tac cgc   1027
Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys Ala Thr Arg Tyr Arg
    295                 300                 305

tac gag cgc cgc gct gaa acc atc ctt cac gag ctc gct cac atg tgg   1075
Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu Leu Ala His Met Trp
310                 315                 320                 325
```

```
ttc ggt gtg ctg gtg acc atg cag tgg tgg gat gat ctg tgg ctc aac   1123
Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp Asp Leu Trp Leu Asn
                330                 335                 340

gag tcc ttc gcc act tgg tcc gcg gca att tct cag gct gag gaa act   1171
Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser Gln Ala Glu Glu Thr
            345                 350                 355

gaa tac aac act gca tgg gtg act ttc gcc aat gtg gag aag tcg tgg   1219
Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn Val Glu Lys Ser Trp
        360                 365                 370

gcg tac cag cag gat cag ctg cct tcc acc cac ccg gtg ttc tct gac   1267
Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His Pro Val Phe Ser Asp
    375                 380                 385

gga tac gac att gag act gtc gac cag aac ttc gac ggc atc acc tac   1315
Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe Asp Gly Ile Thr Tyr
390                 395                 400                 405

gca aag ggc gcc tcg gtg ctc aag cag ctg cag gca tac gtt ggc cgt   1363
Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln Ala Tyr Val Gly Arg
                410                 415                 420

gag gaa ttc ctg gca ggc gta cgc agg cac ttt gcc aac cac gca tgg   1411
Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe Ala Asn His Ala Trp
            425                 430                 435

ggc aac gcc agc ttt gat gat ctg ctc ggc gcc ctc gag cag tcc tcc   1459
Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala Leu Glu Gln Ser Ser
        440                 445                 450

ggc cgc gac ctc tcc gac tgg gca aac cag tgg ctc aag acc acc ggc   1507
Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp Leu Lys Thr Thr Gly
    455                 460                 465

atc aac acc ctc ggc gca aag ttc acc acc gac aac ggc aaa tac acc   1555
Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp Asn Gly Lys Tyr Thr
470                 475                 480                 485

tcc ttc tcc gtc acc cag acc ggc gcc gcg ccg ggt gcc ggt gag ctg   1603
Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro Gly Ala Gly Glu Leu
                490                 495                 500

cgg act cac cgc atc gcg gtg ggt ctt tat aag ctt gtc gac gga tcc   1651
Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys Leu Val Asp Gly Ser
            505                 510                 515

ctc aac cgc tac gca cga gta gaa ctt gac tgc agt ggc gcg tcg aca   1699
Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys Ser Gly Ala Ser Thr
        520                 525                 530

agc gtt gaa gag atc gtt gga ctt gag cag gct gac ttc gtg ctg gtc   1747
Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala Asp Phe Val Leu Val
    535                 540                 545

aac gat gat gat ctg acg tat gcg ctg ctg gat ctg gat gat gat tca   1795
Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp Leu Asp Asp Asp Ser
550                 555                 560                 565

cgc aat ttt gtc atc gac aat att gat aag ttc agc gac cct atg cct   1843
```

```
Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe Ser Asp Pro Met Pro
                570                 575                 580

cgc acg ctg gtg tgg tcc gct gcg tgg gag atg act cgc gct ggt cag   1891
Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met Thr Arg Ala Gly Gln
            585                 590                 595

atg aag gct cgt gat ttc atc gcg ctg gtt gct cgt ggc gct gct gcg   1939
Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala Arg Gly Ala Ala Ala
        600                 605                 610

gaa act gaa att gct gtg ctg gag cgc att ctc gcg cag gct acc tct   1987
Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu Ala Gln Ala Thr Ser
    615                 620                 625

gcg ctg aag agc tac gcc gac cca gcg tgg gca gaa gca act gga aat   2035
Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala Glu Ala Thr Gly Asn
630                 635                 640                 645

gac ctg ctg gcc gat gct ttc ctt gag ggt gct cgc tcc gca gaa cca   2083
Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala Arg Ser Ala Glu Pro
                650                 655                 660

gac tcc gac act cag ttg gcg ttc att cag gct ctg gca aaa gca acg   2131
Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala Leu Ala Lys Ala Thr
            665                 670                 675

ctc aat gat gct gct gcc gat tac ttc cgc gac att ctt gcc ggc aac   2179
Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp Ile Leu Ala Gly Asn
        680                 685                 690

gtc gaa ggc ctg acc gtg gat cct gac ctg cgt tgg tgg gca ctg act   2227
Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg Trp Trp Ala Leu Thr
    695                 700                 705

gcg ctt atc gcc cgt ggt gac atc gag gct gtc gaa gat gca atc gcc   2275
Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val Glu Asp Ala Ile Ala
710                 715                 720                 725

gct gaa ctt tcc cgc gac aac tcc agt gcc tcc ttc ctc gca tca ctt   2323
Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser Phe Leu Ala Ser Leu
                730                 735                 740

cga gcc ggt gcc gct gtg aac act gaa gaa gtg aag gct gct gca tac   2371
Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val Lys Ala Ala Ala Tyr
            745                 750                 755

aag cat gtc acg gca gtt gat agt ggc cta tcc aac ctg gag ctg cgc   2419
Lys His Val Thr Ala Val Asp Ser Gly Leu Ser Asn Leu Glu Leu Arg
        760                 765                 770

cac aag att gaa ggc ctc aca ttc act ggc tct tct gaa ctg ctg caa   2467
His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser Ser Glu Leu Leu Gln
    775                 780                 785

gcc tac aac gag cag tac ttc gaa atc ctt gat gat gtg tgg gcg aac   2515
Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp Asp Val Trp Ala Asn
790                 795                 800                 805

ttc tcc ggc gaa atg gca cag cag atc gtc ctc gga ctg ttc cct tca   2563
Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu Gly Leu Phe Pro Ser
```

```
                  810                 815                 820

tgg aac gtt tcc gaa gag ggt ctc aag cgt acc gac gag ttt ctt gat   2611
Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr Asp Glu Phe Leu Asp
            825                 830                 835

ggc gaa cat gtc gca ggc atc aag cga att gtt tcc gaa tcc ctc gac   2659
Gly Glu His Val Ala Gly Ile Lys Arg Ile Val Ser Glu Ser Leu Asp
        840                 845                 850

cgc act gcc cgt gct ctg cgc aac cgt gcg gca gat gct gcg           2701
Arg Thr Ala Arg Ala Leu Arg Asn Arg Ala Ala Asp Ala Ala
    855                 860                 865

taagtaaaag attctcaatc cca                                        2724
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<210> 152
<211> 867
<212> PRT
<213> Corynebacterium glutamicum

<400> 152

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Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
  1               5                  10                  15

Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
             20                  25                  30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
         35                  40                  45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
     50                  55                  60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
 65                  70                  75                  80

Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
                 85                  90                  95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
            100                 105                 110

Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
        115                 120                 125

Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
    130                 135                 140

Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
145                 150                 155                 160

Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
                165                 170                 175

Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
            180                 185                 190

Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
        195                 200                 205
```

Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
210 215 220

Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
225 230 235 240

Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
245 250 255

Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
260 265 270

Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
275 280 285

Asn Ala Gly Ala Val Thr Ile Arg Asp Glu Tyr Val Phe Ala Ser Lys
290 295 300

Ala Thr Arg Tyr Arg Tyr Glu Arg Arg Ala Glu Thr Ile Leu His Glu
305 310 315 320

Leu Ala His Met Trp Phe Gly Val Leu Val Thr Met Gln Trp Trp Asp
325 330 335

Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile Ser
340 345 350

Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala Asn
355 360 365

Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr His
370 375 380

Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn Phe
385 390 395 400

Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu Gln
405 410 415

Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His Phe
420 425 430

Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly Ala
435 440 445

Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln Trp
450 455 460

Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr Asp
465 470 475 480

Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala Pro
485 490 495

Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr Lys
500 505 510

Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp Cys
515 520 525

```
Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln Ala
    530                 535                 540

Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu Asp
545                 550                 555                 560

Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys Phe
                565                 570                 575

Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu Met
            580                 585                 590

Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val Ala
        595                 600                 605

Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile Leu
    610                 615                 620

Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp Ala
625                 630                 635                 640

Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly Ala
                645                 650                 655

Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln Ala
            660                 665                 670

Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg Asp
        675                 680                 685

Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu Arg
    690                 695                 700

Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala Val
705                 710                 715                 720

Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala Ser
                725                 730                 735

Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu Val
            740                 745                 750

Lys Ala Ala Ala Tyr Lys His Val Thr Ala Val Asp Ser Gly Leu Ser
        755                 760                 765

Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly Ser
    770                 775                 780

Ser Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu Asp
785                 790                 795                 800

Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val Leu
                805                 810                 815

Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg Thr
            820                 825                 830

Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile Val
        835                 840                 845

Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn Arg Ala Ala
```

Replacement Page

```
    850                 855                 860

Asp Ala Ala
865
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<210> 153
<211> 1578
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1578)
<223> FRXA01014

<400> 153

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gat gat ctg tgg ctc aac gag tcc ttc gcc act tgg tcc gcg gca att   48
Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
  1               5                  10                  15

tct cag gct gag gaa act gaa tac aac act gca tgg gtg act ttc gcc   96
Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
             20                  25                  30

aat gtg gag aag tcg tgg gcg tac cag cag gat cag ctg cct tcc acc   144
Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
         35                  40                  45

cac ccg gtg ttc tct gac gga tac gac att gag act gtc gac cag aac   192
His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
     50                  55                  60

ttc gac ggc atc acc tac gca aag ggc gcc tcg gtg ctc aag cag ctg   240
Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65                  70                  75                  80

cag gca tac gtt ggc cgt gag gaa ttc ctg gca ggc gta cgc agg cac   288
Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
                 85                  90                  95

ttt gcc aac cac gca tgg ggc aac gcc agc ttt gat gat ctg ctc ggc   336
Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
            100                 105                 110

gcc ctc gag cag tcc tcc ggc cgc gac ctc tcc gac tgg gca aac cag   384
Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
        115                 120                 125

tgg ctc aag acc acc ggc atc aac acc ctc ggc gca aag ttc acc acc   432
Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
    130                 135                 140

gac aac ggc aaa tac acc tcc ttc tcc gtc acc cag acc ggc gcc gcg   480
Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
145                 150                 155                 160

ccg ggt gcc ggt gag ctg cgg act cac cgc atc gcg gtg ggt ctt tat   528
Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
                165                 170                 175
```

```
aag ctt gtc gac gga tcc ctc aac cgc tac gca cga gta gaa ctt gac   576
Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp
            180                 185                 190

tgc agt ggc gcg tcg aca agc gtt gaa gag atc gtt gga ctt gag cag   624
Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln
        195                 200                 205

gct gac ttc gtg ctg gtc aac gat gat gat ctg acg tat gcg ctg ctg   672
Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu
    210                 215                 220

gat ctg gat gat gat tca cgc aat ttt gtc atc gac aat att gat aag   720
Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys
225                 230                 235                 240

ttc agc gac cct atg cct cgc acg ctg gtg tgg tcc gct gcg tgg gag   768
Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu
                245                 250                 255

atg act cgc gct ggt cag atg aag gct cgt gat ttc atc gcg ctg gtt   816
Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val
            260                 265                 270

gct cgt ggc gct gct gcg gaa act gaa att gct gtg ctg gag cgc att   864
Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile
        275                 280                 285

ctc gcg cag gct acc tct gcg ctg aag agc tac gcc gac cca gcg tgg   912
Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp
    290                 295                 300

gca gaa gca act gga aat gac ctg ctg gcc gat gct ttc ctt gag ggt   960
Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly
305                 310                 315                 320

gct cgc tcc gca gaa cca gac tcc gac act cag ttg gcg ttc att cag   1008
Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln
                325                 330                 335

gct ctg gca aaa gca acg ctc aat gat gct gct gcc gat tac ttc cgc   1056
Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg
            340                 345                 350

gac att ctt gcc ggc aac gtc gaa ggc ctg acc gtg gat cct gac ctg   1104
Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu
        355                 360                 365

cgt tgg tgg gca ctg act gcg ctt atc gcc cgt ggt gac atc gag gct   1152
Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala
    370                 375                 380

gtc gaa gat gca atc gcc gct gaa ctt tcc cgc gac aac tcc agt gcc   1200
Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala
385                 390                 395                 400

tcc ttc ctc gca tca ctt cga gcc ggt gcc gct gtg aac act gaa gaa   1248
Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu
                405                 410                 415

gtg aag gct gct gca tac aag cat gtc ccg gca gtt gat agt ggc cta   1296
```

```
Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu
            420                 425                 430

tcc aac ctg gag ctg cgc cac aag att gaa ggc ctc aca ttc act ggc   1344
Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly
        435                 440                 445

tct ttt gaa ctg ctg caa gcc tac aac gag cag tac ttc gaa atc ctt   1392
Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
    450                 455                 460

gat gat gtg tgg gcg aac ttc tcc ggc gaa atg gca cag cag atc gtc   1440
Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val
465                 470                 475                 480

ctc gga ctg ttc cct tca tgg aac gtt tcc gaa gag ggt ctc aag cgt   1488
Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
                485                 490                 495

acc gac gag ttt ctt gat ggc gaa cat gtc gca ggc atc aag cga att   1536
Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
            500                 505                 510

gtt tcc gaa tcc ctc gac cgc act gcc cgt gct ctg cgc aac           1578
Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
        515                 520                 525
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<210> 154
<211> 526
<212> PRT
<213> Corynebacterium glutamicum

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<400> 154
Asp Asp Leu Trp Leu Asn Glu Ser Phe Ala Thr Trp Ser Ala Ala Ile
  1               5                  10                  15

Ser Gln Ala Glu Glu Thr Glu Tyr Asn Thr Ala Trp Val Thr Phe Ala
             20                  25                  30

Asn Val Glu Lys Ser Trp Ala Tyr Gln Gln Asp Gln Leu Pro Ser Thr
         35                  40                  45

His Pro Val Phe Ser Asp Gly Tyr Asp Ile Glu Thr Val Asp Gln Asn
     50                  55                  60

Phe Asp Gly Ile Thr Tyr Ala Lys Gly Ala Ser Val Leu Lys Gln Leu
 65                  70                  75                  80

Gln Ala Tyr Val Gly Arg Glu Glu Phe Leu Ala Gly Val Arg Arg His
                 85                  90                  95

Phe Ala Asn His Ala Trp Gly Asn Ala Ser Phe Asp Asp Leu Leu Gly
            100                 105                 110

Ala Leu Glu Gln Ser Ser Gly Arg Asp Leu Ser Asp Trp Ala Asn Gln
        115                 120                 125

Trp Leu Lys Thr Thr Gly Ile Asn Thr Leu Gly Ala Lys Phe Thr Thr
    130                 135                 140
```

Asp Asn Gly Lys Tyr Thr Ser Phe Ser Val Thr Gln Thr Gly Ala Ala
145 150 155 160

Pro Gly Ala Gly Glu Leu Arg Thr His Arg Ile Ala Val Gly Leu Tyr
165 170 175

Lys Leu Val Asp Gly Ser Leu Asn Arg Tyr Ala Arg Val Glu Leu Asp
180 185 190

Cys Ser Gly Ala Ser Thr Ser Val Glu Glu Ile Val Gly Leu Glu Gln
195 200 205

Ala Asp Phe Val Leu Val Asn Asp Asp Asp Leu Thr Tyr Ala Leu Leu
210 215 220

Asp Leu Asp Asp Asp Ser Arg Asn Phe Val Ile Asp Asn Ile Asp Lys
225 230 235 240

Phe Ser Asp Pro Met Pro Arg Thr Leu Val Trp Ser Ala Ala Trp Glu
245 250 255

Met Thr Arg Ala Gly Gln Met Lys Ala Arg Asp Phe Ile Ala Leu Val
260 265 270

Ala Arg Gly Ala Ala Ala Glu Thr Glu Ile Ala Val Leu Glu Arg Ile
275 280 285

Leu Ala Gln Ala Thr Ser Ala Leu Lys Ser Tyr Ala Asp Pro Ala Trp
290 295 300

Ala Glu Ala Thr Gly Asn Asp Leu Leu Ala Asp Ala Phe Leu Glu Gly
305 310 315 320

Ala Arg Ser Ala Glu Pro Asp Ser Asp Thr Gln Leu Ala Phe Ile Gln
325 330 335

Ala Leu Ala Lys Ala Thr Leu Asn Asp Ala Ala Ala Asp Tyr Phe Arg
340 345 350

Asp Ile Leu Ala Gly Asn Val Glu Gly Leu Thr Val Asp Pro Asp Leu
355 360 365

Arg Trp Trp Ala Leu Thr Ala Leu Ile Ala Arg Gly Asp Ile Glu Ala
370 375 380

Val Glu Asp Ala Ile Ala Ala Glu Leu Ser Arg Asp Asn Ser Ser Ala
385 390 395 400

Ser Phe Leu Ala Ser Leu Arg Ala Gly Ala Ala Val Asn Thr Glu Glu
405 410 415

Val Lys Ala Ala Ala Tyr Lys His Val Pro Ala Val Asp Ser Gly Leu
420 425 430

Ser Asn Leu Glu Leu Arg His Lys Ile Glu Gly Leu Thr Phe Thr Gly
435 440 445

Ser Phe Glu Leu Leu Gln Ala Tyr Asn Glu Gln Tyr Phe Glu Ile Leu
450 455 460

Asp Asp Val Trp Ala Asn Phe Ser Gly Glu Met Ala Gln Gln Ile Val

```
465                 470                 475                 480

Leu Gly Leu Phe Pro Ser Trp Asn Val Ser Glu Glu Gly Leu Lys Arg
                485                 490                 495

Thr Asp Glu Phe Leu Asp Gly Glu His Val Ala Gly Ile Lys Arg Ile
            500                 505                 510

Val Ser Glu Ser Leu Asp Arg Thr Ala Arg Ala Leu Arg Asn
        515                 520                 525


<210> 155
<211> 964
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(964)
<223> FRXA01018

<400> 155
tcttaaagtt ttctagcaat ccacactagg cgcgaactat cgtggtgtca ttgcgcacct 60

tctaagggta gcgccccctc aaatttcaag gagcattaaa ttg acg tcc act aat   115
                                              Leu Thr Ser Thr Asn
                                                1               5

ctc acc cga cag gaa gct tcg gat cgt tcg agg tta ctg agt gta gaa   163
Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg Leu Leu Ser Val Glu
                10                  15                  20

aac tat gac att gca ctt gat ctc aac aac ggt gat gag ttt ttt agt   211
Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly Asp Glu Phe Phe Ser
            25                  30                  35

tcc tcc acc gtt gtc agc ttc act gtc agg aag gct ggc gat acc ttt   259
Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys Ala Gly Asp Thr Phe
        40                  45                  50

att gat ctc cgc gca gca agc gtt gag gag gtt cgc ctg gac aat gtg   307
Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val Arg Leu Asp Asn Val
    55                  60                  65

tcc atc aaa gat gag gct cta acc ctt ggc aag aac ggc tac gac gag   355
Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys Asn Gly Tyr Asp Glu
70                  75                  80                  85

acg ttc ggc atc gcc ctg aag ggt ctt act ccc ggc gcg cac acc ttg   403
Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro Gly Ala His Thr Leu
                90                  95                  100

cgg gta acg gcg tct atc ccc tat tcc cgc acc ggt gaa ggc ctg cac   451
Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr Gly Glu Gly Leu His
            105                 110                 115

cgc atg gtg gat cca gca gac aat gag gtg tat ttg tac acc cag ttt   499
Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr Leu Tyr Thr Gln Phe
        120                 125                 130
```

```
gag acc gcc gat gcc aag cgt atg ttc gcg tgt ttc gat cag cca gac   547
Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys Phe Asp Gln Pro Asp
    135                 140                 145

ctc aag gct acc tat gat ctg aac atc aaa act cct aag ggt tgg aag   595
Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr Pro Lys Gly Trp Lys
150                 155                 160                 165

atc att tcc aac tct gag cag cag gtt tcc act cag cac act gat tac   643
Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr Gln His Thr Asp Tyr
                170                 175                 180

gat acc cac att tcc cga gtg gac tat ccc ctc tcc acc tac ctg att   691
Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu Ser Thr Tyr Leu Ile
            185                 190                 195

gcg gtg tgc gcg ggt cgt tac cac gag gtg tgc gat gtc tgg aag ggt   739
Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys Asp Val Trp Lys Gly
        200                 205                 210

acg ctc acc cac cat gca gaa aca cct gcc gat cag cca act gag ctg   787
Thr Leu Thr His His Ala Glu Thr Pro Ala Asp Gln Pro Thr Glu Leu
    215                 220                 225

act gtt ccg ctt gct ctc tac tgc cgc agt tct ttg gct aaa gat ctt   835
Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser Leu Ala Lys Asp Leu
230                 235                 240                 245

gat gcg gtg cgt ctg ttt acc gaa acg aag cag ggc ttt gat tgg tac   883
Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln Gly Phe Asp Trp Tyr
                250                 255                 260

cac cgc aac ttc ggt gtg gcg tac cca ttc ggc aag tac gat cag atc   931
His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly Lys Tyr Asp Gln Ile
            265                 270                 275

ttc gtc cct gaa ttt aat gct ggc gcg atg gag                      964
Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
        280                 285
```

Sequence Listing

<210> 156
<211> 288
<212> PRT
<213> Corynebacterium glutamicum

<400> 156

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Leu Thr Ser Thr Asn Leu Thr Arg Gln Glu Ala Ser Asp Arg Ser Arg
  1               5                  10                  15

Leu Leu Ser Val Glu Asn Tyr Asp Ile Ala Leu Asp Leu Asn Asn Gly
            20                  25                  30

Asp Glu Phe Phe Ser Ser Ser Thr Val Val Ser Phe Thr Val Arg Lys
        35                  40                  45

Ala Gly Asp Thr Phe Ile Asp Leu Arg Ala Ala Ser Val Glu Glu Val
    50                  55                  60

Arg Leu Asp Asn Val Ser Ile Lys Asp Glu Ala Leu Thr Leu Gly Lys
65                  70                  75                  80
```

```
Asn Gly Tyr Asp Glu Thr Phe Gly Ile Ala Leu Lys Gly Leu Thr Pro
                 85                  90                  95

Gly Ala His Thr Leu Arg Val Thr Ala Ser Ile Pro Tyr Ser Arg Thr
            100                 105                 110

Gly Glu Gly Leu His Arg Met Val Asp Pro Ala Asp Asn Glu Val Tyr
        115                 120                 125

Leu Tyr Thr Gln Phe Glu Thr Ala Asp Ala Lys Arg Met Phe Ala Cys
    130                 135                 140

Phe Asp Gln Pro Asp Leu Lys Ala Thr Tyr Asp Leu Asn Ile Lys Thr
145                 150                 155                 160

Pro Lys Gly Trp Lys Ile Ile Ser Asn Ser Glu Gln Gln Val Ser Thr
                165                 170                 175

Gln His Thr Asp Tyr Asp Thr His Ile Ser Arg Val Asp Tyr Pro Leu
            180                 185                 190

Ser Thr Tyr Leu Ile Ala Val Cys Ala Gly Arg Tyr His Glu Val Cys
        195                 200                 205

Asp Val Trp Lys Gly Thr Leu Thr His His Ala Glu Thr Pro Ala Asp
    210                 215                 220

Gln Pro Thr Glu Leu Thr Val Pro Leu Ala Leu Tyr Cys Arg Ser Ser
225                 230                 235                 240

Leu Ala Lys Asp Leu Asp Ala Val Arg Leu Phe Thr Glu Thr Lys Gln
                245                 250                 255

Gly Phe Asp Trp Tyr His Arg Asn Phe Gly Val Ala Tyr Pro Phe Gly
            260                 265                 270

Lys Tyr Asp Gln Ile Phe Val Pro Glu Phe Asn Ala Gly Ala Met Glu
        275                 280                 285
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<210> 157
<211> 1902
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1879)
<223> RXN01046

<400> 157
tagcgatcct aggcaaaatg caccagctaa ccccaccgct caaccgccat ctgcccccac 60

ctcacactca tcacagcagg gtctccctcc gggcgccatt atg atc cct ttt cca 115
                                                Met Ile Pro Phe Pro
                                                  1   5

```
ggg caa ccg cag cag caa agc gca ccc aat gac gag acc cgt ttc atc   163
Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp Glu Thr Arg Phe Ile
                 10                  15                  20

gac ctt aac gaa cgt cat aaa gat gat gaa cca gcc ctg ttt cgc gat   211
Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro Ala Leu Phe Arg Asp
             25                  30                  35

gat gtt att gat caa act ctc gct att ttg atc agt aaa aat aag ccc   259
Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile Ser Lys Asn Lys Pro
         40                  45                  50

aat gcg cta ctc gtt ggg cct gcc ggt aca ggt aaa tcc cgt atc gca   307
Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly Lys Ser Arg Ile Ala
     55                  60                  65

gaa gat att gcg cgc cgc ctt gcc aat gat gac gta tct att ccc gat   355
Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp Val Ser Ile Pro Asp
 70                  75                  80                  85

cag ctt gtc ggc cac cgt att ctt gat gtc tcc att gca gag ctt gtt   403
Gln Leu Val Gly His Arg Ile Leu Asp Val Ser Ile Ala Glu Leu Val
                 90                  95                 100

gct ggt gct ggc gtt gtt ggt cag ctc aag aaa cgc att ctg gat ctc   451
Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys Arg Ile Leu Asp Leu
             105                 110                 115

atc aag tat gcg acc gac ccg agt aac aaa gtc att atc ttt att gac   499
Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val Ile Ile Phe Ile Asp
         120                 125                 130

gag att cac caa att gct ggt gat cag tcc agt cac agt gga tcg caa   547
Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser His Ser Gly Ser Gln
     135                 140                 145

gcc aaa gtt gct cag att ctc aaa ccc tat ctt gcc cgt ggt gac ctt   595
Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu Ala Arg Gly Asp Leu
150                 155                 160                 165

cgt gtt att ggt gcc acc acc acc cag gaa gct cgt gac ttc gat cat   643
Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala Arg Asp Phe Asp His
                 170                 175                 180

gat cca gcc ctc aaa cgc cgt ttt agc aga gta aat gtc gat gaa ttt   691
Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val Asn Val Asp Glu Phe
             185                 190                 195

gat cga gat caa acg ctc act att ctt cat gct gca cgt gat ggt tac   739
Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala Ala Arg Asp Gly Tyr
         200                 205                 210

ctc aaa cat ttc aac aac gct gtc acg gta tct gac gac gta ctg ggc   787
Leu Lys His Phe Asn Asn Ala Val Thr Val Ser Asp Asp Val Leu Gly
     215                 220                 225

tat gtc tac acc tac tcg cag caa ttc aac cca ggc aat aca gca caa   835
Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro Gly Asn Thr Ala Gln
230                 235                 240                 245

cct gat gca gca ctg acg ctg ttt gat aag gcg ttg gct tcc cta act   883
```

```
Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala Leu Ala Ser Leu Thr
                250                 255                 260

atg gag aaa cag cgt ctg atc aac aac cat gtc att gcg ccg tcg ctc   931
Met Glu Lys Gln Arg Leu Ile Asn Asn His Val Ile Ala Pro Ser Leu
            265                 270                 275

aag ttc cct gtg tca gaa agg cac atc cat aac acc gct cgc aaa ctt   979
Lys Phe Pro Val Ser Glu Arg His Ile His Asn Thr Ala Arg Lys Leu
        280                 285                 290

gcc ttt ggc tct caa gtg cca gcc tcc atc aat act gat gat gct cgt   1027
Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn Thr Asp Asp Ala Arg
    295                 300                 305

gac aaa ctc gaa acg ttg ttt ggt caa gat cat att att gag cca gta   1075
Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His Ile Ile Glu Pro Val
310                 315                 320                 325

ctc acc gct atc aag cgt gaa cag ctt ggt att ttc cct cgc acc aaa   1123
Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile Phe Pro Arg Thr Lys
                330                 335                 340

cca ttg agc tgg gtg ttt gct ggt tca tct ggt gtg ggt aaa aca gaa   1171
Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly Val Gly Lys Thr Glu
            345                 350                 355

atg gcg cgt att ctc tct cgc gcc att aat ggc ggc gat ccc atc att   1219
Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly Gly Asp Pro Ile Ile
        360                 365                 370

atc aat ggt ccc gaa tac att agt cct gag tcc att act ggc ctt atc   1267
Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser Ile Thr Gly Leu Ile
    375                 380                 385

gga tca tcc gat ggc tat atc ggc tct aat tct aag cgt gct aaa cca   1315
Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser Lys Arg Ala Lys Pro
390                 395                 400                 405

ctc gac ccg ctg att tct aat ccg cgt cag gtg att gtg ctc gat gaa   1363
Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val Ile Val Leu Asp Glu
                410                 415                 420

ttt gag aag tct cac cct cat ttc cag caa ttg ttc atg gca gct ctt   1411
Phe Glu Lys Ser His Pro His Phe Gln Gln Leu Phe Met Ala Ala Leu
            425                 430                 435

gat aca ggc act atg gcg atg gct aat ggc acg aca ttg aat ttc tct   1459
Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr Thr Leu Asn Phe Ser
        440                 445                 450

cag gcc att atc att gcc acc acc aat gca gcc cgc gac aaa atc ggt   1507
Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala Arg Asp Lys Ile Gly
    455                 460                 465

cgt gac agc ttt gga ttc gat tca gat aat tca ggt gtc ctc ggt tct   1555
Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser Gly Val Leu Gly Ser
470                 475                 480                 485

gct caa gca gca act gat ccg cgt gca cag gaa cgc ctc aag tca ctg   1603
Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu Arg Leu Lys Ser Leu
```

Sequence Listing

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                490                 495                 500

atg tcc aag gat ttc ctg ttg aac tgc tca acc gtt tcc aga ata tct   1651
Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr Val Ser Arg Ile Ser
            505                 510                 515

ttg cct tca acc gca ttg atg cag gca cct acc gtg aga ttc tgg aca   1699
Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr Val Arg Phe Trp Thr
        520                 525                 530

atc tct acc agc gtc gcc gtg acg ccg tgc tgc tta gcc acc ccg cat   1747
Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys Leu Ala Thr Pro His
    535                 540                 545

tac gca gca cag atc cct gca gat att gat tca gac act ctt gat cag   1795
Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser Asp Thr Leu Asp Gln
550                 555                 560                 565

ctg gtg gaa acc acc ttt atc tca gat ttt ggt gca cgt cct gct gca   1843
Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly Ala Arg Pro Ala Ala
                570                 575                 580

cgc acc atc gaa gac cac atc gca tcc ttg ctg atg tgaccaacct        1889
Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu Met
            585                 590

tttaggagta cat                                                   1902


<210> 158
<211> 593
<212> PRT
<213> Corynebacterium glutamicum

<400> 158
Met Ile Pro Phe Pro Gly Gln Pro Gln Gln Gln Ser Ala Pro Asn Asp
  1               5                  10                  15

Glu Thr Arg Phe Ile Asp Leu Asn Glu Arg His Lys Asp Asp Glu Pro
             20                  25                  30

Ala Leu Phe Arg Asp Asp Val Ile Asp Gln Thr Leu Ala Ile Leu Ile
         35                  40                  45

Ser Lys Asn Lys Pro Asn Ala Leu Leu Val Gly Pro Ala Gly Thr Gly
     50                  55                  60

Lys Ser Arg Ile Ala Glu Asp Ile Ala Arg Arg Leu Ala Asn Asp Asp
 65                  70                  75                  80

Val Ser Ile Pro Asp Gln Leu Val Gly His Arg Ile Leu Asp Val Ser
                 85                  90                  95

Ile Ala Glu Leu Val Ala Gly Ala Gly Val Val Gly Gln Leu Lys Lys
            100                 105                 110

Arg Ile Leu Asp Leu Ile Lys Tyr Ala Thr Asp Pro Ser Asn Lys Val
        115                 120                 125

Ile Ile Phe Ile Asp Glu Ile His Gln Ile Ala Gly Asp Gln Ser Ser
    130                 135                 140
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His Ser Gly Ser Gln Ala Lys Val Ala Gln Ile Leu Lys Pro Tyr Leu
145                 150                 155                 160

Ala Arg Gly Asp Leu Arg Val Ile Gly Ala Thr Thr Thr Gln Glu Ala
                165                 170                 175

Arg Asp Phe Asp His Asp Pro Ala Leu Lys Arg Arg Phe Ser Arg Val
            180                 185                 190

Asn Val Asp Glu Phe Asp Arg Asp Gln Thr Leu Thr Ile Leu His Ala
        195                 200                 205

Ala Arg Asp Gly Tyr Leu Lys His Phe Asn Asn Ala Val Thr Val Ser
    210                 215                 220

Asp Asp Val Leu Gly Tyr Val Tyr Thr Tyr Ser Gln Gln Phe Asn Pro
225                 230                 235                 240

Gly Asn Thr Ala Gln Pro Asp Ala Ala Leu Thr Leu Phe Asp Lys Ala
                245                 250                 255

Leu Ala Ser Leu Thr Met Glu Lys Gln Arg Leu Ile Asn Asn His Val
            260                 265                 270

Ile Ala Pro Ser Leu Lys Phe Pro Val Ser Glu Arg His Ile His Asn
        275                 280                 285

Thr Ala Arg Lys Leu Ala Phe Gly Ser Gln Val Pro Ala Ser Ile Asn
    290                 295                 300

Thr Asp Asp Ala Arg Asp Lys Leu Glu Thr Leu Phe Gly Gln Asp His
305                 310                 315                 320

Ile Ile Glu Pro Val Leu Thr Ala Ile Lys Arg Glu Gln Leu Gly Ile
                325                 330                 335

Phe Pro Arg Thr Lys Pro Leu Ser Trp Val Phe Ala Gly Ser Ser Gly
            340                 345                 350

Val Gly Lys Thr Glu Met Ala Arg Ile Leu Ser Arg Ala Ile Asn Gly
        355                 360                 365

Gly Asp Pro Ile Ile Ile Asn Gly Pro Glu Tyr Ile Ser Pro Glu Ser
    370                 375                 380

Ile Thr Gly Leu Ile Gly Ser Ser Asp Gly Tyr Ile Gly Ser Asn Ser
385                 390                 395                 400

Lys Arg Ala Lys Pro Leu Asp Pro Leu Ile Ser Asn Pro Arg Gln Val
                405                 410                 415

Ile Val Leu Asp Glu Phe Glu Lys Ser His Pro His Phe Gln Gln Leu
            420                 425                 430

Phe Met Ala Ala Leu Asp Thr Gly Thr Met Ala Met Ala Asn Gly Thr
        435                 440                 445

Thr Leu Asn Phe Ser Gln Ala Ile Ile Ile Ala Thr Thr Asn Ala Ala
    450                 455                 460
```

```
Arg Asp Lys Ile Gly Arg Asp Ser Phe Gly Phe Asp Ser Asp Asn Ser
465                 470                 475                 480

Gly Val Leu Gly Ser Ala Gln Ala Ala Thr Asp Pro Arg Ala Gln Glu
                485                 490                 495

Arg Leu Lys Ser Leu Met Ser Lys Asp Phe Leu Leu Asn Cys Ser Thr
            500                 505                 510

Val Ser Arg Ile Ser Leu Pro Ser Thr Ala Leu Met Gln Ala Pro Thr
        515                 520                 525

Val Arg Phe Trp Thr Ile Ser Thr Ser Val Ala Val Thr Pro Cys Cys
    530                 535                 540

Leu Ala Thr Pro His Tyr Ala Ala Gln Ile Pro Ala Asp Ile Asp Ser
545                 550                 555                 560

Asp Thr Leu Asp Gln Leu Val Glu Thr Thr Phe Ile Ser Asp Phe Gly
                565                 570                 575

Ala Arg Pro Ala Ala Arg Thr Ile Glu Asp His Ile Ala Ser Leu Leu
            580                 585                 590

Met
```

<210> 159
<211> 1908
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1885)
<223> RXN01974

<400> 159

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acaatattta cggggataat ctgcattaac aaattagtta ataaagtgta gtatttaatt 60

aattattaaa ttcaattaac ttttttgtaa aggtgggaag atg acc cag gtt gtg   115
                                            Met Thr Gln Val Val
                                              1               5

gcg ggt acg ttg gtg gga gag tcg att aat cgt gag att gat gaa gac   163
Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg Glu Ile Asp Glu Asp
                  10                  15                  20

aag tac cct tat ttg agc tcg tat gca gcg cct gtt gct gta ccg gtg   211
Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro Val Ala Val Pro Val
              25                  30                  35

cgt gag att att ggg cgc gaa gaa gaa gtc aat aag att atg gcc gcg   259
Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn Lys Ile Met Ala Ala
          40                  45                  50

ctg atg cgt cca gag att tct aat gtc atg ctt gtg ggt cct gct ggt   307
Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu Val Gly Pro Ala Gly
      55                  60                  65
```

```
tcg ggt aaa act acg ttg gta cag caa gca ctg gtg aaa gat cca gag   355
Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu Val Lys Asp Pro Glu
 70                  75                  80                  85

cgt aac tac atc gag gtc gat gta gcg aaa atg gtt gcg gat ttg agc   403
Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met Val Ala Asp Leu Ser
                90                  95                 100

acc ccg gcg caa atg gct gcg cgt att aaa ggt gtg ttt gag gac gcc   451
Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly Val Phe Glu Asp Ala
            105                 110                 115

att gcc tat cgc aag cac gaa ggt cat gaa ttg gtg ctg ttc gtt gat   499
Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu Val Leu Phe Val Asp
        120                 125                 130

gag ttt cac caa att gtg cag ctg tct aat gct gcg gta gag gca atc   547
Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala Ala Val Glu Ala Ile
    135                 140                 145

aag ccg att ttg gcg atg tct ggt gtc ctt ggt gtg cgc gtt atc gct   595
Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly Val Arg Val Ile Ala
150                 155                 160                 165

gcg aca act ctc gaa gaa ttt cac gaa cac atc agg ccg aac caa gca   643
Ala Thr Thr Leu Glu Glu Phe His Glu His Ile Arg Pro Asn Gln Ala
                170                 175                 180

ttg acg gag cgt ttg cag gaa att cga cta acg ccg acc gat cag aag   691
Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr Pro Thr Asp Gln Lys
            185                 190                 195

acc act gtg gcg att ttg cgt ggt atg gca gat cgt tat ggc gta agt   739
Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp Arg Tyr Gly Val Ser
        200                 205                 210

gat cag ttc tat gac gac cac gtt ttt gag cag att tac tcc acc act   787
Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln Ile Tyr Ser Thr Thr
    215                 220                 225

gag cgt ttt atg ccg agt tct gtc cag cct cgt aaa tcc att cgt gtc   835
Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg Lys Ser Ile Arg Val
230                 235                 240                 245

ctt gat gcg atg gtt ggt tgg cat cga ctt tcc ggc aag ccg atg gat   883
Leu Asp Ala Met Val Gly Trp His Arg Leu Ser Gly Lys Pro Met Asp
                250                 255                 260

atg gat ctg ctc ggt gat gtg ctc cac gat gct att ggt gtc gat att   931
Met Asp Leu Leu Gly Asp Val Leu His Asp Ala Ile Gly Val Asp Ile
            265                 270                 275

gca ttc aag gtc gat ggt acg agc att aaa gac aag ctt gat gag aag   979
Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp Lys Leu Asp Glu Lys
        280                 285                 290

gta atg gcg caa agt ctt gcc acc act gtg gta gca cgt cgt ttg cag  1027
Val Met Ala Gln Ser Leu Ala Thr Thr Val Val Ala Arg Arg Leu Gln
    295                 300                 305

ctg gtg gtg gcg gat ctt cat gat aaa tca cgg cca ctg tcg aac ttc  1075
```

```
Leu Val Val Ala Asp Leu His Asp Lys Ser Arg Pro Leu Ser Asn Phe
310                 315                 320                 325

ttg ttc acc ggg cct act ggt gtc ggt aaa aca gag ctg gtc aag caa   1123
Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr Glu Leu Val Lys Gln
                330                 335                 340

cta gca cgg gtg ctc ttt ggt gat gac act ggg cga ttg att cgt ttt   1171
Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly Arg Leu Ile Arg Phe
            345                 350                 355

gac atg tca gag ttc gcc tta gaa tca agt ctt gac ctt ttc agg tct   1219
Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu Asp Leu Phe Arg Ser
        360                 365                 370

gag ctc act cgt cgt gtc gct gac cag ggt aac gct att gtc ctg ctc   1267
Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn Ala Ile Val Leu Leu
    375                 380                 385

gat gag gtt gag aaa gct gat cga gct att gcg cgg ttg tta ctg cag   1315
Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala Arg Leu Leu Leu Gln
390                 395                 400                 405

gta ctt gat gat ggc cga cta tct gac gat tac aac cgt gag gtg agt   1363
Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr Asn Arg Glu Val Ser
                410                 415                 420

ttt ctt aat acc tat atc gtc atg aca act aac gct ggt tct gag att   1411
Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn Ala Gly Ser Glu Ile
            425                 430                 435

ttc gag aca att tcg aac tat gcc act gat gac acg ggc gat ggt cgg   1459
Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp Thr Gly Asp Gly Arg
        440                 445                 450

gcg atc aaa gac ttt gtg aaa aac att cac acg tcg atc aag aat aag   1507
Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr Ser Ile Lys Asn Lys
    455                 460                 465

ggt ttt cca cct gag ctt ctt ggt cgt gta gat gaa att gtg cct ttt   1555
Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp Glu Ile Val Pro Phe
470                 475                 480                 485

caa ccg ctg tcg gag acg aca cag gac agg att att agc aag aag ctg   1603
Gln Pro Leu Ser Glu Thr Thr Gln Asp Arg Ile Ile Ser Lys Lys Leu
                490                 495                 500

cag gat gtg gct act gag gtc tat gaa cgc cac ggc gtg aaa ctg cac   1651
Gln Asp Val Ala Thr Glu Val Tyr Glu Arg His Gly Val Lys Leu His
            505                 510                 515

tgt tca caa aag gtt atg gag ttt ctg ctt gtg gat cag gtg gag gaa   1699
Cys Ser Gln Lys Val Met Glu Phe Leu Leu Val Asp Gln Val Glu Glu
        520                 525                 530

agt gct gaa tct ggt ggt gcc cgt ggt gcg gtg cgg tct ttg cag cgg   1747
Ser Ala Glu Ser Gly Gly Ala Arg Gly Ala Val Arg Ser Leu Gln Arg
    535                 540                 545

gaa gtg gtc act gaa gtg gcg acc ttt att aat acc tac cca gaa gtg   1795
Glu Val Val Thr Glu Val Ala Thr Phe Ile Asn Thr Tyr Pro Glu Val
```

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550                 555                 560                 565

cgt gac att tac gtt gat gtc gat ggt cag atg cgt aat aag act aac   1843
Arg Asp Ile Tyr Val Asp Val Asp Gly Gln Met Arg Asn Lys Thr Asn
                570                 575                 580

cgt gtg tct acg gcc cgt gtg gtg ata aag cgt gtc gaa ggt           1885
Arg Val Ser Thr Ala Arg Val Val Ile Lys Arg Val Glu Gly
            585                 590                 595

taattactct ggggtcgctt aaa                                        1908


<210> 160
<211> 595
<212> PRT
<213> Corynebacterium glutamicum

<400> 160
Met Thr Gln Val Val Ala Gly Thr Leu Val Gly Glu Ser Ile Asn Arg
  1               5                  10                  15

Glu Ile Asp Glu Asp Lys Tyr Pro Tyr Leu Ser Ser Tyr Ala Ala Pro
            20                  25                  30

Val Ala Val Pro Val Arg Glu Ile Ile Gly Arg Glu Glu Glu Val Asn
        35                  40                  45

Lys Ile Met Ala Ala Leu Met Arg Pro Glu Ile Ser Asn Val Met Leu
    50                  55                  60

Val Gly Pro Ala Gly Ser Gly Lys Thr Thr Leu Val Gln Gln Ala Leu
65                  70                  75                  80

Val Lys Asp Pro Glu Arg Asn Tyr Ile Glu Val Asp Val Ala Lys Met
                85                  90                  95

Val Ala Asp Leu Ser Thr Pro Ala Gln Met Ala Ala Arg Ile Lys Gly
            100                 105                 110

Val Phe Glu Asp Ala Ile Ala Tyr Arg Lys His Glu Gly His Glu Leu
        115                 120                 125

Val Leu Phe Val Asp Glu Phe His Gln Ile Val Gln Leu Ser Asn Ala
    130                 135                 140

Ala Val Glu Ala Ile Lys Pro Ile Leu Ala Met Ser Gly Val Leu Gly
145                 150                 155                 160

Val Arg Val Ile Ala Ala Thr Thr Leu Glu Glu Phe His Glu His Ile
                165                 170                 175

Arg Pro Asn Gln Ala Leu Thr Glu Arg Leu Gln Glu Ile Arg Leu Thr
            180                 185                 190

Pro Thr Asp Gln Lys Thr Thr Val Ala Ile Leu Arg Gly Met Ala Asp
        195                 200                 205

Arg Tyr Gly Val Ser Asp Gln Phe Tyr Asp Asp His Val Phe Glu Gln
    210                 215                 220
```

```
Ile Tyr Ser Thr Thr Glu Arg Phe Met Pro Ser Ser Val Gln Pro Arg
225                 230                 235                 240

Lys Ser Ile Arg Val Leu Asp Ala Met Val Gly Trp His Arg Leu Ser
                245                 250                 255

Gly Lys Pro Met Asp Met Asp Leu Leu Gly Asp Val Leu His Asp Ala
            260                 265                 270

Ile Gly Val Asp Ile Ala Phe Lys Val Asp Gly Thr Ser Ile Lys Asp
        275                 280                 285

Lys Leu Asp Glu Lys Val Met Ala Gln Ser Leu Ala Thr Thr Val Val
    290                 295                 300

Ala Arg Arg Leu Gln Leu Val Val Ala Asp Leu His Asp Lys Ser Arg
305                 310                 315                 320

Pro Leu Ser Asn Phe Leu Phe Thr Gly Pro Thr Gly Val Gly Lys Thr
                325                 330                 335

Glu Leu Val Lys Gln Leu Ala Arg Val Leu Phe Gly Asp Asp Thr Gly
            340                 345                 350

Arg Leu Ile Arg Phe Asp Met Ser Glu Phe Ala Leu Glu Ser Ser Leu
        355                 360                 365

Asp Leu Phe Arg Ser Glu Leu Thr Arg Arg Val Ala Asp Gln Gly Asn
    370                 375                 380

Ala Ile Val Leu Leu Asp Glu Val Glu Lys Ala Asp Arg Ala Ile Ala
385                 390                 395                 400

Arg Leu Leu Leu Gln Val Leu Asp Asp Gly Arg Leu Ser Asp Asp Tyr
                405                 410                 415

Asn Arg Glu Val Ser Phe Leu Asn Thr Tyr Ile Val Met Thr Thr Asn
            420                 425                 430

Ala Gly Ser Glu Ile Phe Glu Thr Ile Ser Asn Tyr Ala Thr Asp Asp
        435                 440                 445

Thr Gly Asp Gly Arg Ala Ile Lys Asp Phe Val Lys Asn Ile His Thr
    450                 455                 460

Ser Ile Lys Asn Lys Gly Phe Pro Pro Glu Leu Leu Gly Arg Val Asp
465                 470                 475                 480

Glu Ile Val Pro Phe Gln Pro Leu Ser Glu Thr Thr Gln Asp Arg Ile
                485                 490                 495

Ile Ser Lys Lys Leu Gln Asp Val Ala Thr Glu Val Tyr Glu Arg His
            500                 505                 510

Gly Val Lys Leu His Cys Ser Gln Lys Val Met Glu Phe Leu Leu Val
        515                 520                 525

Asp Gln Val Glu Glu Ser Ala Glu Ser Gly Gly Ala Arg Gly Ala Val
    530                 535                 540

Arg Ser Leu Gln Arg Glu Val Val Thr Glu Val Ala Thr Phe Ile Asn
```

```
545                 550                 555                 560

Thr Tyr Pro Glu Val Arg Asp Ile Tyr Val Asp Val Asp Gly Gln Met
                565                 570                 575

Arg Asn Lys Thr Asn Arg Val Ser Thr Ala Arg Val Val Ile Lys Arg
            580                 585                 590

Val Glu Gly
        595
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<210> 161
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> RXN01120

<400> 161

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acaggtaaag cgctaagatg gaacaaccca ttgccaatat tgttggttag agttgtacgc 60

agtaaatctt ttcaatcgtg gaagcgggtc tcacagtcta atg gca cgt atg cag   115
                                              Met Ala Arg Met Gln
                                                1               5

gaa agc gcc gat ctg ctc aaa tgt tcc ttc tgc gga aag agc caa aag   163
Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys Gly Lys Ser Gln Lys
                10                  15                  20

cag gta aaa aaa ctc atc gcg ggt ggc gcc gta tat atc tgt gat gag   211
Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val Tyr Ile Cys Asp Glu
            25                  30                  35

tgc att gag ctg tgc aac gag att att gaa gaa gaa ctc ggt caa gct   259
Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu Glu Leu Gly Gln Ala
        40                  45                  50

caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att   307
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile
    55                  60                  65

tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt   355
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg
70                  75                  80                  85

atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg   403
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser
                90                  95                  100

gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt   451
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val
            105                 110                 115

aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc   499
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe
        120                 125                 130
```

```
ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg   547
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala
    135                 140                 145

gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa   595
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu
150                 155                 160                 165

aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt   643
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg
                170                 175                 180

gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc   691
Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg
            185                 190                 195

aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg   739
Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val
        200                 205                 210

cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca   787
Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro
    215                 220                 225

ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat   835
Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp
230                 235                 240                 245

acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag   883
Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu
                250                 255                 260

aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg   931
Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val
            265                 270                 275

gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag   979
Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys
        280                 285                 290

gat gtc ctc cct gag gac ctg gtg aag ttt ggt ctc atc cca gaa ttc   1027
Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe
    295                 300                 305

att ggg cgt ctg cca gtc gtt gcc acc gta tcc aac ctg gat cag aaa   1075
Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys
310                 315                 320                 325

tct ctg gtc aag gtt ctc acg gag cct cgt aac tca ttg gtg aag cag   1123
Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln
                330                 335                 340

tat cga cgt ctg ttt gaa atg gat gac gct gtg ttg acc ttt act gat   1171
Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp
            345                 350                 355

gat gct ttg gag gag atc gct aat cag gca ctc gag cgc aaa act ggc   1219
Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly
        360                 365                 370

gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg   1267
```

```
Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile Leu Val Pro Ile Met
    375                 380                 385

tat gac ctc cca gac cgt aaa gac gtt ggc gaa gtc atc atc aac ggt   1315
Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly
390                 395                 400                 405

gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca   1363
Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met Leu Glu Ala Val Ala
                410                 415                 420

gaa gaa aag acc gcg tagttggcag gagttatcac cgg                    1401
Glu Glu Lys Thr Ala
            425


<210> 162
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 162
Met Ala Arg Met Gln Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys
  1               5                  10                  15

Gly Lys Ser Gln Lys Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val
            20                  25                  30

Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
        35                  40                  45

Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
    50                  55                  60

Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
65                  70                  75                  80

Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
                85                  90                  95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
            100                 105                 110

Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
        115                 120                 125

Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
    130                 135                 140

Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
145                 150                 155                 160

Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
                165                 170                 175

Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
            180                 185                 190

Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
        195                 200                 205
```

Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
210 215 220

Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
225 230 235 240

Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
245 250 255

Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
260 265 270

Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile
275 280 285

Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly
290 295 300

Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser
305 310 315 320

Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn
325 330 335

Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val
340 345 350

Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
355 360 365

Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
370 375 380

Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
385 390 395 400

Val Ile Ile Asn Gly Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met
405 410 415

Leu Glu Ala Val Ala Glu Glu Lys Thr Ala
420 425

<210> 163
<211> 1401
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1378)
<223> FRXA01120

<400> 163
acaggtaaag cgctaagatg gaacaaccca ttgccaatat tgttggttag agttgtacgc 60

agtaaatctt ttcaatcgtg gaagcgggtc tcacagtcta atg gca cgt atg cag 115
Met Ala Arg Met Gln
1 5

gaa agc gcc gat ctg ctc aaa tgt tcc ttc tgc gga aag agc caa aag 163

```
Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys Gly Lys Ser Gln Lys
                 10                  15                  20

cag gta aaa aaa ctc atc gcg ggt ggc gcc gta tat atc tgt gat gag   211
Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val Tyr Ile Cys Asp Glu
            25                  30                  35

tgc att gag ctg tgc aac gag att att gaa gaa gaa ctc ggt caa gct   259
Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu Glu Leu Gly Gln Ala
        40                  45                  50

caa cac gac gag cag gag cgc aac gag ctc ccc aag ccg tcg gag att   307
Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro Lys Pro Ser Glu Ile
    55                  60                  65

tca gcc ttc ctt gat act tat gtc atc ggg cag gac cca gca aaa cgt   355
Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln Asp Pro Ala Lys Arg
70                  75                  80                  85

atc ctg tcg gtt gcg gtg tac aac cat tac aag cgt ctc cgc gca tcg   403
Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys Arg Leu Arg Ala Ser
                90                  95                 100

gaa acc atc ggt cgt cgc agg aat gac gag cct gaa acc gaa ctg gtt   451
Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro Glu Thr Glu Leu Val
            105                 110                 115

aag tcc aat att ttg atg ctc ggc ccc act ggc tcc ggc aag act ttc   499
Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly Ser Gly Lys Thr Phe
        120                 125                 130

ctt gcc cag act ttg gca aag ctg ctg gat gtt cct ttt gct atc gcg   547
Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val Pro Phe Ala Ile Ala
    135                 140                 145

gat gcc acc tca ctg acc gag gct ggt tat gtg ggc gag gat gtg gaa   595
Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val Gly Glu Asp Val Glu
150                 155                 160                 165

aac atc ttg ctc aag ctg ctt cag gct gct gat ttt gat gtg gaa cgt   643
Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp Phe Asp Val Glu Arg
                170                 175                 180

gca cag cgc ggc atc att tac atc gat gaa gtg gac aag att tcc cgc   691
Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val Asp Lys Ile Ser Arg
            185                 190                 195

aag tct gaa aac cca tcg atc act cgc gat gtt tcc ggt gaa ggc gtg   739
Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val Ser Gly Glu Gly Val
        200                 205                 210

cag cag gca ctg ctg aaa att ttg gaa ggc act gtc gcc gca atc cca   787
Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr Val Ala Ala Ile Pro
    215                 220                 225

ccg cag gga gga cgc aag cac ccc aac cag gat ttc atc cag ctg gat   835
Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp Phe Ile Gln Leu Asp
230                 235                 240                 245

acc acc aac att ttg ttc atc gtt gct ggt gcg ttc tct ggt ctg gag   883
Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala Phe Ser Gly Leu Glu
```

```
                250                 255                 260

aag gtc atc gcg gac cgc aat ggc aag aaa ggc ttg ggc ttc ggt gtg   931
Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly Leu Gly Phe Gly Val
            265                 270                 275

gag gtc tct tcc aag aag gaa gaa gcc aac att gtg gat atc ttc aag   979
Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile Val Asp Ile Phe Lys
        280                 285                 290

gat gtc ctc cct gag gac ctg gtg aag ttt ggt ctc atc cca gaa ttc   1027
Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly Leu Ile Pro Glu Phe
    295                 300                 305

att ggg cgt ctg cca gtc gtt gcc acc gta tcc aac ctg gat cag aaa   1075
Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser Asn Leu Asp Gln Lys
310                 315                 320                 325

tct ctg gtc aag gtt ctc acg gag cct cgt aac tca ttg gtg aag cag   1123
Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn Ser Leu Val Lys Gln
                330                 335                 340

tat cga cgt ctg ttt gaa atg gat gac gct gtg ttg acc ttt act gat   1171
Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val Leu Thr Phe Thr Asp
            345                 350                 355

gat gct ttg gag gag atc gct aat cag gca ctc gag cgc aaa act ggc   1219
Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu Glu Arg Lys Thr Gly
        360                 365                 370

gcc cgt ggc ctg cgc gcg atc atg gaa gag atc ctg gtt ccg atc atg   1267
Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile Leu Val Pro Ile Met
    375                 380                 385

tat gac ctc cca gac cgt aaa gac gtt ggc gaa gtc atc atc aac ggt   1315
Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu Val Ile Ile Asn Gly
390                 395                 400                 405

gcc gtt gcc cgt ggc gaa gcc gaa cca gag atg ttg gaa gct gtc gca   1363
Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met Leu Glu Ala Val Ala
                410                 415                 420

gaa gaa aag acc gcg tagttggcag gagttatcac cgg                    1401
Glu Glu Lys Thr Ala
            425
```

<210> 164
<211> 426
<212> PRT
<213> Corynebacterium glutamicum

<400> 164

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Met Ala Arg Met Gln Glu Ser Ala Asp Leu Leu Lys Cys Ser Phe Cys
  1               5                  10                  15

Gly Lys Ser Gln Lys Gln Val Lys Lys Leu Ile Ala Gly Gly Ala Val
             20                  25                  30

Tyr Ile Cys Asp Glu Cys Ile Glu Leu Cys Asn Glu Ile Ile Glu Glu
         35                  40                  45
```

Glu Leu Gly Gln Ala Gln His Asp Glu Gln Glu Arg Asn Glu Leu Pro
50 55 60

Lys Pro Ser Glu Ile Ser Ala Phe Leu Asp Thr Tyr Val Ile Gly Gln
65 70 75 80

Asp Pro Ala Lys Arg Ile Leu Ser Val Ala Val Tyr Asn His Tyr Lys
85 90 95

Arg Leu Arg Ala Ser Glu Thr Ile Gly Arg Arg Arg Asn Asp Glu Pro
100 105 110

Glu Thr Glu Leu Val Lys Ser Asn Ile Leu Met Leu Gly Pro Thr Gly
115 120 125

Ser Gly Lys Thr Phe Leu Ala Gln Thr Leu Ala Lys Leu Leu Asp Val
130 135 140

Pro Phe Ala Ile Ala Asp Ala Thr Ser Leu Thr Glu Ala Gly Tyr Val
145 150 155 160

Gly Glu Asp Val Glu Asn Ile Leu Leu Lys Leu Leu Gln Ala Ala Asp
165 170 175

Phe Asp Val Glu Arg Ala Gln Arg Gly Ile Ile Tyr Ile Asp Glu Val
180 185 190

Asp Lys Ile Ser Arg Lys Ser Glu Asn Pro Ser Ile Thr Arg Asp Val
195 200 205

Ser Gly Glu Gly Val Gln Gln Ala Leu Leu Lys Ile Leu Glu Gly Thr
210 215 220

Val Ala Ala Ile Pro Pro Gln Gly Gly Arg Lys His Pro Asn Gln Asp
225 230 235 240

Phe Ile Gln Leu Asp Thr Thr Asn Ile Leu Phe Ile Val Ala Gly Ala
245 250 255

Phe Ser Gly Leu Glu Lys Val Ile Ala Asp Arg Asn Gly Lys Lys Gly
260 265 270

Leu Gly Phe Gly Val Glu Val Ser Ser Lys Lys Glu Glu Ala Asn Ile
275 280 285

Val Asp Ile Phe Lys Asp Val Leu Pro Glu Asp Leu Val Lys Phe Gly
290 295 300

Leu Ile Pro Glu Phe Ile Gly Arg Leu Pro Val Val Ala Thr Val Ser
305 310 315 320

Asn Leu Asp Gln Lys Ser Leu Val Lys Val Leu Thr Glu Pro Arg Asn
325 330 335

Ser Leu Val Lys Gln Tyr Arg Arg Leu Phe Glu Met Asp Asp Ala Val
340 345 350

Leu Thr Phe Thr Asp Asp Ala Leu Glu Glu Ile Ala Asn Gln Ala Leu
355 360 365

```
Glu Arg Lys Thr Gly Ala Arg Gly Leu Arg Ala Ile Met Glu Glu Ile
    370                 375                 380

Leu Val Pro Ile Met Tyr Asp Leu Pro Asp Arg Lys Asp Val Gly Glu
385                 390                 395                 400

Val Ile Ile Asn Gly Ala Val Ala Arg Gly Glu Ala Glu Pro Glu Met
                405                 410                 415

Leu Glu Ala Val Ala Glu Glu Lys Thr Ala
            420                 425
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<210> 165
<211> 924
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(901)
<223> RXN00397

<400> 165

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tttttcgagg ttggggtggc ttttcgggtg gcgtgtatgt attaaaccaa ggagcttgtt 60

tgaggggggag cgcttggttt gattcgacag ttttcgggca ttg agc ctg acg gaa   115
                                              Leu Ser Leu Thr Glu
                                                1               5

ggg gag atc att ccc atc caa aca aag ctc ggc cac tgg cgt gac gtg   163
Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly His Trp Arg Asp Val
                10                  15                  20

cgg gat tcc gaa gat ctg cca ttc caa gta atc gca tcg cgc acc aac   211
Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile Ala Ser Arg Thr Asn
            25                  30                  35

gtg acc att atg gaa aac acc ctg gaa tgg acc aac agc cgc ctt gag   259
Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr Asn Ser Arg Leu Glu
        40                  45                  50

cgt ggc gaa gag ttc acc gag ctc gac att tat gct cac tac ttg gaa   307
Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr Ala His Tyr Leu Glu
    55                  60                  65

gag ttg gaa gat tac gcc ctc caa ttc acc ttc gat gtc gag ccc tac   355
Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe Asp Val Glu Pro Tyr
70                  75                  80                  85

ttc acc aac ctg cac tcc tcc aac aga atg ctc ttc cct gga cct cct   403
Phe Thr Asn Leu His Ser Ser Asn Arg Met Leu Phe Pro Gly Pro Pro
                90                  95                  100

gtg gat ttc ccg atc aac gca gaa acc cga tgc att cag ctc gac gcc   451
Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys Ile Gln Leu Asp Ala
            105                 110                 115

ggt gtt gca gta aag aag gac ggc gtg gtg ctg ggt acc tca gat atg   499
Gly Val Ala Val Lys Lys Asp Gly Val Val Leu Gly Thr Ser Asp Met
        120                 125                 130
```

```
gcg agg tcc ctg cct cga acc gcc gct ggc caa gaa gcc tat gag tac   547
Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln Glu Ala Tyr Glu Tyr
    135                 140                 145

ttc ttc aag gtg gtt cgt gaa ggc atc atc ggg cag ctg cgc ccg ggc   595
Phe Phe Lys Val Val Arg Glu Gly Ile Ile Gly Gln Leu Arg Pro Gly
150                 155                 160                 165

gtg atc tgc gct gac gtg cac gaa gca acc ctt gat tac cta agc ccg   643
Val Ile Cys Ala Asp Val His Glu Ala Thr Leu Asp Tyr Leu Ser Pro
                170                 175                 180

cag cta cct cgc atg att gac atc gga atg ctg ggt gcc gac acc gat   691
Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu Gly Ala Asp Thr Asp
            185                 190                 195

ttc aac acc atc tac cgc aag cgc aat gtt ggc cac ctc atg ggc aag   739
Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly His Leu Met Gly Lys
        200                 205                 210

cag gaa tcc ttt gcc aat gag ctt cgc cct gga tac aag cac att ctt   787
Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly Tyr Lys His Ile Leu
    215                 220                 225

cac cac ggc tcc tat ggt gcc gcg gag atc cct tgg cgc tac aac ggt   835
His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro Trp Arg Tyr Asn Gly
230                 235                 240                 245

gta gcc att ggt acc gag gat ctg tgg tac atc ggc gca gac aag acc   883
Val Ala Ile Gly Thr Glu Asp Leu Trp Tyr Ile Gly Ala Asp Lys Thr
                250                 255                 260

tac att ttg agc cag cgc taaggagaac ccagtgacag aaa                 924
Tyr Ile Leu Ser Gln Arg
            265
```

<210> 166
<211> 267
<212> PRT
<213> Corynebacterium glutamicum

<400> 166

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Leu Ser Leu Thr Glu Gly Glu Ile Ile Pro Ile Gln Thr Lys Leu Gly
  1               5                  10                  15

His Trp Arg Asp Val Arg Asp Ser Glu Asp Leu Pro Phe Gln Val Ile
             20                  25                  30

Ala Ser Arg Thr Asn Val Thr Ile Met Glu Asn Thr Leu Glu Trp Thr
         35                  40                  45

Asn Ser Arg Leu Glu Arg Gly Glu Glu Phe Thr Glu Leu Asp Ile Tyr
     50                  55                  60

Ala His Tyr Leu Glu Glu Leu Glu Asp Tyr Ala Leu Gln Phe Thr Phe
 65                  70                  75                  80

Asp Val Glu Pro Tyr Phe Thr Asn Leu His Ser Ser Asn Arg Met Leu
                 85                  90                  95
```

```
Phe Pro Gly Pro Pro Val Asp Phe Pro Ile Asn Ala Glu Thr Arg Cys
            100                 105                 110

Ile Gln Leu Asp Ala Gly Val Ala Val Lys Lys Asp Gly Val Val Leu
        115                 120                 125

Gly Thr Ser Asp Met Ala Arg Ser Leu Pro Arg Thr Ala Ala Gly Gln
    130                 135                 140

Glu Ala Tyr Glu Tyr Phe Phe Lys Val Val Arg Glu Gly Ile Ile Gly
145                 150                 155                 160

Gln Leu Arg Pro Gly Val Ile Cys Ala Asp Val His Glu Ala Thr Leu
                165                 170                 175

Asp Tyr Leu Ser Pro Gln Leu Pro Arg Met Ile Asp Ile Gly Met Leu
            180                 185                 190

Gly Ala Asp Thr Asp Phe Asn Thr Ile Tyr Arg Lys Arg Asn Val Gly
        195                 200                 205

His Leu Met Gly Lys Gln Glu Ser Phe Ala Asn Glu Leu Arg Pro Gly
    210                 215                 220

Tyr Lys His Ile Leu His His Gly Ser Tyr Gly Ala Ala Glu Ile Pro
225                 230                 235                 240

Trp Arg Tyr Asn Gly Val Ala Ile Gly Thr Glu Asp Leu Trp Tyr Ile
                245                 250                 255

Gly Ala Asp Lys Thr Tyr Ile Leu Ser Gln Arg
            260                 265
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<210> 167
<211> 2049
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2026)
<223> RXN01868

<400> 167

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tgacaggcta ccttctgggg tggacatgat ccccaacgct caacccactt gtggcaccaa 60

ccacaaaccc tgtggcggta aatcccctag agtaggccac atg aag gat ctt tat   115
                                              Met Lys Asp Leu Tyr
                                                1               5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat   163
Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
                  10                  15                  20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa   211
Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
              25                  30                  35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt   259
```

```
Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
         40                  45                  50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca   307
Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
     55                  60                  65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt   355
Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
 70                  75                  80                  85

ttc gca gct gct ctc ggc gaa ctg gac cgt gaa ggc gtt ggc gcg cca   403
Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu Gly Val Gly Ala Pro
                 90                  95                 100

gta ggt ttc tgg gtg gag aag gat tct tcc tcc aac gaa tcc gtc gcc   451
Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser Asn Glu Ser Val Ala
            105                 110                 115

tat gtc atc cag tcc ggc ctc ggc ctg ccc gat gag gct tat tac cgc   499
Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp Glu Ala Tyr Tyr Arg
        120                 125                 130

gag gag gca cac gcc gaa act ctc gcg gcc tac aaa gag cac gtt gag   547
Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr Lys Glu His Val Glu
    135                 140                 145

cgc atg ctc ggc tac ttg gat aac agc cgc ctc ttc ggt ctg tcg gct   595
Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu Phe Gly Leu Ser Ala
150                 155                 160                 165

gct tcc gct gcc gca cga att gtc gcc ctg gaa acg gaa atc gct gct   643
Ala Ser Ala Ala Ala Arg Ile Val Ala Leu Glu Thr Glu Ile Ala Ala
                170                 175                 180

ggc cac tgg gat gtc gtg aag acc cgc gac gcc gta gcc acc tac aac   691
Gly His Trp Asp Val Val Lys Thr Arg Asp Ala Val Ala Thr Tyr Asn
            185                 190                 195

ccc acc gaa ctc ggc gcg ctg cca cca aag gtc cgc acg ctg ctc agt   739
Pro Thr Glu Leu Gly Ala Leu Pro Pro Lys Val Arg Thr Leu Leu Ser
        200                 205                 210

tcc gca ggc ctc ccg gac cag cgc ctg gta tcg atg atg ccg tca tac   787
Ser Ala Gly Leu Pro Asp Gln Arg Leu Val Ser Met Met Pro Ser Tyr
    215                 220                 225

ctc gac cac ctc aac ggc ttg ctt gtc gac gac cgc ctc ccc gat tgg   835
Leu Asp His Leu Asn Gly Leu Leu Val Asp Asp Arg Leu Pro Asp Trp
230                 235                 240                 245

cag cta tgg gca acc tgg cac atc ttg agg tct cga gca gga ctg ttg   883
Gln Leu Trp Ala Thr Trp His Ile Leu Arg Ser Arg Ala Gly Leu Leu
                250                 255                 260

acc gag gaa att agc caa gca aac ttc gac ttc tat ggc acc aaa ctg   931
Thr Glu Glu Ile Ser Gln Ala Asn Phe Asp Phe Tyr Gly Thr Lys Leu
            265                 270                 275

tcc ggc gcc acc gag caa aaa gat cga tgg aag cgt gct gtc ggc ctg   979
Ser Gly Ala Thr Glu Gln Lys Asp Arg Trp Lys Arg Ala Val Gly Leu
```

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        280                 285                 290

gca gag cgc atg gtg ggc gag gaa atc ggg caa cga ttc gtc gaa agg   1027
Ala Glu Arg Met Val Gly Glu Glu Ile Gly Gln Arg Phe Val Glu Arg
    295                 300                 305

cat ttt cct gca agc tcc aag gag cac atg ctt gag ctc gtc gac tac   1075
His Phe Pro Ala Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr
310                 315                 320                 325

ctg gtt gcc gcc tac cgt gat cgc att tcc aac ctc gaa tgg atg acg   1123
Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr
                330                 335                 340

ccc gcc acc cgc gag cgt gcc ctg gaa aag ttg ggc aaa ttc aac gcg   1171
Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala
            345                 350                 355

aaa atc ggc tac ccc gac aag tgg cgc tcc tac gaa ggc ctc gaa ttc   1219
Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe
        360                 365                 370

ggc tcc gac ctg gtg gac aac tcc cgc aag ggc tcc gcg ttc ctc cat   1267
Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His
    375                 380                 385

gac tat gag ctg ggc aag atc ggc aaa cca gcc gac cgc gac gaa tgg   1315
Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp
390                 395                 400                 405

gtc acc acc cca caa acc gtc aac gcc ttc tac aac ccc gtg gtc aac   1363
Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn
                410                 415                 420

gac atc acc ttc ccc gca gcc atc ctg cgc gca cca ttc ttc gac ccc   1411
Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro
            425                 430                 435

gaa gca gaa gcc gca gaa aac ttc ggt gca atc ggt gct gtg atc gga   1459
Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly
        440                 445                 450

cac gaa atc ggc cac ggc ttt gac gat caa ggc agc caa tac gac ggc   1507
His Glu Ile Gly His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly
    455                 460                 465

gac ggc aac ctc aac tcc tgg tgg acc gac gaa gac cgc tcc gca ttc   1555
Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe
470                 475                 480                 485

gag cag ctc acc tca cgt ctg gtc acc caa ttc agc gga ctc gtc cct   1603
Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro
                490                 495                 500

gcc gtc ctg acc tct gaa gga atc gac acc gac ggc gtc aac ggt gaa   1651
Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu
            505                 510                 515

ttc act ctc ggc gaa aac atc ggt gac ctc ggc gga ttg ggc atc gct   1699
Phe Thr Leu Gly Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala
        520                 525                 530
```

```
gtc gtt gcc tac gaa aag tac ctc gca gac cgt ggc caa acc ttt gaa   1747
Val Val Ala Tyr Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu
    535                 540                 545

acc tca cca gtc caa aaa ttc gaa gca gaa ggc gcc gag gaa ggc ctg   1795
Thr Ser Pro Val Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu
550                 555                 560                 565

gcc gag caa gaa ttc aac ggt ctc caa cgc ctc ttc ctg tcc tgg gct   1843
Ala Glu Gln Glu Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala
                570                 575                 580

cgc gtg tgg cgc acc aaa atc cgc cca cag atg gcc gtc caa tac ctg   1891
Arg Val Trp Arg Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu
            585                 590                 595

gcc atc gac cca cac tcc cct gca gaa ttc cgc tgc aat gtc atc gcc   1939
Ala Ile Asp Pro His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala
        600                 605                 610

gga aac gtc gct gaa ttc tac gaa gca ttc gac gtc ccc gaa gat gca   1987
Gly Asn Val Ala Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala
    615                 620                 625

cct gtg tac atc aag cca gaa gag cgc cta gct atc tgg tagttgttag   2036
Pro Val Tyr Ile Lys Pro Glu Glu Arg Leu Ala Ile Trp
630                 635                 640

ttggtattga aaa                                                  2049
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<210> 168
<211> 642
<212> PRT
<213> Corynebacterium glutamicum

<400> 168

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Met Lys Asp Leu Tyr Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His
  1               5                  10                  15

Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
             20                  25                  30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
         35                  40                  45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
     50                  55                  60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val
 65                  70                  75                  80

Ala Asn Ser Ser Phe Phe Ala Ala Ala Leu Gly Glu Leu Asp Arg Glu
                 85                  90                  95

Gly Val Gly Ala Pro Val Gly Phe Trp Val Glu Lys Asp Ser Ser Ser
            100                 105                 110

Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu Pro Asp
        115                 120                 125
```

Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala Ala Tyr
130 135 140

Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser Arg Leu
145 150 155 160

Phe Gly Leu Ser Ala Ala Ser Ala Ala Ala Arg Ile Val Ala Leu Glu
165 170 175

Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg Asp Ala
180 185 190

Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro Lys Val
195 200 205

Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu Val Ser
210 215 220

Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val Asp Asp
225 230 235 240

Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu Arg Ser
245 250 255

Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe Asp Phe
260 265 270

Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg Trp Lys
275 280 285

Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile Gly Gln
290 295 300

Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His Met Leu
305 310 315 320

Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile Ser Asn
325 330 335

Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu Lys Leu
340 345 350

Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg Ser Tyr
355 360 365

Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg Lys Gly
370 375 380

Ser Ala Phe Leu His Asp Tyr Glu Leu Gly Lys Ile Gly Lys Pro Ala
385 390 395 400

Asp Arg Asp Glu Trp Val Thr Thr Pro Gln Thr Val Asn Ala Phe Tyr
405 410 415

Asn Pro Val Val Asn Asp Ile Thr Phe Pro Ala Ala Ile Leu Arg Ala
420 425 430

Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly Ala Ile
435 440 445

```
Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp Gln Gly
    450                 455                 460

Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr Asp Glu
465                 470                 475                 480

Asp Arg Ser Ala Phe Glu Gln Leu Thr Ser Arg Leu Val Thr Gln Phe
                485                 490                 495

Ser Gly Leu Val Pro Ala Val Leu Thr Ser Glu Gly Ile Asp Thr Asp
            500                 505                 510

Gly Val Asn Gly Glu Phe Thr Leu Gly Glu Asn Ile Gly Asp Leu Gly
        515                 520                 525

Gly Leu Gly Ile Ala Val Val Ala Tyr Glu Lys Tyr Leu Ala Asp Arg
    530                 535                 540

Gly Gln Thr Phe Glu Thr Ser Pro Val Gln Lys Phe Glu Ala Glu Gly
545                 550                 555                 560

Ala Glu Glu Gly Leu Ala Glu Gln Glu Phe Asn Gly Leu Gln Arg Leu
                565                 570                 575

Phe Leu Ser Trp Ala Arg Val Trp Arg Thr Lys Ile Arg Pro Gln Met
            580                 585                 590

Ala Val Gln Tyr Leu Ala Ile Asp Pro His Ser Pro Ala Glu Phe Arg
        595                 600                 605

Cys Asn Val Ile Ala Gly Asn Val Ala Glu Phe Tyr Glu Ala Phe Asp
    610                 615                 620

Val Pro Glu Asp Ala Pro Val Tyr Ile Lys Pro Glu Glu Arg Leu Ala
625                 630                 635                 640

Ile Trp
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09611P-US

<210> 169
<211> 1734
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1711)
<223> FRXA01868

<400> 169
atgcggatct gaacaggctg tctgttgcta actcatcgtt ttcgcagctg ctctcggcga 60

actggaccgt gaaggcgttg gcgcgccagt aggtttctgg gtg gag aag gat tct 115
                                    Val Glu Lys Asp Ser
                                      1   5

tcc tcc aac gaa tcc gtc gcc tat gtc atc cag tcc ggc ctc ggc ctg 163
Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln Ser Gly Leu Gly Leu
                  10   15   20

```
ccc gat gag gct tat tac cgc gag gag gca cac gcc gaa act ctc gcg   211
Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His Ala Glu Thr Leu Ala
             25                  30                  35

gcc tac aaa gag cac gtt gag cgc atg ctc ggc tac ttg gat aac agc   259
Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly Tyr Leu Asp Asn Ser
         40                  45                  50

cgc ctc ttc ggt ctg tcg gct gct tcc gct gcc gca cga att gtc gcc   307
Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala Ala Arg Ile Val Ala
     55                  60                  65

ctg gaa acg gaa atc gct gct ggc cac tgg gat gtc gtg aag acc cgc   355
Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp Val Val Lys Thr Arg
 70                  75                  80                  85

gac gcc gta gcc acc tac aac ccc acc gaa ctc ggc gcg ctg cca cca   403
Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu Gly Ala Leu Pro Pro
                 90                  95                 100

aag gtc cgc acg ctg ctc agt tcc gca ggc ctc ccg gac cag cgc ctg   451
Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu Pro Asp Gln Arg Leu
            105                 110                 115

gta tcg atg atg ccg tca tac ctc gac cac ctc aac ggc ttg ctt gtc   499
Val Ser Met Met Pro Ser Tyr Leu Asp His Leu Asn Gly Leu Leu Val
        120                 125                 130

gac gac cgc ctc ccc gat tgg cag cta tgg gca acc tgg cac atc ttg   547
Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala Thr Trp His Ile Leu
    135                 140                 145

agg tct cga gca gga ctg ttg acc gag gaa att agc caa gca aac ttc   595
Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile Ser Gln Ala Asn Phe
150                 155                 160                 165

gac ttc tat ggc acc aaa ctg tcc ggc gcc acc gag caa aaa gat cga   643
Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr Glu Gln Lys Asp Arg
                170                 175                 180

tgg aag cgt gct gtc ggc ctg gca gag cgc atg gtg ggc gag gaa atc   691
Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met Val Gly Glu Glu Ile
            185                 190                 195

ggg caa cga ttc gtc gaa agg cat ttt cct gca agc tcc aag gag cac   739
Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala Ser Ser Lys Glu His
        200                 205                 210

atg ctt gag ctc gtc gac tac ctg gtt gcc gcc tac cgt gat cgc att   787
Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala Tyr Arg Asp Arg Ile
    215                 220                 225

tcc aac ctc gaa tgg atg acg ccc gcc acc cgc gag cgt gcc ctg gaa   835
Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg Glu Arg Ala Leu Glu
230                 235                 240                 245

aag ttg ggc aaa ttc aac gcg aaa atc ggc tac ccc gac aag tgg cgc   883
Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr Pro Asp Lys Trp Arg
                250                 255                 260

tcc tac gaa ggc ctc gaa ttc ggc tcc gac ctg gtg gac aac tcc cgc   931
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```
Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu Val Asp Asn Ser Arg
            265                 270                 275

aag ggc tcc gcg ttc ctc cat gac tat gag ctg ggc aag atc ggc aaa   979
Lys Gly Ser Ala Phe Leu His Asp Tyr Glu Leu Gly Lys Ile Gly Lys
        280                 285                 290

cca gcc gac cgc gac gaa tgg gtc acc acc cca caa acc gtc aac gcc   1027
Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro Gln Thr Val Asn Ala
    295                 300                 305

ttc tac aac ccc gtg gtc aac gac atc acc ttc ccc gca gcc atc ctg   1075
Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe Pro Ala Ala Ile Leu
310                 315                 320                 325

cgc gca cca ttc ttc gac ccc gaa gca gaa gcc gca gaa aac ttc ggt   1123
Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala Ala Glu Asn Phe Gly
                330                 335                 340

gca atc ggt gct gtg atc gga cac gaa atc ggc cac ggc ttt gac gat   1171
Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly His Gly Phe Asp Asp
            345                 350                 355

caa ggc agc caa tac gac ggc gac ggc aac ctc aac tcc tgg tgg acc   1219
Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu Asn Ser Trp Trp Thr
        360                 365                 370

gac gaa gac cgc tcc gca ttc gag cag ctc acc tca cgt ctg gtc acc   1267
Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr Ser Arg Leu Val Thr
    375                 380                 385

caa ttc agc gga ctc gtc cct gcc gtc ctg acc tct gaa gga atc gac   1315
Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr Ser Glu Gly Ile Asp
390                 395                 400                 405

acc gac ggc gtc aac ggt gaa ttc act ctc ggc gaa aac atc ggt gac   1363
Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly Glu Asn Ile Gly Asp
                410                 415                 420

ctc ggc gga ttg ggc atc gct gtc gtt gcc tac gaa aag tac ctc gca   1411
Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr Glu Lys Tyr Leu Ala
            425                 430                 435

gac cgt ggc caa acc ttt gaa acc tca cca gtc caa aaa ttc gaa gca   1459
Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val Gln Lys Phe Glu Ala
        440                 445                 450

gaa ggc gcc gag gaa ggc ctg gcc gag caa gaa ttc aac ggt ctc caa   1507
Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu Phe Asn Gly Leu Gln
    455                 460                 465

cgc ctc ttc ctg tcc tgg gct cgc gtg tgg cgc acc aaa atc cgc cca   1555
Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg Thr Lys Ile Arg Pro
470                 475                 480                 485

cag atg gcc gtc caa tac ctg gcc atc gac cca cac tcc cct gca gaa   1603
Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro His Ser Pro Ala Glu
                490                 495                 500

ttc cgc tgc aat gtc atc gcc gga aac gtc gct gaa ttc tac gaa gca   1651
Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala Glu Phe Tyr Glu Ala
```

505 510 515

ttc gac gtc ccc gaa gat gca cct gtg tac atc aag cca gaa gag cgc 1699
Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile Lys Pro Glu Glu Arg
520 525 530

cta gct atc tgg tagttgttag ttggtattga aaa 1734
Leu Ala Ile Trp
535

<210> 170
<211> 537
<212> PRT
<213> Corynebacterium glutamicum

<400> 170
Val Glu Lys Asp Ser Ser Ser Asn Glu Ser Val Ala Tyr Val Ile Gln
1 5 10 15

Ser Gly Leu Gly Leu Pro Asp Glu Ala Tyr Tyr Arg Glu Glu Ala His
20 25 30

Ala Glu Thr Leu Ala Ala Tyr Lys Glu His Val Glu Arg Met Leu Gly
35 40 45

Tyr Leu Asp Asn Ser Arg Leu Phe Gly Leu Ser Ala Ala Ser Ala Ala
50 55 60

Ala Arg Ile Val Ala Leu Glu Thr Glu Ile Ala Ala Gly His Trp Asp
65 70 75 80

Val Val Lys Thr Arg Asp Ala Val Ala Thr Tyr Asn Pro Thr Glu Leu
85 90 95

Gly Ala Leu Pro Pro Lys Val Arg Thr Leu Leu Ser Ser Ala Gly Leu
100 105 110

Pro Asp Gln Arg Leu Val Ser Met Met Pro Ser Tyr Leu Asp His Leu
115 120 125

Asn Gly Leu Leu Val Asp Asp Arg Leu Pro Asp Trp Gln Leu Trp Ala
130 135 140

Thr Trp His Ile Leu Arg Ser Arg Ala Gly Leu Leu Thr Glu Glu Ile
145 150 155 160

Ser Gln Ala Asn Phe Asp Phe Tyr Gly Thr Lys Leu Ser Gly Ala Thr
165 170 175

Glu Gln Lys Asp Arg Trp Lys Arg Ala Val Gly Leu Ala Glu Arg Met
180 185 190

Val Gly Glu Glu Ile Gly Gln Arg Phe Val Glu Arg His Phe Pro Ala
195 200 205

Ser Ser Lys Glu His Met Leu Glu Leu Val Asp Tyr Leu Val Ala Ala
210 215 220

Tyr Arg Asp Arg Ile Ser Asn Leu Glu Trp Met Thr Pro Ala Thr Arg
225 230 235 240

Glu Arg Ala Leu Glu Lys Leu Gly Lys Phe Asn Ala Lys Ile Gly Tyr
245 250 255

Pro Asp Lys Trp Arg Ser Tyr Glu Gly Leu Glu Phe Gly Ser Asp Leu
260 265 270

Val Asp Asn Ser Arg Lys Gly Ser Ala Phe Leu His Asp Tyr Glu Leu
275 280 285

Gly Lys Ile Gly Lys Pro Ala Asp Arg Asp Glu Trp Val Thr Thr Pro
290 295 300

Gln Thr Val Asn Ala Phe Tyr Asn Pro Val Val Asn Asp Ile Thr Phe
305 310 315 320

Pro Ala Ala Ile Leu Arg Ala Pro Phe Phe Asp Pro Glu Ala Glu Ala
325 330 335

Ala Glu Asn Phe Gly Ala Ile Gly Ala Val Ile Gly His Glu Ile Gly
340 345 350

His Gly Phe Asp Asp Gln Gly Ser Gln Tyr Asp Gly Asp Gly Asn Leu
355 360 365

Asn Ser Trp Trp Thr Asp Glu Asp Arg Ser Ala Phe Glu Gln Leu Thr
370 375 380

Ser Arg Leu Val Thr Gln Phe Ser Gly Leu Val Pro Ala Val Leu Thr
385 390 395 400

Ser Glu Gly Ile Asp Thr Asp Gly Val Asn Gly Glu Phe Thr Leu Gly
405 410 415

Glu Asn Ile Gly Asp Leu Gly Gly Leu Gly Ile Ala Val Val Ala Tyr
420 425 430

Glu Lys Tyr Leu Ala Asp Arg Gly Gln Thr Phe Glu Thr Ser Pro Val
435 440 445

Gln Lys Phe Glu Ala Glu Gly Ala Glu Glu Gly Leu Ala Glu Gln Glu
450 455 460

Phe Asn Gly Leu Gln Arg Leu Phe Leu Ser Trp Ala Arg Val Trp Arg
465 470 475 480

Thr Lys Ile Arg Pro Gln Met Ala Val Gln Tyr Leu Ala Ile Asp Pro
485 490 495

His Ser Pro Ala Glu Phe Arg Cys Asn Val Ile Ala Gly Asn Val Ala
500 505 510

Glu Phe Tyr Glu Ala Phe Asp Val Pro Glu Asp Ala Pro Val Tyr Ile
515 520 525

Lys Pro Glu Glu Arg Leu Ala Ile Trp
530 535

<210> 171
<211> 426

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(403)
<223> FRXA01869

<400> 171
tgacaggcta ccttctgggg tggacatgat ccccaacgct caacccactt gtggcaccaa 60

ccacaaaccc tgtggcggta aatcccctag agtaggccac atg aag gat ctt tat 115
Met Lys Asp Leu Tyr
1 5

cgc ttt gtc aat ggc ctg tgg ctt gac acc cac atc att ccc gac gat 163
Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His Ile Ile Pro Asp Asp
10 15 20

cgc gcg gtg gac ggc acg ttc cac aag ctg cgc gat gat gct gaa gaa 211
Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg Asp Asp Ala Glu Glu
25 30 35

gac gtc cat gag atc gtc aag gaa gac act gga cgc gca ggc aca ctt 259
Asp Val His Glu Ile Val Lys Glu Asp Thr Gly Arg Ala Gly Thr Leu
40 45 50

tat gcc tca ttt atg gat act gac gcc atc aac gct gct ggt gtt gca 307
Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn Ala Ala Gly Val Ala
55 60 65

ccg ctc gat gcg gat ctg aac agg ctg tct gtt gct aac tca tcg ttt 355
Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val Ala Asn Ser Ser Phe
70 75 80 85

tcg cag ctg ctc tcg gcg aac tgg acc gtg aag gcg ttg gcg cgc cag 403
Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys Ala Leu Ala Arg Gln
90 95 100

taggtttctg ggtggagaag gat 426

<210> 172
<211> 101
<212> PRT
<213> Corynebacterium glutamicum

<400> 172
Met Lys Asp Leu Tyr Arg Phe Val Asn Gly Leu Trp Leu Asp Thr His
1 5 10 15

Ile Ile Pro Asp Asp Arg Ala Val Asp Gly Thr Phe His Lys Leu Arg
20 25 30

Asp Asp Ala Glu Glu Asp Val His Glu Ile Val Lys Glu Asp Thr Gly
35 40 45

Arg Ala Gly Thr Leu Tyr Ala Ser Phe Met Asp Thr Asp Ala Ile Asn
50 55 60

Ala Ala Gly Val Ala Pro Leu Asp Ala Asp Leu Asn Arg Leu Ser Val

65 70 75 80

Ala Asn Ser Ser Phe Ser Gln Leu Leu Ser Ala Asn Trp Thr Val Lys
85 90 95

Ala Leu Ala Arg Gln
100

<210> 173
<211> 1404
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1381)
<223> RXN00499

<400> 173
tgccaacagg ggatatgcca ctgtgtaccc cacggcgatg atcggtaaaa tcctcggcgc 60

gcagatattg ttcttgctgc tctaaggtga ttttgggca gtg gtg ggg gtg gtg 115
Val Val Gly Val Val
1 5

tcc acc cct gcg cgt aac ctg gga agc atg act aaa aca ctt ggt tcc 163
Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr Lys Thr Leu Gly Ser
10 15 20

ctt cag ctg gaa gaa atc acg ctg acc ctc cct ctg act gaa gat gtg 211
Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro Leu Thr Glu Asp Val
25 30 35

gcc gat gaa cgc acc att gat gtg ttc gca cgc att gcc aca cgc gtc 259
Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg Ile Ala Thr Arg Val
40 45 50

ggt ggg gaa gac ctt cca tat tta gta ttc ctg cag ggt ggg cct ggc 307
Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu Gln Gly Gly Pro Gly
55 60 65

aat gaa gct cca cgt cca agc ctt aat ccc ctc aac ccc aat tgg ttg 355
Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu Asn Pro Asn Trp Leu
70 75 80 85

ggc gtg gcc ttg gag gaa tac cgc gtg gtc atg ttg gat caa cgt ggc 403
Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met Leu Asp Gln Arg Gly
90 95 100

acc ggc cgt tcc acc cca gtg ggt aat gat att ttg gaa aaa ccc aca 451
Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile Leu Glu Lys Pro Thr
105 110 115

gca gaa gta gtg gag tac tta tcc cac ctg cgc gca gat ggc att gtg 499
Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg Ala Asp Gly Ile Val
120 125 130

cga gat gct gaa gcc ctg cgt aag cat ttg ggt gtg aat cag tgg aac 547
Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly Val Asn Gln Trp Asn
135 140 145

```
ctt tta ggc cag tcc ttc gga ggt ttc acc acc ctg cat tac ttg tcc   595
Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr Leu His Tyr Leu Ser
150                 155                 160                 165

cgg cac gcc gat tcc ttg gac aac gtg ttt att acc ggc ggt ctc agc   643
Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile Thr Gly Gly Leu Ser
                170                 175                 180

gct att gat cgc cca gca gaa gac gtg tat gcc aac tgt tac aac cgc   691
Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala Asn Cys Tyr Asn Arg
            185                 190                 195

atg cgc cga aac tct gag gaa ttc tac cgt cgc ttc ccg caa tta cgg   739
Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg Phe Pro Gln Leu Arg
        200                 205                 210

gaa act ttc cga ggg ttg gtt aat cgt gct cgc gcc ggg gag att gtg   787
Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg Ala Gly Glu Ile Val
    215                 220                 225

ctt ccc acc ggc gaa gtt gtg tca gaa acc agg ctg cga tcc ctt ggt   835
Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg Leu Arg Ser Leu Gly
230                 235                 240                 245

cac ttg ttg ggt agc aat gac ggc tgg ttt gat ctg tac aac ctg ctg   883
His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp Leu Tyr Asn Leu Leu
                250                 255                 260

gaa tta gat ccc acc tcc aac gct ttt gtc cat gac ctg gca gga ctt   931
Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His Asp Leu Ala Gly Leu
            265                 270                 275

ttg cct ttc ggc aac cgc aac cca att tat tac gtg ctc cat gag tcc   979
Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr Val Leu His Glu Ser
        280                 285                 290

tct tac gcc gac ggt gtg gtg aca aat tgg gca gca gag cgt gtg ctt   1027
Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala Ala Glu Arg Val Leu
    295                 300                 305

cca gag gat ttc cgc gag gat cca aca ctg ctc acc ggt gag cac gtg   1075
Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu Thr Gly Glu His Val
310                 315                 320                 325

ttc cag gag tgg aca gac acc gtg ccg tcg ctc aag ccg tgg aag gac   1123
Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu Lys Pro Trp Lys Asp
                330                 335                 340

gtt gcc ctg gca ttg gct cag cag gaa tgg ccc aag ctt tat gat gcg   1171
Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro Lys Leu Tyr Asp Ala
            345                 350                 355

aag gca ttg gaa aac tca cag gcc aag ggc gct gca gca gtg tat gcc   1219
Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala Ala Ala Val Tyr Ala
        360                 365                 370

aat gac gtt ttc gtc cca gtg gat tac tct ctg gaa acc gca caa cac   1267
Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu Glu Thr Ala Gln His
    375                 380                 385
```

```
ctg ccc ggt gtg cag ctg ttt atc acc agc cag cat gaa cac aat gga   1315
Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln His Glu His Asn Gly
390                 395                 400                 405

ctt cgt gcc agc tca ggc gca gta ctg aag cac ctt ttc gat ctg gcc   1363
Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His Leu Phe Asp Leu Ala
                410                 415                 420

cac ggc cga gag gta cgc tgattcctcg tgttagtact agc                1404
His Gly Arg Glu Val Arg
            425
```

<210> 174
<211> 427
<212> PRT
<213> Corynebacterium glutamicum

<400> 174

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Val Val Gly Val Val Ser Thr Pro Ala Arg Asn Leu Gly Ser Met Thr
  1               5                  10                  15

Lys Thr Leu Gly Ser Leu Gln Leu Glu Glu Ile Thr Leu Thr Leu Pro
             20                  25                  30

Leu Thr Glu Asp Val Ala Asp Glu Arg Thr Ile Asp Val Phe Ala Arg
         35                  40                  45

Ile Ala Thr Arg Val Gly Gly Glu Asp Leu Pro Tyr Leu Val Phe Leu
     50                  55                  60

Gln Gly Gly Pro Gly Asn Glu Ala Pro Arg Pro Ser Leu Asn Pro Leu
 65                  70                  75                  80

Asn Pro Asn Trp Leu Gly Val Ala Leu Glu Glu Tyr Arg Val Val Met
                 85                  90                  95

Leu Asp Gln Arg Gly Thr Gly Arg Ser Thr Pro Val Gly Asn Asp Ile
            100                 105                 110

Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu Ser His Leu Arg
        115                 120                 125

Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg Lys His Leu Gly
    130                 135                 140

Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly Gly Phe Thr Thr
145                 150                 155                 160

Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp Asn Val Phe Ile
                165                 170                 175

Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu Asp Val Tyr Ala
            180                 185                 190

Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu Phe Tyr Arg Arg
        195                 200                 205

Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val Asn Arg Ala Arg
    210                 215                 220
```

```
Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val Ser Glu Thr Arg
225                 230                 235                 240

Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp Gly Trp Phe Asp
                245                 250                 255

Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn Ala Phe Val His
            260                 265                 270

Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn Pro Ile Tyr Tyr
        275                 280                 285

Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val Thr Asn Trp Ala
    290                 295                 300

Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp Pro Thr Leu Leu
305                 310                 315                 320

Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr Val Pro Ser Leu
                325                 330                 335

Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln Gln Glu Trp Pro
            340                 345                 350

Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln Ala Lys Gly Ala
        355                 360                 365

Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val Asp Tyr Ser Leu
    370                 375                 380

Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe Ile Thr Ser Gln
385                 390                 395                 400

His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala Val Leu Lys His
                405                 410                 415

Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
            420                 425
```

09604.doc

<210> 175
<211> 980
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(957)
<223> FRXA00499

<400> 175

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ggt aat gat att ttg gaa aaa ccc aca gca gaa gta gtg gag tac tta   48
Gly Asn Asp Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu
  1               5                  10                  15

tcc cac ctg cgc gca gat ggc att gtg cga gat gct gaa gcc ctg cgt   96
Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
             20                  25                  30

aag cat ttg ggt gtg aat cag tgg aac ctt tta ggc cag tcc ttc gga  144
Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
```

```
         35                  40                  45

ggt ttc acc acc ctg cat tac ttg tcc cgg cac gcc gat tcc ttg gac   192
Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
     50                  55                  60

aac gtg ttt att acc ggc ggt ctc agc gct att gat cgc cca gca gaa   240
Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
 65                  70                  75                  80

gac gtg tat gcc aac tgt tac aac cgc atg cgc cga aac tct gag gaa   288
Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
                 85                  90                  95

ttc tac cgt cgc ttc ccg caa tta cgg gaa act ttc cga ggg ttg gtt   336
Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
            100                 105                 110

aat cgt gct cgc gcc ggg gag att gtg ctt ccc acc ggc gaa gtt gtg   384
Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
        115                 120                 125

tca gaa acc agg ctg cga tcc ctt ggt cac ttg ttg ggt agc aat gac   432
Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
    130                 135                 140

ggc tgg ttt gat ctg tac aac ctg ctg gaa tta gat ccc acc tcc aac   480
Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
145                 150                 155                 160

gct ttt gtc cat gac ctg gca gga ctt ttg cct ttc ggc aac cgc aac   528
Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
                165                 170                 175

cca att tat tac gtg ctc cat gag tcc tct tac gcc gac ggt gtg gtg   576
Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
            180                 185                 190

aca aat tgg gca gca gag cgt gtg ctt cca gag gat ttc cgc gag gat   624
Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
        195                 200                 205

cca aca ctg ctc acc ggt gag cac gtg ttc cag gag tgg aca gac acc   672
Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
    210                 215                 220

gtg ccg tcg ctc aag ccg tgg aag gac gtt gcc ctg gca ttg gct cag   720
Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln
225                 230                 235                 240

cag gaa tgg ccc aag ctt tat gat gcg aag gca ttg gaa aac tca cag   768
Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln
                245                 250                 255

gcc aag ggc gct gca gca gtg tat gcc aat gac gtt ttc gtc cca gtg   816
Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val
            260                 265                 270

gat tac tct ctg gaa acc gca caa cac ctg ccc ggt gtg cag ctg ttt   864
Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe
        275                 280                 285
```

```
atc acc agc cag cat gaa cac aat gga ctt cgt gcc agc tca ggc gca   912
Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
    290                 295                 300

gta ctg aag cac ctt ttc gat ctg gcc cac ggc cga gag gta cgc       957
Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
305                 310                 315

tgattcctcg tgttagtact agc                                        980
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<210> 176
<211> 319
<212> PRT
<213> Corynebacterium glutamicum

<400> 176

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Gly Asn Asp Ile Leu Glu Lys Pro Thr Ala Glu Val Val Glu Tyr Leu
  1               5                  10                  15

Ser His Leu Arg Ala Asp Gly Ile Val Arg Asp Ala Glu Ala Leu Arg
             20                  25                  30

Lys His Leu Gly Val Asn Gln Trp Asn Leu Leu Gly Gln Ser Phe Gly
         35                  40                  45

Gly Phe Thr Thr Leu His Tyr Leu Ser Arg His Ala Asp Ser Leu Asp
     50                  55                  60

Asn Val Phe Ile Thr Gly Gly Leu Ser Ala Ile Asp Arg Pro Ala Glu
 65                  70                  75                  80

Asp Val Tyr Ala Asn Cys Tyr Asn Arg Met Arg Arg Asn Ser Glu Glu
                 85                  90                  95

Phe Tyr Arg Arg Phe Pro Gln Leu Arg Glu Thr Phe Arg Gly Leu Val
            100                 105                 110

Asn Arg Ala Arg Ala Gly Glu Ile Val Leu Pro Thr Gly Glu Val Val
        115                 120                 125

Ser Glu Thr Arg Leu Arg Ser Leu Gly His Leu Leu Gly Ser Asn Asp
    130                 135                 140

Gly Trp Phe Asp Leu Tyr Asn Leu Leu Glu Leu Asp Pro Thr Ser Asn
145                 150                 155                 160

Ala Phe Val His Asp Leu Ala Gly Leu Leu Pro Phe Gly Asn Arg Asn
                165                 170                 175

Pro Ile Tyr Tyr Val Leu His Glu Ser Ser Tyr Ala Asp Gly Val Val
            180                 185                 190

Thr Asn Trp Ala Ala Glu Arg Val Leu Pro Glu Asp Phe Arg Glu Asp
        195                 200                 205

Pro Thr Leu Leu Thr Gly Glu His Val Phe Gln Glu Trp Thr Asp Thr
    210                 215                 220

Val Pro Ser Leu Lys Pro Trp Lys Asp Val Ala Leu Ala Leu Ala Gln
```

```
225                 230                 235                 240

Gln Glu Trp Pro Lys Leu Tyr Asp Ala Lys Ala Leu Glu Asn Ser Gln
                245                 250                 255

Ala Lys Gly Ala Ala Ala Val Tyr Ala Asn Asp Val Phe Val Pro Val
            260                 265                 270

Asp Tyr Ser Leu Glu Thr Ala Gln His Leu Pro Gly Val Gln Leu Phe
        275                 280                 285

Ile Thr Ser Gln His Glu His Asn Gly Leu Arg Ala Ser Ser Gly Ala
    290                 295                 300

Val Leu Lys His Leu Phe Asp Leu Ala His Gly Arg Glu Val Arg
305                 310                 315
```

<210> 177
<211> 2127
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2104)
<223> RXN01277

<400> 177

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tactactcgg ttcacgttta cgtcggctga tccaattgga ggcgccctcg gaagccgcct 60

taaaaaacct gccggtcaaa agatcactaa cctgaacttc atg act gat tac acg   115
                                            Met Thr Asp Tyr Thr
                                              1               5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa   163
Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
                10                  15                  20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc   211
Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
            25                  30                  35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc   259
Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
        40                  45                  50

tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg   307
Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
    55                  60                  65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa   355
Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
70                  75                  80                  85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg   403
Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
                90                  95                  100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg   451
Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
```

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            105                 110                 115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat   499
Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
        120                 125                 130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat   547
Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
    135                 140                 145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt   595
Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val
150                 155                 160                 165

gat ctg gat acg ttg ctg gtg ggc acg gat acc ggc gag ggg tca ctg   643
Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu
                170                 175                 180

acg gat tct ggg tac ccg gcg cgg gtg ctc acg tgg aag cgt ggg act   691
Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr
            185                 190                 195

ccg ctt gag cag gcg gag ttg ttc ttt gag ggg tcg cgt cag gat gtg   739
Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val
        200                 205                 210

gcg act cat gcg tgg cgg gat tca aca cct ggt ttt gag cgg acg ttt   787
Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly Phe Glu Arg Thr Phe
    215                 220                 225

gtg tca agg tcg ttg gat ttc tat aat tcg gag acg tcg ctg gaa acc   835
Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu Thr Ser Leu Glu Thr
230                 235                 240                 245

gag ggt ggc ctg gtc aag ctt gat gtg ccg acc gat tgc gat gtc att   883
Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr Asp Cys Asp Val Ile
                250                 255                 260

gtg aag aag cag tgg att ttt gtg agt cct cgg acg gat ttc gct ggg   931
Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg Thr Asp Phe Ala Gly
            265                 270                 275

att cca gca ggt ggc ttg gga gtg ctg ctg tta aag gag ttc ctt gag   979
Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu Lys Glu Phe Leu Glu
        280                 285                 290

ggc ggg cgc gat ttt cag cct gtg ttt acg cct act gag tcg acg tcg   1027
Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser
    295                 300                 305

ctg cag gga ttg gcc acg aca aag aat ttc ctg gtt tta acg ctc ctt   1075
Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu Val Leu Thr Leu Leu
310                 315                 320                 325

aat aat gtc tcc aca gaa atc gtc aca gtg ccg ctc aat gat ccg aca   1123
Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro Leu Asn Asp Pro Thr
                330                 335                 340

acg gag cat gaa cac att gac ctc cca gag cat gtc acc gcg cat gtg   1171
Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val
            345                 350                 355
```

```
gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg   1219
Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala
        360                 365                 370

agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg   1267
Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala
    375                 380                 385

ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag   1315
Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln
390                 395                 400                 405

gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg   1363
Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro
                410                 415                 420

tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc   1411
Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val
            425                 430                 435

cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg   1459
His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro
        440                 445                 450

acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc   1507
Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala
    455                 460                 465

aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca   1555
Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala
470                 475                 480                 485

acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc   1603
Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu
                490                 495                 500

gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att   1651
Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile
            505                 510                 515

cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag   1699
Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln
        520                 525                 530

tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat   1747
Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp
    535                 540                 545

atg ttg cgc tat cac acc tgg tca gcg ggt gct tcg tgg atg gcg gag   1795
Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala Ser Trp Met Ala Glu
550                 555                 560                 565

tac ggc aac cct gac gat ccg gag gaa cgg gcg gtg att gag cag tac   1843
Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala Val Ile Glu Gln Tyr
                570                 575                 580

tcg ccg gtg cag gcg gtg gtg ggc gtc gag aag cga att tat cca ccc   1891
Ser Pro Val Gln Ala Val Val Gly Val Glu Lys Arg Ile Tyr Pro Pro
            585                 590                 595
```

```
gca ttg gtg acg acc tca acc cgg gac gac cgc gtc cac ccc gcg cac   1939
Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg Val His Pro Ala His
        600                 605                 610

gcg cgc ctt ttt gct caa gct ttg ctt gat gcg ggc cag gcc gtg gat   1987
Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala Gly Gln Ala Val Asp
    615                 620                 625

tac tac gaa aac acc gag ggc ggc cat gcc ggc gcg gcg gat aac aag   2035
Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly Ala Ala Asp Asn Lys
630                 635                 640                 645

cag acc gcg ttt gtg gaa tcg ctg atc tac acc tgg atc gag aag act   2083
Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr Trp Ile Glu Lys Thr
                650                 655                 660

ttg gat cag cag ggt agc att taatacctat gattatgcga agg             2127
Leu Asp Gln Gln Gly Ser Ile
            665
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<210> 178
<211> 668
<212> PRT
<213> Corynebacterium glutamicum

<400> 178

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Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
  1               5                  10                  15

Ala Trp Ala Glu Lys Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser
             20                  25                  30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
         35                  40                  45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
     50                  55                  60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
 65                  70                  75                  80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
                 85                  90                  95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
            100                 105                 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
        115                 120                 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
    130                 135                 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
145                 150                 155                 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
                165                 170                 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
```

```
            180                 185                 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
        195                 200                 205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
    210                 215                 220

Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
225                 230                 235                 240

Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr
                245                 250                 255

Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
            260                 265                 270

Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
        275                 280                 285

Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
    290                 295                 300

Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
305                 310                 315                 320

Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
                325                 330                 335

Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
            340                 345                 350

Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
        355                 360                 365

Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
    370                 375                 380

Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
385                 390                 395                 400

Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
                405                 410                 415

Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
            420                 425                 430

Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
        435                 440                 445

Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
    450                 455                 460

Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
465                 470                 475                 480

Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
                485                 490                 495

His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
            500                 505                 510
```

Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
515 520 525

Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
530 535 540

Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Ala
545 550 555 560

Ser Trp Met Ala Glu Tyr Gly Asn Pro Asp Asp Pro Glu Glu Arg Ala
565 570 575

Val Ile Glu Gln Tyr Ser Pro Val Gln Ala Val Val Gly Val Glu Lys
580 585 590

Arg Ile Tyr Pro Pro Ala Leu Val Thr Thr Ser Thr Arg Asp Asp Arg
595 600 605

Val His Pro Ala His Ala Arg Leu Phe Ala Gln Ala Leu Leu Asp Ala
610 615 620

Gly Gln Ala Val Asp Tyr Tyr Glu Asn Thr Glu Gly Gly His Ala Gly
625 630 635 640

Ala Ala Asp Asn Lys Gln Thr Ala Phe Val Glu Ser Leu Ile Tyr Thr
645 650 655

Trp Ile Glu Lys Thr Leu Asp Gln Gln Gly Ser Ile
660 665

<210> 179
<211> 1812
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1789)
<223> FRXA01277

<400> 179
tactactcgg ttcacgttta cgtcggctga tccaattgga ggcgccctcg gaagccgcct 60

taaaaaacct gccggtcaaa agatcactaa cctgaacttc atg act gat tac acg 115
Met Thr Asp Tyr Thr
1 5

ttc ctc gaa gac att gac acc ccg gaa gcg ctc gcg tgg gcg gaa aaa 163
Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu Ala Trp Ala Glu Lys
10 15 20

tgg tcg ggg gaa agc gtc gaa aag cta aaa agc cca gcc aag gac gcc 211
Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser Pro Ala Lys Asp Ala
25 30 35

ctg gaa gcc agg ctg ctg gct gcg ttg gac acc gat gat cgc att gcc 259
Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr Asp Asp Arg Ile Ala
40 45 50

```
tac gtg agc cgg cgc ggt gag aag ctg tac aac ttt tgg cgg gac gcg   307
Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn Phe Trp Arg Asp Ala
     55                  60                  65

cag cat ccg cgt gga gtg tgg cgc acg acc acg ttg gag tcg tat gaa   355
Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr Leu Glu Ser Tyr Glu
 70                  75                  80                  85

agt gac cag ccg gag tgg gac gtg ctc att gat gtg gat gcg ttg gcg   403
Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp Val Asp Ala Leu Ala
                 90                  95                 100

gag gat gag ggc gaa aac tgg gta tgg aag ggc gcg gtt gtg cgc tcg   451
Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly Ala Val Val Arg Ser
            105                 110                 115

ccg gag ttt gat cgg gcg ttg gtg aag ttc tcg cgg ggc ggg gct gat   499
Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser Arg Gly Gly Ala Asp
        120                 125                 130

gcg acg gtg att agg gag ttt gat ctg gcc acg gct gct ttc gtg gat   547
Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr Ala Ala Phe Val Asp
    135                 140                 145

gat tcg ccg ttt gaa ttg aag gag gcg aag tcc gat gtc acg tgg gtt   595
Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser Asp Val Thr Trp Val
150                 155                 160                 165

gat ctg gat acg ttg ctg gtg ggc acg gat acc ggc gag ggg tca ctg   643
Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr Gly Glu Gly Ser Leu
                170                 175                 180

acg gat tct ggg tac ccg gcg cgg gtg ctc acg tgg aag cgt ggg act   691
Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr Trp Lys Arg Gly Thr
            185                 190                 195

ccg ctt gag cag gcg gag ttg ttc ttt gag ggg tcg cgt cag gat gtg   739
Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly Ser Arg Gln Asp Val
        200                 205                 210

gcg act cat gcg tgg cgg gat tca aca cct ggt ttt gag cgg acg ttt   787
Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly Phe Glu Arg Thr Phe
    215                 220                 225

gtg tca agg tcg ttg gat ttc tat aat tcg gag acg tcg ctg gaa acc   835
Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu Thr Ser Leu Glu Thr
230                 235                 240                 245

gag ggt ggc ctg gtc aag ctt gat gtg ccg acc gat tgc gat gtc att   883
Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr Asp Cys Asp Val Ile
                250                 255                 260

gtg aag aag cag tgg att ttt gtg agt cct cgg acg gat ttc gct ggg   931
Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg Thr Asp Phe Ala Gly
            265                 270                 275

att cca gca ggt ggc ttg gga gtg ctg ctg tta aag gag ttc ctt gag   979
Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu Lys Glu Phe Leu Glu
        280                 285                 290

ggc ggg cgc gat ttt cag cct gtg ttt acg cct act gag tcg acg tcg   1027
```

```
Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro Thr Glu Ser Thr Ser
    295                 300                 305

ctg cag gga ttg gcc acg aca aag aat ttc ctg gtt tta acg ctc ctt   1075
Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu Val Leu Thr Leu Leu
310                 315                 320                 325

aat aat gtc tcc aca gaa atc gtc aca gtg ccg ctc aat gat ccg aca   1123
Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro Leu Asn Asp Pro Thr
                330                 335                 340

acg gag cat gaa cac att gac ctc cca gag cat gtc acc gcg cat gtg   1171
Thr Glu His Glu His Ile Asp Leu Pro Glu His Val Thr Ala His Val
            345                 350                 355

gtt gct acc tcc ccg ttg gat ggc gat gaa att tgg gtg cag gca gcg   1219
Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile Trp Val Gln Ala Ala
        360                 365                 370

agt ttc acc gaa gcg cca acg ttg ctg cgt gcg gag ctg cct ggt gcg   1267
Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala Glu Leu Pro Gly Ala
    375                 380                 385

ctt gag gct gtg aag aag gcg ccg ttg cag ttt gaa aat gct ggt cag   1315
Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe Glu Asn Ala Gly Gln
390                 395                 400                 405

gag act cgt cag cat tgg gca acc tcg gcg gat gga acg aag att ccg   1363
Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp Gly Thr Lys Ile Pro
                410                 415                 420

tac ttt att aca gga gcc ttc gag gag gaa cca caa aac acc ctg gtc   1411
Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro Gln Asn Thr Leu Val
            425                 430                 435

cac gcc tac ggc ggc ttc gag gtt tcc ctt acc cca agc cac tcc ccg   1459
His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr Pro Ser His Ser Pro
        440                 445                 450

acc cgc ggc atc gca tgg ttg gaa aag ggc tac tac ttt gtg gaa gcc   1507
Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr Tyr Phe Val Glu Ala
    455                 460                 465

aac ctg cgt ggt ggc ggt gaa ttc ggt ccg gaa tgg cat tcg cag gca   1555
Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu Trp His Ser Gln Ala
470                 475                 480                 485

acc aag ctg aac cgc atg aag gtg tgg gag gat cac cgc gcg gtg ctc   1603
Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp His Arg Ala Val Leu
                490                 495                 500

gcc gac ctt gtg gag cgc ggc tac gca acg ccg gag cag att gcg att   1651
Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro Glu Gln Ile Ala Ile
            505                 510                 515

cgt ggc gga tcc aac ggt ggt ttg ctg aca agt ggc gcg tta act cag   1699
Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser Gly Ala Leu Thr Gln
        520                 525                 530

tac cca gaa gca ttc ggt gcg gca gtt gtg cag gtg ccg ttg gct gat   1747
Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln Val Pro Leu Ala Asp
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535 540 545

atg ttg cgc tat cac acc tgg tca gcg ggt acc tcg tgg atg 1789
Met Leu Arg Tyr His Thr Trp Ser Ala Gly Thr Ser Trp Met
550 555 560

taggtgtcgg caaccatggg aac 1812

<210> 180
<211> 563
<212> PRT
<213> Corynebacterium glutamicum

<400> 180
Met Thr Asp Tyr Thr Phe Leu Glu Asp Ile Asp Thr Pro Glu Ala Leu
1 5 10 15

Ala Trp Ala Glu Lys Trp Ser Gly Glu Ser Val Glu Lys Leu Lys Ser
20 25 30

Pro Ala Lys Asp Ala Leu Glu Ala Arg Leu Leu Ala Ala Leu Asp Thr
35 40 45

Asp Asp Arg Ile Ala Tyr Val Ser Arg Arg Gly Glu Lys Leu Tyr Asn
50 55 60

Phe Trp Arg Asp Ala Gln His Pro Arg Gly Val Trp Arg Thr Thr Thr
65 70 75 80

Leu Glu Ser Tyr Glu Ser Asp Gln Pro Glu Trp Asp Val Leu Ile Asp
85 90 95

Val Asp Ala Leu Ala Glu Asp Glu Gly Glu Asn Trp Val Trp Lys Gly
100 105 110

Ala Val Val Arg Ser Pro Glu Phe Asp Arg Ala Leu Val Lys Phe Ser
115 120 125

Arg Gly Gly Ala Asp Ala Thr Val Ile Arg Glu Phe Asp Leu Ala Thr
130 135 140

Ala Ala Phe Val Asp Asp Ser Pro Phe Glu Leu Lys Glu Ala Lys Ser
145 150 155 160

Asp Val Thr Trp Val Asp Leu Asp Thr Leu Leu Val Gly Thr Asp Thr
165 170 175

Gly Glu Gly Ser Leu Thr Asp Ser Gly Tyr Pro Ala Arg Val Leu Thr
180 185 190

Trp Lys Arg Gly Thr Pro Leu Glu Gln Ala Glu Leu Phe Phe Glu Gly
195 200 205

Ser Arg Gln Asp Val Ala Thr His Ala Trp Arg Asp Ser Thr Pro Gly
210 215 220

Phe Glu Arg Thr Phe Val Ser Arg Ser Leu Asp Phe Tyr Asn Ser Glu
225 230 235 240

Thr Ser Leu Glu Thr Glu Gly Gly Leu Val Lys Leu Asp Val Pro Thr

```
                245                 250                 255

Asp Cys Asp Val Ile Val Lys Lys Gln Trp Ile Phe Val Ser Pro Arg
            260                 265                 270

Thr Asp Phe Ala Gly Ile Pro Ala Gly Gly Leu Gly Val Leu Leu Leu
        275                 280                 285

Lys Glu Phe Leu Glu Gly Gly Arg Asp Phe Gln Pro Val Phe Thr Pro
    290                 295                 300

Thr Glu Ser Thr Ser Leu Gln Gly Leu Ala Thr Thr Lys Asn Phe Leu
305                 310                 315                 320

Val Leu Thr Leu Leu Asn Asn Val Ser Thr Glu Ile Val Thr Val Pro
                325                 330                 335

Leu Asn Asp Pro Thr Thr Glu His Glu His Ile Asp Leu Pro Glu His
            340                 345                 350

Val Thr Ala His Val Val Ala Thr Ser Pro Leu Asp Gly Asp Glu Ile
        355                 360                 365

Trp Val Gln Ala Ala Ser Phe Thr Glu Ala Pro Thr Leu Leu Arg Ala
    370                 375                 380

Glu Leu Pro Gly Ala Leu Glu Ala Val Lys Lys Ala Pro Leu Gln Phe
385                 390                 395                 400

Glu Asn Ala Gly Gln Glu Thr Arg Gln His Trp Ala Thr Ser Ala Asp
                405                 410                 415

Gly Thr Lys Ile Pro Tyr Phe Ile Thr Gly Ala Phe Glu Glu Glu Pro
            420                 425                 430

Gln Asn Thr Leu Val His Ala Tyr Gly Gly Phe Glu Val Ser Leu Thr
        435                 440                 445

Pro Ser His Ser Pro Thr Arg Gly Ile Ala Trp Leu Glu Lys Gly Tyr
    450                 455                 460

Tyr Phe Val Glu Ala Asn Leu Arg Gly Gly Gly Glu Phe Gly Pro Glu
465                 470                 475                 480

Trp His Ser Gln Ala Thr Lys Leu Asn Arg Met Lys Val Trp Glu Asp
                485                 490                 495

His Arg Ala Val Leu Ala Asp Leu Val Glu Arg Gly Tyr Ala Thr Pro
            500                 505                 510

Glu Gln Ile Ala Ile Arg Gly Gly Ser Asn Gly Gly Leu Leu Thr Ser
        515                 520                 525

Gly Ala Leu Thr Gln Tyr Pro Glu Ala Phe Gly Ala Ala Val Val Gln
    530                 535                 540

Val Pro Leu Ala Asp Met Leu Arg Tyr His Thr Trp Ser Ala Gly Thr
545                 550                 555                 560

Ser Trp Met
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<210> 181
<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXN00675

<400> 181
gtggaagtac tcacctcaag gtggccggaa ccgcatgcat tgtgcggtgc cggccacctt 60

tggttttaac agtttaattt gaagaaagag acgtggaagc atg ggt ttc cgt tcc 115
Met Gly Phe Arg Ser
1 5

aag aag aag gtt att gcg gca aag acc gcc gct gag ctg gac gcg atg 163
Lys Lys Lys Val Ile Ala Ala Lys Thr Ala Ala Glu Leu Asp Ala Met
10 15 20

cag gcg gcg ggt gag atc gtc ggc aag gct ttg cag gct gtg cgc gct 211
Gln Ala Ala Gly Glu Ile Val Gly Lys Ala Leu Gln Ala Val Arg Ala
25 30 35

gag gct aaa gct ggc atg agc acg tgg gat ctg gat cag atc gcg gag 259
Glu Ala Lys Ala Gly Met Ser Thr Trp Asp Leu Asp Gln Ile Ala Glu
40 45 50

cag gtt atc cgc gat gct ggc gcc gtt cct aca ttc ctg ggt tac cag 307
Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr Phe Leu Gly Tyr Gln
55 60 65

ggt ttt ccg gca tca gtg tgc gct tcg gtc aat gag gtg att gtt cac 355
Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn Glu Val Ile Val His
70 75 80 85

ggc att cca tcc aag gag acc atc ttg gag gaa ggc gat ctg gtg tcc 403
Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu Gly Asp Leu Val Ser
90 95 100

atc gac tgc ggc gca acc ttt gat ggt tgg gtc ggc gat tcc gcg tgg 451
Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp
105 110 115

agc ttc ggc atc ggc gag ctg gac gag gac gtc cag ggt ctc aac ttg 499
Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu
120 125 130

gct acc gag tgg gtc ctc atg gaa ggc atg aag gcc atg gtt cca ggc 547
Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly
135 140 145

aac cgt ttg acc gat gtc tcc cac gct ctc gag gtc gca acc cgc aag 595
Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys
150 155 160 165

gct gag tcc aag ttc ggc gtc gcg ctc ggc atc gtc gat ggc tac ggc 643
Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly

```
                170                 175                 180

gga cac ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat   691
Gly His Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn
            185                 190                 195

gag ggc aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc   739
Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu
        200                 205                 210

gcc att gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg   787
Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu
    215                 220                 225

gaa gat gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac   835
Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His
230                 235                 240                 245

tgg gag cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg   883
Trp Glu His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr
                250                 255                 260

ccg cgt tat taaaatgatg cttttcgacg cat                            915
Pro Arg Tyr
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<210> 182
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 182

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Met Gly Phe Arg Ser Lys Lys Lys Val Ile Ala Ala Lys Thr Ala Ala
  1               5                  10                  15

Glu Leu Asp Ala Met Gln Ala Ala Gly Glu Ile Val Gly Lys Ala Leu
             20                  25                  30

Gln Ala Val Arg Ala Glu Ala Lys Ala Gly Met Ser Thr Trp Asp Leu
         35                  40                  45

Asp Gln Ile Ala Glu Gln Val Ile Arg Asp Ala Gly Ala Val Pro Thr
     50                  55                  60

Phe Leu Gly Tyr Gln Gly Phe Pro Ala Ser Val Cys Ala Ser Val Asn
 65                  70                  75                  80

Glu Val Ile Val His Gly Ile Pro Ser Lys Glu Thr Ile Leu Glu Glu
                 85                  90                  95

Gly Asp Leu Val Ser Ile Asp Cys Gly Ala Thr Phe Asp Gly Trp Val
            100                 105                 110

Gly Asp Ser Ala Trp Ser Phe Gly Ile Gly Glu Leu Asp Glu Asp Val
        115                 120                 125

Gln Gly Leu Asn Leu Ala Thr Glu Trp Val Leu Met Glu Gly Met Lys
    130                 135                 140

Ala Met Val Pro Gly Asn Arg Leu Thr Asp Val Ser His Ala Leu Glu
```

```
145                 150                 155                 160

Val Ala Thr Arg Lys Ala Glu Ser Lys Phe Gly Val Ala Leu Gly Ile
                165                 170                 175

Val Asp Gly Tyr Gly Gly His Gly Ile Gly Arg His Met His Glu Glu
            180                 185                 190

Pro Tyr Leu Ala Asn Glu Gly Lys Ala Gly Lys Gly Pro Val Ile Gln
        195                 200                 205

Glu Gly Ser Val Leu Ala Ile Glu Pro Met Leu Thr Leu Gly Thr Glu
    210                 215                 220

Asp Ser Ala Val Leu Glu Asp Asp Trp Thr Val Val Thr Leu Asp Gly
225                 230                 235                 240

Ser Trp Ala Ser His Trp Glu His Thr Val Ala Ala Thr Lys Gly Gly
                245                 250                 255

Pro Arg Ile Leu Thr Pro Arg Tyr
            260
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<210> 183
<211> 506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(483)
<223> FRXA00675

<400> 183

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tgc ggc gca acc ttt gat ggt tgg gtc ggc gat tcc gcg tgg agc ttc   48
Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp Ser Phe
  1               5                  10                  15

ggc atc ggc gag ctg gac gag gac gtc cag ggt ctc aac ttg gct acc   96
Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu Ala Thr
             20                  25                  30

gag tgg gtc ctc atg gaa ggc atg aag gcc atg gtt cca ggc aac cgt   144
Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
         35                  40                  45

ttg acc gat gtc tcc cac gct ctc gag gtc gca acc cgc aag gct gag   192
Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
     50                  55                  60

tcc aag ttc ggc gtc gcg ctc ggc atc gtc gat ggc tac ggc gga cac   240
Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
 65                  70                  75                  80

ggc att ggc cgc cac atg cac gag gag cca tac ttg gct aat gag ggc   288
Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
                 85                  90                  95

aag gcc ggc aag ggc cct gtg att cag gag ggc tcc gtg ctc gcc att   336
Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
```

```
            100                 105                 110

gag cct atg ctc acc ctc ggc acc gaa gat tcc gca gtg ctg gaa gat   384
Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
        115                 120                 125

gat tgg act gtc gtg act ctc gac ggt tca tgg gca tca cac tgg gag   432
Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His Trp Glu
    130                 135                 140

cac acc gtt gca gcc acc aag ggc ggc ccg cgc atc ctc acg ccg cgt   480
His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr Pro Arg
145                 150                 155                 160

tat taaaatgatg cttttcgacg cat                                    506
Tyr
```

<210> 184
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 184

```
Cys Gly Ala Thr Phe Asp Gly Trp Val Gly Asp Ser Ala Trp Ser Phe
  1               5                  10                  15

Gly Ile Gly Glu Leu Asp Glu Asp Val Gln Gly Leu Asn Leu Ala Thr
             20                  25                  30

Glu Trp Val Leu Met Glu Gly Met Lys Ala Met Val Pro Gly Asn Arg
         35                  40                  45

Leu Thr Asp Val Ser His Ala Leu Glu Val Ala Thr Arg Lys Ala Glu
     50                  55                  60

Ser Lys Phe Gly Val Ala Leu Gly Ile Val Asp Gly Tyr Gly Gly His
 65                  70                  75                  80

Gly Ile Gly Arg His Met His Glu Glu Pro Tyr Leu Ala Asn Glu Gly
                 85                  90                  95

Lys Ala Gly Lys Gly Pro Val Ile Gln Glu Gly Ser Val Leu Ala Ile
            100                 105                 110

Glu Pro Met Leu Thr Leu Gly Thr Glu Asp Ser Ala Val Leu Glu Asp
        115                 120                 125

Asp Trp Thr Val Val Thr Leu Asp Gly Ser Trp Ala Ser His Trp Glu
    130                 135                 140

His Thr Val Ala Ala Thr Lys Gly Gly Pro Arg Ile Leu Thr Pro Arg
145                 150                 155                 160

Tyr
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<210> 185
<211> 1788

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1765)
<223> RXN00877

<400> 185
aaataatggg gctcgccggt gatggttccc gccgggcatt caacggtgac ggaagaggtg 60

gcagacatga tgaaaactct agcaactagt atcggtcact atg act gtt gaa cac 115
Met Thr Val Glu His
1 5

ctg ctc aag ccc agc acc ttg ccc tac cag ctg ccc gat ttc gca gcg 163
Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu Pro Asp Phe Ala Ala
10 15 20

atc aag gtg gct gat ttc ccg ccc gcc ttc gaa ctc gca tta gct gaa 211
Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu Leu Ala Leu Ala Glu
25 30 35

cac gat gct gaa att aca gcg atc gct acc aat gag gac gct cct acc 259
His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn Glu Asp Ala Pro Thr
40 45 50

tgg gag aac acc att gag gcc ctg gaa cgc gca ggc ctg tcc ctc aac 307
Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala Gly Leu Ser Leu Asn
55 60 65

cgc gtc gcc gcc gta ttc ttc aac ttg cag ggc acc gat tcc tcc cct 355
Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly Thr Asp Ser Ser Pro
70 75 80 85

gaa atg gat gaa atc gca gcc act atc gcg ccg aaa ctc tcc gcg cat 403
Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro Lys Leu Ser Ala His
90 95 100

tcg gat gcg att ttc cac aat gct gcg ctt ttc gcg cgc att gag gcc 451
Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe Ala Arg Ile Glu Ala
105 110 115

gta gaa gca ccg gcc gac gag gaa tcg caa cgc ctg ttg tcc cac acc 499
Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg Leu Leu Ser His Thr
120 125 130

aag cgc gct ttt cga cgt cgc ggt gca gca ctc aac gcc gac ggc aag 547
Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu Asn Ala Asp Gly Lys
135 140 145

gcc cga ctg agc acc atc aac cag cgc cta tcg gca ctg tcc gaa cag 595
Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser Ala Leu Ser Glu Gln
150 155 160 165

ttc ggc cgc aac ctg ctt cag gac acc cgc gat ctg gcg gtc aac ttt 643
Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp Leu Ala Val Asn Phe
170 175 180

gaa gaa tct gaa ctt gcc ggt ttt agc gaa gcc cgc ata tcc gcc gcc 691
Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala Arg Ile Ser Ala Ala

```
            185                 190                 195

gct gac tac gca gca gca gtt ggc acc gaa ggc tac gtg gtt cca ctg   739
Ala Asp Tyr Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu
        200                 205                 210

gaa ctg ccc acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc   787
Glu Leu Pro Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala
    215                 220                 225

tcg cgt gca aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg   835
Ser Arg Ala Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu
230                 235                 240                 245

aac aag gac gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc   883
Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala
                250                 255                 260

aca ctt tta ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa   931
Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu
            265                 270                 275

acc gcc gat gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc   979
Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala
        280                 285                 290

cca gcc gcc tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa  1027
Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu
    295                 300                 305

gaa gca gaa gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc  1075
Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe
310                 315                 320                 325

tgg gaa gcc aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa  1123
Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu
                330                 335                 340

ctg cgc aac tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc  1171
Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe
            345                 350                 355

ttc gct gct aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac  1219
Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp
        360                 365                 370

ctg cgc ggt tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct  1267
Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser
    375                 380                 385

gac ggc tcc ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca  1315
Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro
390                 395                 400                 405

tcc aag cgg ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag  1363
Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu
                410                 415                 420

ctg cta ggc acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa  1411
Leu Leu Gly Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys
            425                 430                 435
```

```
cca acc acc ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc   1459
Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile
        440                 445                 450

ttc cac gaa ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc   1507
Phe His Glu Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg
    455                 460                 465

tac cca agc ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc   1555
Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe
470                 475                 480                 485

ccc tcc cag atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc   1603
Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg
                490                 495                 500

aac tac gcc cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg   1651
Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu
            505                 510                 515

ctt gag gca gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat   1699
Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His
        520                 525                 530

gtg agt act tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt   1747
Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys
    535                 540                 545

cca cag cgg atg ccg cac tagtcaatga cattgaccaa tta                 1788
Pro Gln Arg Met Pro His
550                 555
```

<210> 186
<211> 555
<212> PRT
<213> Corynebacterium glutamicum

<400> 186

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Met Thr Val Glu His Leu Leu Lys Pro Ser Thr Leu Pro Tyr Gln Leu
  1               5                  10                  15

Pro Asp Phe Ala Ala Ile Lys Val Ala Asp Phe Pro Pro Ala Phe Glu
             20                  25                  30

Leu Ala Leu Ala Glu His Asp Ala Glu Ile Thr Ala Ile Ala Thr Asn
         35                  40                  45

Glu Asp Ala Pro Thr Trp Glu Asn Thr Ile Glu Ala Leu Glu Arg Ala
     50                  55                  60

Gly Leu Ser Leu Asn Arg Val Ala Ala Val Phe Phe Asn Leu Gln Gly
 65                  70                  75                  80

Thr Asp Ser Ser Pro Glu Met Asp Glu Ile Ala Ala Thr Ile Ala Pro
                 85                  90                  95

Lys Leu Ser Ala His Ser Asp Ala Ile Phe His Asn Ala Ala Leu Phe
            100                 105                 110
```

```
Ala Arg Ile Glu Ala Val Glu Ala Pro Ala Asp Glu Glu Ser Gln Arg
        115                 120                 125

Leu Leu Ser His Thr Lys Arg Ala Phe Arg Arg Arg Gly Ala Ala Leu
    130                 135                 140

Asn Ala Asp Gly Lys Ala Arg Leu Ser Thr Ile Asn Gln Arg Leu Ser
145                 150                 155                 160

Ala Leu Ser Glu Gln Phe Gly Arg Asn Leu Leu Gln Asp Thr Arg Asp
                165                 170                 175

Leu Ala Val Asn Phe Glu Glu Ser Glu Leu Ala Gly Phe Ser Glu Ala
            180                 185                 190

Arg Ile Ser Ala Ala Ala Asp Tyr Ala Ala Ala Val Gly Thr Glu Gly
        195                 200                 205

Tyr Val Val Pro Leu Glu Leu Pro Thr Val Gln Ser Glu Gln Ala Val
    210                 215                 220

Leu Thr Glu Ser Ala Ser Arg Ala Lys Leu Tyr Glu Ala Ser Gln Lys
225                 230                 235                 240

Arg Gly Ala Ser Leu Asn Lys Asp Val Leu Leu Glu Thr Val Arg Leu
                245                 250                 255

Arg Ala Glu Arg Ala Thr Leu Leu Gly Tyr Asp Thr His Ala Asp Tyr
            260                 265                 270

Val Ile Glu Glu Glu Thr Ala Asp Asp Val Ala Ala Val Arg Ala Leu
        275                 280                 285

Leu Tyr Asp Leu Ala Pro Ala Ala Ser Ala Asn Ala Lys Ala Glu Tyr
    290                 295                 300

Lys Leu Ser Ala Glu Glu Ala Glu Glu His Gly Gln Lys Val Gly Ala
305                 310                 315                 320

Ala Asp Trp Ser Phe Trp Glu Ala Lys Val Arg Ala Arg Asp Tyr Ala
                325                 330                 335

Leu Asp Glu Thr Glu Leu Arg Asn Tyr Phe Pro Leu Asn Gln Val Leu
            340                 345                 350

Arg Asp Gly Val Phe Phe Ala Ala Asn Arg Leu Tyr Gly Ile Thr Val
        355                 360                 365

Glu Pro Arg Pro Asp Leu Arg Gly Tyr Ala Glu Gly Val Asp Val Trp
    370                 375                 380

Glu Val Leu Asp Ser Asp Gly Ser Gly Ile Gly Leu Ile Leu Thr Asp
385                 390                 395                 400

Tyr Tyr Gly Arg Pro Ser Lys Arg Gly Gly Ala Trp Met Ser Ser Phe
                405                 410                 415

Val Asp Gln Ser Glu Leu Leu Gly Thr Lys Pro Val Val Val Asn Val
            420                 425                 430

Met Gly Ile Thr Lys Pro Thr Thr Gly Glu Ala Leu Leu Ser Leu Asp
```

```
        435                 440                 445

Glu Val Thr Thr Ile Phe His Glu Phe Gly His Gly Leu His Gly Leu
    450                 455                 460

Leu Ser Lys Val Arg Tyr Pro Ser Phe Ser Gly Thr Ser Val Pro Arg
465                 470                 475                 480

Asp Tyr Val Glu Phe Pro Ser Gln Ile Asn Glu Asn Trp Ala Phe Asp
                485                 490                 495

Pro Ala Val Val Arg Asn Tyr Ala Arg His Val Asp Thr Gly Asp Ile
            500                 505                 510

Ile Pro Asp Ser Leu Leu Glu Ala Val Glu Ala Cys Gly Ile Ser Asp
        515                 520                 525

Arg Val Val Glu His Val Ser Thr Cys Pro His Leu Leu Ser Thr Cys
    530                 535                 540

Pro Val Ser Pro Cys Pro Gln Arg Met Pro His
545                 550                 555
```

Sequence Listing

<210> 187
<211> 1088
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(1065)
<223> FRXA00877

<400> 187

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gca gca gca gtt ggc acc gaa ggc tac gtg gtt cca ctg gaa ctg ccc   48
Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu Glu Leu Pro
  1               5                  10                  15

acc gtg cag tca gag cag gca gta tta acc gaa tcc gcc tcg cgt gca   96
Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala
             20                  25                  30

aag ctt tat gaa gcc tcc cag aag cgt ggc gcc agc ctg aac aag gac  144
Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp
         35                  40                  45

gtg ctg ctc gaa acc gtg cgt ctg cgt gct gaa cgc gcc aca ctt tta  192
Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu
     50                  55                  60

ggc tac gac acc cac gcc gat tac gtc atc gaa gaa gaa acc gcc gat  240
Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp
 65                  70                  75                  80

gac gtc gca gcc gtg cgc gcc ttg ctt tat gat ctc gcc cca gcc gcc  288
Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala
                 85                  90                  95

tct gcc aat gcg aaa gcc gaa tac aaa ctc tcc gca gaa gaa gca gaa  336
Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu
```

```
            100                 105                 110

gaa cac ggc caa aaa gtc ggc gca gct gac tgg agc ttc tgg gaa gcc   384
Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala
        115                 120                 125

aaa gtc cgc gcc cgc gac tac gcc ctg gac gaa acc gaa ctg cgc aac   432
Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn
    130                 135                 140

tac ttc cca ttg aac caa gta ctc cgt gac ggc gtc ttc ttc gct gct   480
Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala
145                 150                 155                 160

aac cgc ctc tac gga atc acc gtg gaa cca cgc cct gac ctg cgc ggt   528
Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly
                165                 170                 175

tac gcc gag ggc gtg gac gtc tgg gaa gtc ctc gat tct gac ggc tcc   576
Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser
            180                 185                 190

ggc atc ggc ctg atc ctt acc gac tac tac ggc cga cca tcc aag cgg   624
Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg
        195                 200                 205

ggc ggc gct tgg atg tcc agc ttt gtc gac caa tcc gag ctg cta ggc   672
Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly
    210                 215                 220

acc aag cca gtc gtg gtc aac gtt atg ggt att acc aaa cca acc acc   720
Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr
225                 230                 235                 240

ggc gaa gca cta ctc agc ctc gat gaa gta acc acc atc ttc cac gaa   768
Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu
                245                 250                 255

ttc ggc cac ggc ctg cac ggc ttg ctg tcc aag gtg cgc tac cca agc   816
Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser
            260                 265                 270

ttc tcc gga acc tcc gtg ccc cgc gac tac gta gaa ttc ccc tcc cag   864
Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
        275                 280                 285

atc aac gaa aac tgg gca ttc gac cct gca gta gtc cgc aac tac gcc   912
Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
    290                 295                 300

cgc cac gtg gac acc ggc gac atc att cca gac tcc ctg ctt gag gca   960
Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
305                 310                 315                 320

gtg gaa gca tgt ggc att tca gac aga gtg gtg gaa cat gtg agt act  1008
Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
                325                 330                 335

tgt ccc cat cta tta tcg acc tgc cct gtc tct ccc tgt cca cag cgg  1056
Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
            340                 345                 350
```

atg ccg cac tagtcaatga cattgaccaa tta 1088
Met Pro His
355

<210> 188
<211> 355
<212> PRT
<213> Corynebacterium glutamicum

<400> 188
Ala Ala Ala Val Gly Thr Glu Gly Tyr Val Val Pro Leu Glu Leu Pro
1 5 10 15

Thr Val Gln Ser Glu Gln Ala Val Leu Thr Glu Ser Ala Ser Arg Ala
20 25 30

Lys Leu Tyr Glu Ala Ser Gln Lys Arg Gly Ala Ser Leu Asn Lys Asp
35 40 45

Val Leu Leu Glu Thr Val Arg Leu Arg Ala Glu Arg Ala Thr Leu Leu
50 55 60

Gly Tyr Asp Thr His Ala Asp Tyr Val Ile Glu Glu Glu Thr Ala Asp
65 70 75 80

Asp Val Ala Ala Val Arg Ala Leu Leu Tyr Asp Leu Ala Pro Ala Ala
85 90 95

Ser Ala Asn Ala Lys Ala Glu Tyr Lys Leu Ser Ala Glu Glu Ala Glu
100 105 110

Glu His Gly Gln Lys Val Gly Ala Ala Asp Trp Ser Phe Trp Glu Ala
115 120 125

Lys Val Arg Ala Arg Asp Tyr Ala Leu Asp Glu Thr Glu Leu Arg Asn
130 135 140

Tyr Phe Pro Leu Asn Gln Val Leu Arg Asp Gly Val Phe Phe Ala Ala
145 150 155 160

Asn Arg Leu Tyr Gly Ile Thr Val Glu Pro Arg Pro Asp Leu Arg Gly
165 170 175

Tyr Ala Glu Gly Val Asp Val Trp Glu Val Leu Asp Ser Asp Gly Ser
180 185 190

Gly Ile Gly Leu Ile Leu Thr Asp Tyr Tyr Gly Arg Pro Ser Lys Arg
195 200 205

Gly Gly Ala Trp Met Ser Ser Phe Val Asp Gln Ser Glu Leu Leu Gly
210 215 220

Thr Lys Pro Val Val Val Asn Val Met Gly Ile Thr Lys Pro Thr Thr
225 230 235 240

Gly Glu Ala Leu Leu Ser Leu Asp Glu Val Thr Thr Ile Phe His Glu
245 250 255

Phe Gly His Gly Leu His Gly Leu Leu Ser Lys Val Arg Tyr Pro Ser

```
            260                 265                 270

Phe Ser Gly Thr Ser Val Pro Arg Asp Tyr Val Glu Phe Pro Ser Gln
        275                 280                 285

Ile Asn Glu Asn Trp Ala Phe Asp Pro Ala Val Val Arg Asn Tyr Ala
    290                 295                 300

Arg His Val Asp Thr Gly Asp Ile Ile Pro Asp Ser Leu Leu Glu Ala
305                 310                 315                 320

Val Glu Ala Cys Gly Ile Ser Asp Arg Val Val Glu His Val Ser Thr
                325                 330                 335

Cys Pro His Leu Leu Ser Thr Cys Pro Val Ser Pro Cys Pro Gln Arg
            340                 345                 350

Met Pro His
        355
```

<210> 189
<211> 663
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(640)
<223> RXN01226

<400> 189
cgtgcgggga aatttaaagt gatgacagtg cacgatcatc atggaggttt cctcacatgg 60

tggcggggcc tgtttttgct tgtggtggac tcatggttgg atg ggg gat gtg aat 115
Met Gly Asp Val Asn
1 5

aac tct ccc ctt tta gtt gtt ggc ctg gga aat ccc ggc ccg aaa tac 163
Asn Ser Pro Leu Leu Val Val Gly Leu Gly Asn Pro Gly Pro Lys Tyr
10 15 20

gtt ggc acc cgc cac aat att ggc ttt gag gtt gca gaa gaa cta gtg 211
Val Gly Thr Arg His Asn Ile Gly Phe Glu Val Ala Glu Glu Leu Val
25 30 35

tcg cgc agc ttt gga tca ttt agt gtg cac aag cgc tcc aac acc gat 259
Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys Arg Ser Asn Thr Asp
40 45 50

atc gcg cag ctt cct ggg cta att gtg gcc aag ccg cgc agc ttt atg 307
Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys Pro Arg Ser Phe Met
55 60 65

aac ctg tcg gga act ccg att cgg gcg ctg tgt gac ttc ttt aag att 355
Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys Asp Phe Phe Lys Ile
70 75 80 85

tcc cca gcc aat gtc atc gtg gtg cat gat gaa ttg gag ctt gat ttc 403
Ser Pro Ala Asn Val Ile Val Val His Asp Glu Leu Glu Leu Asp Phe
90 95 100

```
ggc tca gtg aag cta cgt cag ggt ggc ggg gat cat ggg cac aat ggt   451
Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp His Gly His Asn Gly
            105                 110                 115

ctg aaa tcc acg tcc aaa tct ttg gga act aag gac tat tgg aag ctc   499
Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys Asp Tyr Trp Lys Leu
        120                 125                 130

agc atg ggt atc ggt agg cca ccg ggt cgg atg gat ccg gca agt ttt   547
Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met Asp Pro Ala Ser Phe
    135                 140                 145

gtg ttg aag cct ttt ggc aag caa gaa ctg gcg gat att ccc atc atg   595
Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala Asp Ile Pro Ile Met
150                 155                 160                 165

gcg gct gac gct gca gat ctc gtc gaa aag cat ttg cag cag ggc       640
Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His Leu Gln Gln Gly
                170                 175                 180

tagctacttg cgccgcgcct ctt                                        663
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SEQUENCE LISTING

<210> 190
<211> 180
<212> PRT
<213> Corynebacterium glutamicum

<400> 190

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Met Gly Asp Val Asn Asn Ser Pro Leu Leu Val Val Gly Leu Gly Asn
  1               5                  10                  15

Pro Gly Pro Lys Tyr Val Gly Thr Arg His Asn Ile Gly Phe Glu Val
            20                  25                  30

Ala Glu Glu Leu Val Ser Arg Ser Phe Gly Ser Phe Ser Val His Lys
        35                  40                  45

Arg Ser Asn Thr Asp Ile Ala Gln Leu Pro Gly Leu Ile Val Ala Lys
    50                  55                  60

Pro Arg Ser Phe Met Asn Leu Ser Gly Thr Pro Ile Arg Ala Leu Cys
65                  70                  75                  80

Asp Phe Phe Lys Ile Ser Pro Ala Asn Val Ile Val Val His Asp Glu
                85                  90                  95

Leu Glu Leu Asp Phe Gly Ser Val Lys Leu Arg Gln Gly Gly Gly Asp
            100                 105                 110

His Gly His Asn Gly Leu Lys Ser Thr Ser Lys Ser Leu Gly Thr Lys
        115                 120                 125

Asp Tyr Trp Lys Leu Ser Met Gly Ile Gly Arg Pro Pro Gly Arg Met
    130                 135                 140

Asp Pro Ala Ser Phe Val Leu Lys Pro Phe Gly Lys Gln Glu Leu Ala
145                 150                 155                 160

Asp Ile Pro Ile Met Ala Ala Asp Ala Ala Asp Leu Val Glu Lys His
```

```
                165                 170                 175

Leu Gln Gln Gly
            180


<210> 191
<211> 784
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXN01963

<400> 191
cagattttct ctgtgtgagc tggggttttc tgcatttccc acttgttttt ctccaacact 60

ccacacacac accttcaaag aagaaagttc gaaagattct atg aaa aac cgt aaa   115
                                        Met Lys Asn Arg Lys
                                          1               5

aaa atc atg tct acc ctc acc act gtc tgc gcc gta ctg ggt ata gtt   163
Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala Val Leu Gly Ile Val
                 10                  15                  20

gca gct cat cca ttc cac gcc tct gct gtc atc ggc ggc tct gtc cca   211
Ala Ala His Pro Phe His Ala Ser Ala Val Ile Gly Gly Ser Val Pro
             25                  30                  35

tca act gat tcc gtt gcc aac gct gtc gca aaa atc gga cca ggc gca   259
Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys Ile Gly Pro Gly Ala
         40                  45                  50

ttg aac tgc agc ggt gtc atg atc tca cca tcg tgg gca ctc acc gca   307
Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser Trp Ala Leu Thr Ala
     55                  60                  65

cgc cac tgt gtc gat gac atc aac ata ctc ggc gac atc gac acc atc   355
Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly Asp Ile Asp Thr Ile
 70                  75                  80                  85

acg cct att act cca ggt att cat cgc aat gaa ggt aac tat atg ggt   403
Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu Gly Asn Tyr Met Gly
                 90                  95                 100

gag gtt tac cgc gca ccg tcc ggt gat cta gcg ctc att aat atc aac   451
Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala Leu Ile Asn Ile Asn
             105                 110                 115

ggc gtg cac aag ggc acc att gcg cag ctc ccc aca caa gaa tat cca   499
Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro Thr Gln Glu Tyr Pro
         120                 125                 130

ctg gga acc gct gca cag tca gtc ggt ttt ggt ggc ggt ggt gtc aat   547
Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly Gly Gly Gly Val Asn
     135                 140                 145

atc cgc acc gct gaa tcg gtc aac atg att ctc acc gac ata tat agc   595
Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu Thr Asp Ile Tyr Ser
```

```
150                 155                 160                 165

gtg agg tca ggg aaa ttc cat cac ggt gtc ggt cga tca cac tat ctc   643
Val Arg Ser Gly Lys Phe His His Gly Val Gly Arg Ser His Tyr Leu
                170                 175                 180

ctc ttt gat tat gac agt gct gaa act ggt cga atc cac aaa ggt gat   691
Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg Ile His Lys Gly Asp
            185                 190                 195

tct ggg ggc ccc atc ttc att ggt gac gag gtt gtg ggc att atg tct   739
Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val Val Gly Ile Met Ser
        200                 205                 210

cac ggc aca ata aat aag aac gac ggg tct ttt gat gac gaa tcc       784
His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe Asp Asp Glu Ser
    215                 220                 225


<210> 192
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

<400> 192
Met Lys Asn Arg Lys Lys Ile Met Ser Thr Leu Thr Thr Val Cys Ala
  1               5                  10                  15

Val Leu Gly Ile Val Ala Ala His Pro Phe His Ala Ser Ala Val Ile
             20                  25                  30

Gly Gly Ser Val Pro Ser Thr Asp Ser Val Ala Asn Ala Val Ala Lys
         35                  40                  45

Ile Gly Pro Gly Ala Leu Asn Cys Ser Gly Val Met Ile Ser Pro Ser
     50                  55                  60

Trp Ala Leu Thr Ala Arg His Cys Val Asp Asp Ile Asn Ile Leu Gly
 65                  70                  75                  80

Asp Ile Asp Thr Ile Thr Pro Ile Thr Pro Gly Ile His Arg Asn Glu
                 85                  90                  95

Gly Asn Tyr Met Gly Glu Val Tyr Arg Ala Pro Ser Gly Asp Leu Ala
            100                 105                 110

Leu Ile Asn Ile Asn Gly Val His Lys Gly Thr Ile Ala Gln Leu Pro
        115                 120                 125

Thr Gln Glu Tyr Pro Leu Gly Thr Ala Ala Gln Ser Val Gly Phe Gly
    130                 135                 140

Gly Gly Gly Val Asn Ile Arg Thr Ala Glu Ser Val Asn Met Ile Leu
145                 150                 155                 160

Thr Asp Ile Tyr Ser Val Arg Ser Gly Lys Phe His His Gly Val Gly
                165                 170                 175

Arg Ser His Tyr Leu Leu Phe Asp Tyr Asp Ser Ala Glu Thr Gly Arg
            180                 185                 190
```

Ile His Lys Gly Asp Ser Gly Gly Pro Ile Phe Ile Gly Asp Glu Val
195 200 205

Val Gly Ile Met Ser His Gly Thr Ile Asn Lys Asn Asp Gly Ser Phe
210 215 220

Asp Asp Glu Ser
225

<210> 193
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> RXN00621

<400> 193
aaatgaatcc gggtttttca gtttcggggt gcaaatcaga atgtcgccaa tggcgaacac 60

acgagcgtgc agaagatgtg cgtgactaag atcgggggct atg tct gaa cgc cta 115
Met Ser Glu Arg Leu
1 5

aac gct ccg caa gca cca atc cat ccc atc acc cga acc cac cac ggt 163
Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr Arg Thr His His Gly
10 15 20

att gat ttc gta gac aac tat gaa tgg ctg agg gat aaa gaa tcc caa 211
Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg Asp Lys Glu Ser Gln
25 30 35

gaa acc ttg gac tac ctg gag gcg gag aat gcg ttc acc aag cag gag 259
Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala Phe Thr Lys Gln Glu
40 45 50

act gaa cag cta gcc aca ctg cgg gac aac atc tat gaa gag att aag 307
Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile Tyr Glu Glu Ile Lys
55 60 65

tca cgc gtt aaa gaa acc gac atg tcc atc cca gtg cgt gcc gga aag 355
Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro Val Arg Ala Gly Lys
70 75 80 85

cac tgg tat tac tct cgc act gaa gaa ggc aag agc tac ggc tat tcc 403
His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys Ser Tyr Gly Tyr Ser
90 95 100

tgc cgc att cca gtg act gaa ggg tcg gat gca tgg acc cct cct gtt 451
Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala Trp Thr Pro Pro Val
105 110 115

atc cct gag ggt gag cca gcg cag ggt gaa acc atc atc atg gat gcc 499
Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr Ile Ile Met Asp Ala
120 125 130

aac gag ttg gca gaa ggc cac gaa ttc ttc tcc atg ggt gca tca tct 547
Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser Met Gly Ala Ser Ser

```
    135                 140                 145

gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc   595
Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
150                 155                 160                 165

gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg   643
Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
                170                 175                 180

ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg   691
Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
            185                 190                 195

gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat   739
Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
        200                 205                 210

act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg   787
Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
    215                 220                 225

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act   835
Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
230                 235                 240                 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc   883
Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
                250                 255                 260

tgaagtacgc gtgcttcctt tcg                                        906


<210> 194
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 194
Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
  1               5                  10                  15

Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
             20                  25                  30

Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
         35                  40                  45

Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
     50                  55                  60

Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
 65                  70                  75                  80

Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
                 85                  90                  95

Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
            100                 105                 110

Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
```

```
        115                 120                 125

Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
    130                 135                 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
145                 150                 155                 160

Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
                165                 170                 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
            180                 185                 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
        195                 200                 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
    210                 215                 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
225                 230                 235                 240

Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
                245                 250                 255

Leu Gln Asp His Leu
            260
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09501.1 SEQ LIST

<210> 195
<211> 906
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(883)
<223> FRXA00621

<400> 195
aaatgaatcc gggtttttca gtttcggggt gcaaatcaga atgtcgccaa tggcgaacac 60

acgagcgtgc agaagatgtg cgtgactaag atcgggggct atg tct gaa cgc cta 115
                                    Met Ser Glu Arg Leu
                                      1   5

aac gct ccg caa gca cca atc cat ccc atc acc cga acc cac cac ggt 163
Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr Arg Thr His His Gly
                  10   15   20

att gat ttc gta gac aac tat gaa tgg ctg agg gat aaa gaa tcc caa 211
Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg Asp Lys Glu Ser Gln
              25   30   35

gaa acc ttg gac tac ctg gag gcg gag aat gcg ttc acc aag cag gag 259
Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala Phe Thr Lys Gln Glu
          40   45   50

act gaa cag cta gcc aca ctg cgg gac aac atc tat gaa gag att aag 307
Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile Tyr Glu Glu Ile Lys
```
```

```
     55                  60                  65

tca cgc gtt aaa gaa acc gac atg tcc atc cca gtg cgt gcc gga aag   355
Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro Val Arg Ala Gly Lys
 70                  75                  80                  85

cac tgg tat tac tct cgc act gaa gaa ggc aag agc tac ggc tat tcc   403
His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys Ser Tyr Gly Tyr Ser
                 90                  95                 100

tgc cgc att cca gtg act gaa ggg tcg gat gca tgg acc cct cct gtt   451
Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala Trp Thr Pro Pro Val
            105                 110                 115

atc cct gag ggt gag cca gcg cag ggt gaa acc atc atc atg gat gcc   499
Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr Ile Ile Met Asp Ala
        120                 125                 130

aac gag ttg gca gaa ggc cac gaa ttc ttc tcc atg ggt gca tca tct   547
Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser Met Gly Ala Ser Ser
    135                 140                 145

gtc acc acc tct ggc cgc tac ctt gcg tat tcc acc gat gtc acg ggc   595
Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser Thr Asp Val Thr Gly
150                 155                 160                 165

gaa gag cgc ttt acg ttg cgc atc aag gat cta gaa act ggc gag ctg   643
Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu Glu Thr Gly Glu Leu
                170                 175                 180

ctt cct gat acc ctg act ggc att ttc tac ggt gct act tgg gtg ggg   691
Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly Ala Thr Trp Val Gly
            185                 190                 195

gag gag tac ctc ttt tac cag cgc gtt gat gat gcg tgg cgt cca gat   739
Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp Ala Trp Arg Pro Asp
        200                 205                 210

act gtg tgg cgc cac aag gtg ggt acc ccg gtt gaa gaa gac gtg ttg   787
Thr Val Trp Arg His Lys Val Gly Thr Pro Val Glu Glu Asp Val Leu
    215                 220                 225

gtg tac cac gag cct gat gaa cgt tat tcc acc tgg gtg ggc acc act   835
Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr Trp Val Gly Thr Thr
230                 235                 240                 245

cgt tca gaa aaa gtt cat cct ttt tgg ttg cgc ctc caa gat cac ctc   883
Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg Leu Gln Asp His Leu
                250                 255                 260

tgaagtacgc gtgcttcctt tcg                                        906
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<210> 196
<211> 261
<212> PRT
<213> Corynebacterium glutamicum

<400> 196

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Met Ser Glu Arg Leu Asn Ala Pro Gln Ala Pro Ile His Pro Ile Thr
  1               5                  10                  15
```

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Arg Thr His His Gly Ile Asp Phe Val Asp Asn Tyr Glu Trp Leu Arg
            20                  25                  30

Asp Lys Glu Ser Gln Glu Thr Leu Asp Tyr Leu Glu Ala Glu Asn Ala
        35                  40                  45

Phe Thr Lys Gln Glu Thr Glu Gln Leu Ala Thr Leu Arg Asp Asn Ile
    50                  55                  60

Tyr Glu Glu Ile Lys Ser Arg Val Lys Glu Thr Asp Met Ser Ile Pro
65                  70                  75                  80

Val Arg Ala Gly Lys His Trp Tyr Tyr Ser Arg Thr Glu Glu Gly Lys
                85                  90                  95

Ser Tyr Gly Tyr Ser Cys Arg Ile Pro Val Thr Glu Gly Ser Asp Ala
            100                 105                 110

Trp Thr Pro Pro Val Ile Pro Glu Gly Glu Pro Ala Gln Gly Glu Thr
        115                 120                 125

Ile Ile Met Asp Ala Asn Glu Leu Ala Glu Gly His Glu Phe Phe Ser
    130                 135                 140

Met Gly Ala Ser Ser Val Thr Thr Ser Gly Arg Tyr Leu Ala Tyr Ser
145                 150                 155                 160

Thr Asp Val Thr Gly Glu Glu Arg Phe Thr Leu Arg Ile Lys Asp Leu
                165                 170                 175

Glu Thr Gly Glu Leu Leu Pro Asp Thr Leu Thr Gly Ile Phe Tyr Gly
            180                 185                 190

Ala Thr Trp Val Gly Glu Glu Tyr Leu Phe Tyr Gln Arg Val Asp Asp
        195                 200                 205

Ala Trp Arg Pro Asp Thr Val Trp Arg His Lys Val Gly Thr Pro Val
    210                 215                 220

Glu Glu Asp Val Leu Val Tyr His Glu Pro Asp Glu Arg Tyr Ser Thr
225                 230                 235                 240

Trp Val Gly Thr Thr Arg Ser Glu Lys Val His Pro Phe Trp Leu Arg
                245                 250                 255

Leu Gln Asp His Leu
            260
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<210> 197
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> RXN00622

<400> 197

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ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cacgagcctg atg aac gtt att cca   115
                                            Met Asn Val Ile Pro
                                              1               5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc   163
Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
                 10                  15                  20

gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca   211
Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
             25                  30                  35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac   259
Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
         40                  45                  50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca   307
Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr
     55                  60                  65

cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac   355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp
 70                  75                  80                  85

aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat   403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp
                 90                  95                 100

gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg   451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu
             105                 110                 115

ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc   499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile
         120                 125                 130

gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc   547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile
     135                 140                 145

tac acc gtc gca tcg ggc gga aac cca gaa tgg gac gcc ccc gtc att   595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile
150                 155                 160                 165

cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac   643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr
                170                 175                 180

tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc   691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu
             185                 190                 195

ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act   739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr
         200                 205                 210

gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac   787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp
     215                 220                 225
```

```
ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc   835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser
230                 235                 240                 245

tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg   883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu
                250                 255                 260

atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc   931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly
            265                 270                 275

gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa   979
Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys
        280                 285                 290

aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag   1027
Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln
    295                 300                 305

aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt   1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
310                 315                 320                 325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag   1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
                330                 335                 340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc   1171
Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
            345                 350                 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat   1219
Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
        360                 365                 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca   1267
Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
    375                 380                 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca   1315
Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
390                 395                 400                 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta   1363
Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
                410                 415                 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act   1411
Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
            425                 430                 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg   1459
Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
        440                 445                 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt   1507
Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
    455                 460                 465
```

gtg acc gaa taaaacttgt tcgactagcg aac 1539
Val Thr Glu
470

<210> 198
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 198
Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
1 5 10 15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
20 25 30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
35 40 45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
50 55 60

Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
65 70 75 80

Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
85 90 95

Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg
100 105 110

Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala
115 120 125

Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu
130 135 140

Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp
145 150 155 160

Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala
165 170 175

Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys
180 185 190

Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser
195 200 205

Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu
210 215 220

Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu
225 230 235 240

Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile
245 250 255

Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His
260 265 270

Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys
275 280 285

Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp
290 295 300

Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu
305 310 315 320

Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala
325 330 335

Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro
340 345 350

Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp
355 360 365

Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met
370 375 380

Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
385 390 395 400

Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
405 410 415

Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
420 425 430

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
465 470

<210> 199
<211> 1539
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1516)
<223> FRXA00622

<400> 199
ttttaccagc gcgttgatga tgcgtggcgt ccagatactg tgtggcgcca caaggtgggt 60

accccggttg aagaagacgt gttggtgtac cacgagcctg atg aac gtt att cca 115
Met Asn Val Ile Pro
1 5

cct ggg tgg gca cca ctc gtt cag aaa aag ttc atc ctt ttt ggt tgc 163
Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe Ile Leu Phe Gly Cys
10 15 20

```
gcc tcc aag atc acc tct gaa gta cgc gtg ctt cct ttc gac cag cca   211
Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu Pro Phe Asp Gln Pro
             25                  30                  35

gag ggc acc cct gag gtg ctg att ccg cgc gcg gag ggt gtg gaa tac   259
Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala Glu Gly Val Glu Tyr
         40                  45                  50

gac gtc gat cat gca gtc gta gac ggc tcc gat att tgg ttg gtc aca   307
Asp Val Asp His Ala Val Val Asp Gly Ser Asp Ile Trp Leu Val Thr
     55                  60                  65

cac aac gcc gag ggc ccg aac ttt tcg gtg ggg tgg gct ggc gtc gac   355
His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly Trp Ala Gly Val Asp
 70                  75                  80                  85

aag ctc aat tct ttg gac gcg ctg gcg cca ctc gtc gcg cac aag gat   403
Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu Val Ala His Lys Asp
                 90                  95                 100

gac gtg cgc att gag ggt gtc gat acc tac cgc gat ttc atc atc ctg   451
Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg Asp Phe Ile Ile Leu
             105                 110                 115

ggc tac agg tcc ggc gcg atc ggc cag gtc gcg atc atg aag ctt atc   499
Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala Ile Met Lys Leu Ile
         120                 125                 130

gac gga acc ttc ggc gat ttc caa cag ctg gaa ttt gac gag gaa atc   547
Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu Phe Asp Glu Glu Ile
     135                 140                 145

tac acc gtc gca tcg ggc gga aac cca gaa tgg gac gcc ccc gtc att   595
Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp Asp Ala Pro Val Ile
150                 155                 160                 165

cgc ctt tct tac gga tca ttc acc acc ccg gcg cag ctg ttt aac tac   643
Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala Gln Leu Phe Asn Tyr
                170                 175                 180

tgg att gaa tcc ggc gaa cgc acg ctg ctg aag cag cag gaa gtg ctc   691
Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys Gln Gln Glu Val Leu
             185                 190                 195

ggc gga tac aag ccg tca gac tat gtg gcc tcc cga ttg tgg gtc act   739
Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser Arg Leu Trp Val Thr
         200                 205                 210

gcg aaa gat ggc gcg cag att cca gtg tcc ttg gtg cac cgc acc gac   787
Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu Val His Arg Thr Asp
     215                 220                 225

ctg gat gta tcc aag ccc aac ccc acg ttg ctc tac ggc tat ggt tcc   835
Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu Tyr Gly Tyr Gly Ser
230                 235                 240                 245

tac gaa tca tcc att gat cca ggc ttc tct atc gcg cgt ttg tca ctg   883
Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile Ala Arg Leu Ser Leu
                250                 255                 260
```

```
atg gat cgt ggc atg att ttt gcg att gcc cac gtt cgt ggc ggt ggc   931
Met Asp Arg Gly Met Ile Phe Ala Ile Ala His Val Arg Gly Gly Gly
            265                 270                 275

gaa atg ggt cgt ggc tgg tac gac aac ggc aaa acc acc acg aag aaa   979
Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys Thr Thr Thr Lys Lys
        280                 285                 290

aac acc ttc acc gac ttc att gat gtt gcc gac gcc ctc atc gag cag   1027
Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp Ala Leu Ile Glu Gln
    295                 300                 305

aag att tct gcc cct gaa atg ctg gtt gca gaa ggc ggc tca gct ggt   1075
Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu Gly Gly Ser Ala Gly
310                 315                 320                 325

ggc atg ctc atg ggc gcc att gcc aac atg gcc ggt gac cgc ttc aag   1123
Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala Gly Asp Arg Phe Lys
                330                 335                 340

gcg atc gaa gcc aac gtg cca ttc gtc gat ccg ctg acc tct atg ctc   1171
Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro Leu Thr Ser Met Leu
            345                 350                 355

atg ccg gaa ctg cca ctg acg gtt atc gaa tgg gat gag tgg ggc gat   1219
Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp Asp Glu Trp Gly Asp
        360                 365                 370

cca ctc cac gat aag gac gtc tat gaa tac atg gcg tcg tat gcc cca   1267
Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met Ala Ser Tyr Ala Pro
    375                 380                 385

tat gaa aac atc gag gca aag aac tac ccc aat atc ttg gcc gta aca   1315
Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn Ile Leu Ala Val Thr
390                 395                 400                 405

tcg ctc aac gac acc cga gtg ttg tac gtc gaa cca gcc aaa tgg gta   1363
Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu Pro Ala Lys Trp Val
                410                 415                 420

gcg cag ctt cgg gcg act gca acc ggt gga gaa ttc ctt ctg aaa act   1411
Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu Phe Leu Leu Lys Thr
            425                 430                 435

gaa atg gtt gcc gga cac ggc ggt gtg tca gga cgc tac gaa aag tgg   1459
Glu Met Val Ala Gly His Gly Gly Val Ser Gly Arg Tyr Glu Lys Trp
        440                 445                 450

cgt gag act gca ttt gag tac ggc tgg ttg atc aac caa gca acc ggt   1507
Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile Asn Gln Ala Thr Gly
    455                 460                 465

gtg acc gaa taaaacttgt tcgactagcg aac                            1539
Val Thr Glu
470
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<210> 200
<211> 472
<212> PRT
<213> Corynebacterium glutamicum

<400> 200

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Met Asn Val Ile Pro Pro Gly Trp Ala Pro Leu Val Gln Lys Lys Phe
 1               5                  10                  15

Ile Leu Phe Gly Cys Ala Ser Lys Ile Thr Ser Glu Val Arg Val Leu
            20                  25                  30

Pro Phe Asp Gln Pro Glu Gly Thr Pro Glu Val Leu Ile Pro Arg Ala
        35                  40                  45

Glu Gly Val Glu Tyr Asp Val Asp His Ala Val Val Asp Gly Ser Asp
    50                  55                  60

Ile Trp Leu Val Thr His Asn Ala Glu Gly Pro Asn Phe Ser Val Gly
65                  70                  75                  80

Trp Ala Gly Val Asp Lys Leu Asn Ser Leu Asp Ala Leu Ala Pro Leu
                85                  90                  95

Val Ala His Lys Asp Asp Val Arg Ile Glu Gly Val Asp Thr Tyr Arg
            100                 105                 110

Asp Phe Ile Ile Leu Gly Tyr Arg Ser Gly Ala Ile Gly Gln Val Ala
        115                 120                 125

Ile Met Lys Leu Ile Asp Gly Thr Phe Gly Asp Phe Gln Gln Leu Glu
    130                 135                 140

Phe Asp Glu Glu Ile Tyr Thr Val Ala Ser Gly Gly Asn Pro Glu Trp
145                 150                 155                 160

Asp Ala Pro Val Ile Arg Leu Ser Tyr Gly Ser Phe Thr Thr Pro Ala
                165                 170                 175

Gln Leu Phe Asn Tyr Trp Ile Glu Ser Gly Glu Arg Thr Leu Leu Lys
            180                 185                 190

Gln Gln Glu Val Leu Gly Gly Tyr Lys Pro Ser Asp Tyr Val Ala Ser
        195                 200                 205

Arg Leu Trp Val Thr Ala Lys Asp Gly Ala Gln Ile Pro Val Ser Leu
    210                 215                 220

Val His Arg Thr Asp Leu Asp Val Ser Lys Pro Asn Pro Thr Leu Leu
225                 230                 235                 240

Tyr Gly Tyr Gly Ser Tyr Glu Ser Ser Ile Asp Pro Gly Phe Ser Ile
                245                 250                 255

Ala Arg Leu Ser Leu Met Asp Arg Gly Met Ile Phe Ala Ile Ala His
            260                 265                 270

Val Arg Gly Gly Gly Glu Met Gly Arg Gly Trp Tyr Asp Asn Gly Lys
        275                 280                 285

Thr Thr Thr Lys Lys Asn Thr Phe Thr Asp Phe Ile Asp Val Ala Asp
    290                 295                 300

Ala Leu Ile Glu Gln Lys Ile Ser Ala Pro Glu Met Leu Val Ala Glu
305                 310                 315                 320
```

Gly Gly Ser Ala Gly Gly Met Leu Met Gly Ala Ile Ala Asn Met Ala
325 330 335

Gly Asp Arg Phe Lys Ala Ile Glu Ala Asn Val Pro Phe Val Asp Pro
340 345 350

Leu Thr Ser Met Leu Met Pro Glu Leu Pro Leu Thr Val Ile Glu Trp
355 360 365

Asp Glu Trp Gly Asp Pro Leu His Asp Lys Asp Val Tyr Glu Tyr Met
370 375 380

Ala Ser Tyr Ala Pro Tyr Glu Asn Ile Glu Ala Lys Asn Tyr Pro Asn
385 390 395 400

Ile Leu Ala Val Thr Ser Leu Asn Asp Thr Arg Val Leu Tyr Val Glu
405 410 415

Pro Ala Lys Trp Val Ala Gln Leu Arg Ala Thr Ala Thr Gly Gly Glu
420 425 430

Phe Leu Leu Lys Thr Glu Met Val Ala Gly His Gly Gly Val Ser Gly
435 440 445

Arg Tyr Glu Lys Trp Arg Glu Thr Ala Phe Glu Tyr Gly Trp Leu Ile
450 455 460

Asn Gln Ala Thr Gly Val Thr Glu
465 470

<210> 201
<211> 750
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(727)
<223> RXN02146

<400> 201
ggttctctcg cagagagaga aggagtgggg ataggggcct tccgctccga acccgacagc 60

taactcggtc agcaaacagg aagaatttgg agtttcatca gtg ggt aag cac cgt 115
Val Gly Lys His Arg
1 5

cgc aac aat tca aac gca act cgc aag gct gta gca gca tct gca gtt 163
Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val Ala Ala Ser Ala Val
10 15 20

gcg ctt gga gca acc gca gct atc gcc tcc cca gca cag gca gct gag 211
Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro Ala Gln Ala Ala Glu
25 30 35

gtt gtt gtt cct ggc acc gga atc agc gtt gac atc gct ggc atc gag 259
Val Val Val Pro Gly Thr Gly Ile Ser Val Asp Ile Ala Gly Ile Glu
40 45 50

```
acc act cca ggt ctt aac aac gtt cca gga atc gat cag tgg atc cct   307
Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile Asp Gln Trp Ile Pro
     55                  60                  65

tcc ctt agc agc cag gca gct cct act gct tac gca gcc gtc att gat   355
Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr Ala Ala Val Ile Asp
 70                  75                  80                  85

gca cct gca gca cag gct gca cct gca gca agc acc ggt cag gca atc   403
Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser Thr Gly Gln Ala Ile
                 90                  95                 100

gtt gat gca gcg cgc acc aag att ggt tcc cca tac ggt tgg ggt gct   451
Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro Tyr Gly Trp Gly Ala
            105                 110                 115

acc ggt cct aac gct ttc gac tgc tcc ggc ctt acc tca tgg gca tac   499
Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu Thr Ser Trp Ala Tyr
        120                 125                 130

agc cag gtt ggc aag tcc atc cca cgt acc tcc cag gct cag gct gca   547
Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser Gln Ala Gln Ala Ala
    135                 140                 145

cag ggc acc cct gtt gct tac tct gac ctt cag gct ggc gac atc gtt   595
Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln Ala Gly Asp Ile Val
150                 155                 160                 165

gcg ttc tac tcc ggc gct acc cac gtt ggt atc tac tcc ggc cac ggc   643
Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile Tyr Ser Gly His Gly
                170                 175                 180

acc gtt atc cac gca ctg aac agc agc acc cct ctg tct gag cac tcc   691
Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro Leu Ser Glu His Ser
            185                 190                 195

ttg gat tac atg cca ttc cac tct gca gtt cgt ttc taatctgcat        737
Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg Phe
        200                 205

aaagtcttaa gct                                                   750
```

<210> 202
<211> 209
<212> PRT
<213> Corynebacterium glutamicum

<400> 202

```
Val Gly Lys His Arg Arg Asn Asn Ser Asn Ala Thr Arg Lys Ala Val
  1               5                  10                  15

Ala Ala Ser Ala Val Ala Leu Gly Ala Thr Ala Ala Ile Ala Ser Pro
             20                  25                  30

Ala Gln Ala Ala Glu Val Val Val Pro Gly Thr Gly Ile Ser Val Asp
         35                  40                  45

Ile Ala Gly Ile Glu Thr Thr Pro Gly Leu Asn Asn Val Pro Gly Ile
     50                  55                  60
```

```
Asp Gln Trp Ile Pro Ser Leu Ser Ser Gln Ala Ala Pro Thr Ala Tyr
 65                  70                  75                  80

Ala Ala Val Ile Asp Ala Pro Ala Ala Gln Ala Ala Pro Ala Ala Ser
                 85                  90                  95

Thr Gly Gln Ala Ile Val Asp Ala Ala Arg Thr Lys Ile Gly Ser Pro
            100                 105                 110

Tyr Gly Trp Gly Ala Thr Gly Pro Asn Ala Phe Asp Cys Ser Gly Leu
        115                 120                 125

Thr Ser Trp Ala Tyr Ser Gln Val Gly Lys Ser Ile Pro Arg Thr Ser
    130                 135                 140

Gln Ala Gln Ala Ala Gln Gly Thr Pro Val Ala Tyr Ser Asp Leu Gln
145                 150                 155                 160

Ala Gly Asp Ile Val Ala Phe Tyr Ser Gly Ala Thr His Val Gly Ile
                165                 170                 175

Tyr Ser Gly His Gly Thr Val Ile His Ala Leu Asn Ser Ser Thr Pro
            180                 185                 190

Leu Ser Glu His Ser Leu Asp Tyr Met Pro Phe His Ser Ala Val Arg
        195                 200                 205

Phe
```

Sequence Listing

<210> 203
<211> 807
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(784)
<223> RXN03133

<400> 203

```
ggcgtcaagc acgcactcca ccacatcgat cttcgccccg ccctcgaatg ggacatcatg 60

ggatttcccg aatcccccga cacgctgccc attttgctca gtg acc tgc gcg acc   115
                                            Val Thr Cys Ala Thr
                                              1               5

ccc ctt acg cca cca ctg ctg tgc cac ctc aat cca cgc cac gct ccg   163
Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn Pro Arg His Ala Pro
                  10                  15                  20

ctc acc gat cca cac att gac gct tcc agg cgc cac cgc ggt ccc ttc   211
Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg His Arg Gly Pro Phe
              25                  30                  35

cac gcc act ccc agc tac gca ggc ttt cac ccc tca ttt acc gac gac   259
His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro Ser Phe Thr Asp Asp
          40                  45                  50

acc gcc cgc atg ctg ggc aac cta gcc aaa att ggc gcg gtt gcc acc   307
```

```
Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile Gly Ala Val Ala Thr
     55                  60                  65

tgg gaa aag acg ctt gtc gac gcc gca agc tgg gcc gaa ctc ccc cac   355
Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp Ala Glu Leu Pro His
 70                  75                  80                  85

cca cca gtc atc gtc ggg gat acc ccg ccc tcg act gtc acg ccg gac   403
Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser Thr Val Thr Pro Asp
                 90                  95                 100

aac gcc tgg tac cag ttt cgc gtc ggc aag cat ctt ggt cgc gat gcg   451
Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His Leu Gly Arg Asp Ala
            105                 110                 115

ttc gcg gaa atc gtc atg tgc ctt ggc cac gtg ttt tgc cat cat gtc   499
Phe Ala Glu Ile Val Met Cys Leu Gly His Val Phe Cys His His Val
        120                 125                 130

ccc cag gta tgg tcg aca acc tgc gca tct cag gac gct gat tcc acc   547
Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln Asp Ala Asp Ser Thr
    135                 140                 145

acg atg ctc att gaa gcc gag acc gcg ggg gca ttg gcc atc gct cgc   595
Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala Leu Ala Ile Ala Arg
150                 155                 160                 165

gtc ggc ggc ccg acc cgt cga ggt ggt tcc ttc ttc ggc gat gcc ctt   643
Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe Phe Gly Asp Ala Leu
                170                 175                 180

ctc aaa gag ggg acg cca ctt cct gct ggt ttc cga cta gat gtt gtt   691
Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe Arg Leu Asp Val Val
            185                 190                 195

cta cac gcc gcc tca gaa att gag gat ctg ctg cgc ggt gac acc aca   739
Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu Arg Gly Asp Thr Thr
        200                 205                 210

gcc gtt gtc agc ggc gct tgg tct gtg gag gat cgc cga ggt tac       784
Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp Arg Arg Gly Tyr
    215                 220                 225

taacaaatag gcccaacaaa gag                                        807
```

<210> 204
<211> 228
<212> PRT
<213> Corynebacterium glutamicum

```
<400> 204
Val Thr Cys Ala Thr Pro Leu Thr Pro Pro Leu Leu Cys His Leu Asn
  1               5                  10                  15

Pro Arg His Ala Pro Leu Thr Asp Pro His Ile Asp Ala Ser Arg Arg
             20                  25                  30

His Arg Gly Pro Phe His Ala Thr Pro Ser Tyr Ala Gly Phe His Pro
         35                  40                  45
```

```
Ser Phe Thr Asp Asp Thr Ala Arg Met Leu Gly Asn Leu Ala Lys Ile
     50                  55                  60

Gly Ala Val Ala Thr Trp Glu Lys Thr Leu Val Asp Ala Ala Ser Trp
 65                  70                  75                  80

Ala Glu Leu Pro His Pro Pro Val Ile Val Gly Asp Thr Pro Pro Ser
                 85                  90                  95

Thr Val Thr Pro Asp Asn Ala Trp Tyr Gln Phe Arg Val Gly Lys His
            100                 105                 110

Leu Gly Arg Asp Ala Phe Ala Glu Ile Val Met Cys Leu Gly His Val
        115                 120                 125

Phe Cys His His Val Pro Gln Val Trp Ser Thr Thr Cys Ala Ser Gln
    130                 135                 140

Asp Ala Asp Ser Thr Thr Met Leu Ile Glu Ala Glu Thr Ala Gly Ala
145                 150                 155                 160

Leu Ala Ile Ala Arg Val Gly Gly Pro Thr Arg Arg Gly Gly Ser Phe
                165                 170                 175

Phe Gly Asp Ala Leu Leu Lys Glu Gly Thr Pro Leu Pro Ala Gly Phe
            180                 185                 190

Arg Leu Asp Val Val Leu His Ala Ala Ser Glu Ile Glu Asp Leu Leu
        195                 200                 205

Arg Gly Asp Thr Thr Ala Val Val Ser Gly Ala Trp Ser Val Glu Asp
    210                 215                 220

Arg Arg Gly Tyr
225
```

<210> 205
<211> 1411
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1411)
<223> RXN02820

<400> 205
caacgaaaca aatgcaagcc cccaatcatg ggtttctacc aattaaattt tctttcagaa 60

aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
                                        Met Lys Val Thr Gln
                                          1   5

agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc 163
Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
                 10   15   20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc 211
Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
             25   30   35

```
acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt   259
Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
         40                  45                  50

gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa   307
Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
     55                  60                  65

ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc   355
Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
 70                  75                  80                  85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg   403
Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val
                 90                  95                 100

gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga   451
Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg
            105                 110                 115

gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg   499
Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu
        120                 125                 130

gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att   547
Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Gly Tyr Ile
    135                 140                 145

ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt   595
Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr Ala Ile Asp Gly Arg
150                 155                 160                 165

gaa aca gcg cca gtt gct gct gat gaa aac tat ctc att cat gtt tct   643
Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr Leu Ile His Val Ser
                170                 175                 180

gca gag gat caa acg gca cct gtt cct gat gcc cga cgt tcc ggc agg   691
Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala Arg Arg Ser Gly Arg
            185                 190                 195

tca att ggt gtg cca gga atc gtg gca gcc ctt gga cag ctg cat gat   739
Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu Gly Gln Leu His Asp
        200                 205                 210

tca ttc gga aag acc tcc tgg cag gac gtg ctg aca act ccg cag cag   787
Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu Thr Thr Pro Gln Gln
    215                 220                 225

ctc gca act gat ggt ttt tcc atc agc cct cgc atg tca gca tca att   835
Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg Met Ser Ala Ser Ile
230                 235                 240                 245

gct aac tcc gct gag gat ctc tcc cac gat ccg gaa gct gcc gca tat   883
Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
                250                 255                 260

ttc ctt gat gaa aac ggt gat gcg aag gca ccc ggc aca ctt tta caa   931
Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
            265                 270                 275
```

```
aac cct gac tat gca gaa acg att cgt ctc atc tct gaa ggt ggc ccc   979
Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
        280                 285                 290

gat gcg ttc tac acg ggt gag att gca gca gac atc gtg gaa cgc gcc   1027
Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
    295                 300                 305

acc cgt gag gtt gac ggt ttc aca cca tca ctg atg agc acg gca gat   1075
Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
310                 315                 320                 325

ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac   1123
Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
                330                 335                 340

cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc   1171
Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
            345                 350                 355

aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa   1219
Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
        360                 365                 370

tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa   1267
Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
    375                 380                 385

gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc   1315
Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
390                 395                 400                 405

gat gct tac atc ggt gat cct gct ttc gtg gaa gtt cca gca ggt ggt   1363
Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu Val Pro Ala Gly Gly
                410                 415                 420

gtc caa cag tgg atc aac cat gtc cac acg ggc gaa cac tcc aaa ctt   1411
Val Gln Gln Trp Ile Asn His Val His Thr Gly Glu His Ser Lys Leu
            425                 430                 435
```

<210> 206
<211> 437
<212> PRT
<213> Corynebacterium glutamicum

<400> 206

```
Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr
  1               5                  10                  15

Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
             20                  25                  30

Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
         35                  40                  45

Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
     50                  55                  60

Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
 65                  70                  75                  80
```

Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
85 90 95

Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
100 105 110

Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr
115 120 125

Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
130 135 140

Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
145 150 155 160

Ala Ile Asp Gly Arg Glu Thr Ala Pro Val Ala Ala Asp Glu Asn Tyr
165 170 175

Leu Ile His Val Ser Ala Glu Asp Gln Thr Ala Pro Val Pro Asp Ala
180 185 190

Arg Arg Ser Gly Arg Ser Ile Gly Val Pro Gly Ile Val Ala Ala Leu
195 200 205

Gly Gln Leu His Asp Ser Phe Gly Lys Thr Ser Trp Gln Asp Val Leu
210 215 220

Thr Thr Pro Gln Gln Leu Ala Thr Asp Gly Phe Ser Ile Ser Pro Arg
225 230 235 240

Met Ser Ala Ser Ile Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro
245 250 255

Glu Ala Ala Ala Tyr Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro
260 265 270

Gly Thr Leu Leu Gln Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile
275 280 285

Ser Glu Gly Gly Pro Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp
290 295 300

Ile Val Glu Arg Ala Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu
305 310 315 320

Met Ser Thr Ala Asp Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala
325 330 335

Leu Cys Ala Pro Tyr Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser
340 345 350

Ser Ser Gly Gly Val Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn
355 360 365

Phe Asp Leu Ala Gln Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly
370 375 380

Leu Pro Asn Ala Glu Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu
385 390 395 400

Sequence Listing

```
Ala Tyr Ala Asp Arg Asp Ala Tyr Ile Gly Asp Pro Ala Phe Val Glu
                405                 410                 415

Val Pro Ala Gly Gly Val Gln Gln Trp Ile Asn His Val His Thr Gly
            420                 425                 430

Glu His Ser Lys Leu
        435
```

<210> 207
<211> 507
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(507)
<223> FRXA02820

<400> 207

```
gct aac tcc gct gag gat ctc tcc cac gat ccg gaa gct gcc gca tat   48
Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
  1               5                  10                  15

ttc ctt gat gaa aac ggt gat gcg aag gca ccc ggc aca ctt tta caa   96
Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
             20                  25                  30

aac cct gac tat gca gaa acg att cgt ctc atc tct gaa ggt ggc ccc  144
Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
         35                  40                  45

gat gcg ttc tac acg ggt gag att gca gca gac atc gtg gaa cgc gcc  192
Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
     50                  55                  60

acc cgt gag gtt gac ggt ttc aca cca tca ctg atg agc acg gca gat  240
Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
 65                  70                  75                  80

ttg gct gcc tac act ccg gaa act cgt gaa gct ttg tgt gct ccc tac  288
Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
                 85                  90                  95

cgc gac aag att gtt tgt ggc atg cca ccg tca tca tcg ggt ggc gtc  336
Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
            100                 105                 110

aca gtg atg gaa acc ctg ggt atc ttg aac aac ttt gat ctc gcc caa  384
Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
        115                 120                 125

tac cca ccc act gag gtt ggt ttg gat ggc gga ttg cca aat gcg gaa  432
Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
    130                 135                 140

gct gtt cac ctg att tca gag gct gag cgc ctg gct tat gct gat cgc  480
Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
145                 150                 155                 160
```

gat gct tac atc ggt gat cct gct ttc 507
Asp Ala Tyr Ile Gly Asp Pro Ala Phe
165

<210> 208
<211> 169
<212> PRT
<213> Corynebacterium glutamicum

<400> 208
Ala Asn Ser Ala Glu Asp Leu Ser His Asp Pro Glu Ala Ala Ala Tyr
1 5 10 15

Phe Leu Asp Glu Asn Gly Asp Ala Lys Ala Pro Gly Thr Leu Leu Gln
20 25 30

Asn Pro Asp Tyr Ala Glu Thr Ile Arg Leu Ile Ser Glu Gly Gly Pro
35 40 45

Asp Ala Phe Tyr Thr Gly Glu Ile Ala Ala Asp Ile Val Glu Arg Ala
50 55 60

Thr Arg Glu Val Asp Gly Phe Thr Pro Ser Leu Met Ser Thr Ala Asp
65 70 75 80

Leu Ala Ala Tyr Thr Pro Glu Thr Arg Glu Ala Leu Cys Ala Pro Tyr
85 90 95

Arg Asp Lys Ile Val Cys Gly Met Pro Pro Ser Ser Ser Gly Gly Val
100 105 110

Thr Val Met Glu Thr Leu Gly Ile Leu Asn Asn Phe Asp Leu Ala Gln
115 120 125

Tyr Pro Pro Thr Glu Val Gly Leu Asp Gly Gly Leu Pro Asn Ala Glu
130 135 140

Ala Val His Leu Ile Ser Glu Ala Glu Arg Leu Ala Tyr Ala Asp Arg
145 150 155 160

Asp Ala Tyr Ile Gly Asp Pro Ala Phe
165

<210> 209
<211> 604
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(604)
<223> FRXA02000

<400> 209
caacgaaaca aatgcaagcc cccaatcatg ggtttctacc aattaaattt tctttcagaa 60

aatatctccc cacataaaag ttccttgata ggctcgagag atg aaa gtg acc caa 115
Met Lys Val Thr Gln
1 5

```
agc aca ttc ctt aaa tcg gta gct gcg ttc act gtc gca gcc tta acc   163
Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr Val Ala Ala Leu Thr
                 10                  15                  20

ctg acc atc tct tcg tgt tcc agc ggt gaa gac acc tcc gca agc tcc   211
Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp Thr Ser Ala Ser Ser
             25                  30                  35

acg gat act gaa aac tcc tca acc caa gca gca gcg tct ccc cca ctt   259
Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala Ala Ser Pro Pro Leu
         40                  45                  50

gcg cct tgt gaa ctt ccc gcc gac gct tct gct gaa gag gaa gta gaa   307
Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala Glu Glu Glu Val Glu
     55                  60                  65

ggc act cac aca ggt gaa gat att tct gtt gcc ccg gaa atc ggt acc   355
Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala Pro Glu Ile Gly Thr
 70                  75                  80                  85

ggc tac cgc gag ggc atg acc cct gtt caa acc caa ggt tat gcg gtg   403
Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr Gln Gly Tyr Ala Val
                 90                  95                 100

gca act gca aac ccc atc gct tct gaa gca gcc tgc gcg gtg tta aga   451
Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala Cys Ala Val Leu Arg
             105                 110                 115

gaa ggc ggc act gca gct gat gct ctt gtc acc gcg cag ttt gtt ttg   499
Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr Ala Gln Phe Val Leu
         120                 125                 130

gga ctg acg gaa ccg cag tcg tct ggc ctt ggt ggt ggc gga tac att   547
Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly Gly Gly Gly Tyr Ile
     135                 140                 145

ctg tac tac gac gcc gaa gcc aat gcg gtg aca gcc att gat ggc cgt   595
Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr Ala Ile Asp Gly Arg
150                 155                 160                 165

gaa aca gcg                                                      604
Glu Thr Ala
```

<210> 210
<211> 168
<212> PRT
<213> Corynebacterium glutamicum

<400> 210

```
Met Lys Val Thr Gln Ser Thr Phe Leu Lys Ser Val Ala Ala Phe Thr
  1               5                  10                  15

Val Ala Ala Leu Thr Leu Thr Ile Ser Ser Cys Ser Ser Gly Glu Asp
             20                  25                  30

Thr Ser Ala Ser Ser Thr Asp Thr Glu Asn Ser Ser Thr Gln Ala Ala
         35                  40                  45
```

Ala Ser Pro Pro Leu Ala Pro Cys Glu Leu Pro Ala Asp Ala Ser Ala
50 55 60

Glu Glu Glu Val Glu Gly Thr His Thr Gly Glu Asp Ile Ser Val Ala
65 70 75 80

Pro Glu Ile Gly Thr Gly Tyr Arg Glu Gly Met Thr Pro Val Gln Thr
85 90 95

Gln Gly Tyr Ala Val Ala Thr Ala Asn Pro Ile Ala Ser Glu Ala Ala
100 105 110

Cys Ala Val Leu Arg Glu Gly Gly Thr Ala Ala Asp Ala Leu Val Thr
115 120 125

Ala Gln Phe Val Leu Gly Leu Thr Glu Pro Gln Ser Ser Gly Leu Gly
130 135 140

Gly Gly Gly Tyr Ile Leu Tyr Tyr Asp Ala Glu Ala Asn Ala Val Thr
145 150 155 160

Ala Ile Asp Gly Arg Glu Thr Ala
165

<210> 211
<211> 753
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (53)..(730)
<223> RXN02944

<400> 211
ggggaggtcc caacaggtgg tggcgaagag gtgaccagcg aggtcaacag gggtg aac 58
Val Asn
1

gct cag aat ctt att gat cca gag cat tca atg ggt cag gca act gct 106
Ala Gln Asn Leu Ile Asp Pro Glu His Ser Met Gly Gln Ala Thr Ala
5 10 15

ggt gtg agc cag aac cca gtc atg gct gcc ctg ccg gaa agt ggc acc 154
Gly Val Ser Gln Asn Pro Val Met Ala Ala Leu Pro Glu Ser Gly Thr
20 25 30

agc cat att tcc atc atc gat tcc tat ggc aac gca gca tcg ttg acc 202
Ser His Ile Ser Ile Ile Asp Ser Tyr Gly Asn Ala Ala Ser Leu Thr
35 40 45 50

acc agt gtg gaa gct gct ttc ggt tcc ttc cac ttc acc cgt ggt ttc 250
Thr Ser Val Glu Ala Ala Phe Gly Ser Phe His Phe Thr Arg Gly Phe
55 60 65

att ttg aat aat cag ctg aca gat ttc tcc gct gaa cca ctt gat gag 298
Ile Leu Asn Asn Gln Leu Thr Asp Phe Ser Ala Glu Pro Leu Asp Glu
70 75 80

gac ggc gag ccc gtg gcc aat cgt gtc gag tca gca aag cgc cca cgg 346

```
Asp Gly Glu Pro Val Ala Asn Arg Val Glu Ser Ala Lys Arg Pro Arg
         85                  90                  95

tct tcc atg tcg cca atg cta gtg ttc aac gcc agt ggc gat ggt gaa   394
Ser Ser Met Ser Pro Met Leu Val Phe Asn Ala Ser Gly Asp Gly Glu
    100                 105                 110

atc gcg gat ctg aat atg gtg ctg ggc tcc cct ggc gga tcc ttg att   442
Ile Ala Asp Leu Asn Met Val Leu Gly Ser Pro Gly Gly Ser Leu Ile
115                 120                 125                 130

att cag tac gtg gtg aaa acc ctg gtc aac atc atc gac tgg gat atg   490
Ile Gln Tyr Val Val Lys Thr Leu Val Asn Ile Ile Asp Trp Asp Met
                135                 140                 145

gat cca cag cag gca gtg tct gcg ccc aac ttt ggt gcg atg aac cag   538
Asp Pro Gln Gln Ala Val Ser Ala Pro Asn Phe Gly Ala Met Asn Gln
            150                 155                 160

cct aag act gga ctg gga agc gag cat ccg ctg atc gcc aat gat tca   586
Pro Lys Thr Gly Leu Gly Ser Glu His Pro Leu Ile Ala Asn Asp Ser
        165                 170                 175

gca gag ctt gta tct gaa ctg gaa agc aaa ggc cac gaa gtt aat gtg   634
Ala Glu Leu Val Ser Glu Leu Glu Ser Lys Gly His Glu Val Asn Val
    180                 185                 190

ggc gag caa tcc agt ggc cta tcg gcg ttg gtg aaa aac ggc gac acc   682
Gly Glu Gln Ser Ser Gly Leu Ser Ala Leu Val Lys Asn Gly Asp Thr
195                 200                 205                 210

att gtc ggt ggc gcc gat cca cgt aga gaa ggc gtg gtc ttg ggt ggc   730
Ile Val Gly Gly Ala Asp Pro Arg Arg Glu Gly Val Val Leu Gly Gly
                215                 220                 225

taattagcgc gcagaccacg cag                                        753
```

Deposited Sequence

<210> 212
<211> 226
<212> PRT
<213> Corynebacterium glutamicum

<400> 212

```
Val Asn Ala Gln Asn Leu Ile Asp Pro Glu His Ser Met Gly Gln Ala
  1               5                  10                  15

Thr Ala Gly Val Ser Gln Asn Pro Val Met Ala Ala Leu Pro Glu Ser
             20                  25                  30

Gly Thr Ser His Ile Ser Ile Ile Asp Ser Tyr Gly Asn Ala Ala Ser
         35                  40                  45

Leu Thr Thr Ser Val Glu Ala Ala Phe Gly Ser Phe His Phe Thr Arg
     50                  55                  60

Gly Phe Ile Leu Asn Asn Gln Leu Thr Asp Phe Ser Ala Glu Pro Leu
 65                  70                  75                  80

Asp Glu Asp Gly Glu Pro Val Ala Asn Arg Val Glu Ser Ala Lys Arg
                 85                  90                  95
```

```
Pro Arg Ser Ser Met Ser Pro Met Leu Val Phe Asn Ala Ser Gly Asp
            100                 105                 110

Gly Glu Ile Ala Asp Leu Asn Met Val Leu Gly Ser Pro Gly Gly Ser
        115                 120                 125

Leu Ile Ile Gln Tyr Val Val Lys Thr Leu Val Asn Ile Ile Asp Trp
    130                 135                 140

Asp Met Asp Pro Gln Gln Ala Val Ser Ala Pro Asn Phe Gly Ala Met
145                 150                 155                 160

Asn Gln Pro Lys Thr Gly Leu Gly Ser Glu His Pro Leu Ile Ala Asn
                165                 170                 175

Asp Ser Ala Glu Leu Val Ser Glu Leu Glu Ser Lys Gly His Glu Val
            180                 185                 190

Asn Val Gly Glu Gln Ser Ser Gly Leu Ser Ala Leu Val Lys Asn Gly
        195                 200                 205

Asp Thr Ile Val Gly Gly Ala Asp Pro Arg Arg Glu Gly Val Val Leu
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Gly Gly
225
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SEQUENCE LISTING

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<213> Corynebacterium glutamicum

<220>
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<223> RXS00197

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cggttggcaa ccaacttgta agctaaggag cttccgcctc gtg gca gcc tat ctt   115
                                              Val Ala Ala Tyr Leu
                                                1               5

ctt ggt gtc gta tta ttt ttc ctc ggc atc gca gta acc atc gcg ctt   163
Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala Val Thr Ile Ala Leu
                10                  15                  20

cac gag tgg ggg cac ttc atc aca gcg cgc att ttc gga atg aaa gtg   211
His Glu Trp Gly His Phe Ile Thr Ala Arg Ile Phe Gly Met Lys Val
            25                  30                  35

cgg cgt ttc ttc atc ggt ttc ggc ccg acg gtg ttt gcc aaa aga cgc   259
Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val Phe Ala Lys Arg Arg
        40                  45                  50

ggc gaa acc gtg tac ggc ctt aaa gcg att ccg gtc ggc ggt ttt tgt   307
Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro Val Gly Gly Phe Cys
    55                  60                  65
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gac atc gcg ggg atg act gcc caa gat gaa ctt gat ccg gaa gac ctg   355
Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu Asp Pro Glu Asp Leu
 70                  75                  80                  85

ccg cgc gcc atg tat cta aag ccc tgg tgg cag cgc ata att gtg ctt   403
Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln Arg Ile Ile Val Leu
                90                  95                 100

tcc ggc ggc gtg atc atg aat ctg atc gtc ggc ttt ttg gtg ctt tac   451
Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly Phe Leu Val Leu Tyr
            105                 110                 115

ggc gtg gcg gtg agc tcc gga atc ccg aat ccg gat gtg gat acc acc   499
Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro Asp Val Asp Thr Thr
        120                 125                 130

gcg aca gtc gac acc gtt cag tgc gtg ccg gaa acc caa att tcc gca   547
Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu Thr Gln Ile Ser Ala
    135                 140                 145

act gaa ctg tcc tcc tgc gta ggt tca ggc cca gcg ggc gac gcc ggc   595
Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro Ala Gly Asp Ala Gly
150                 155                 160                 165

att gag cac ggc gat aag att ttg gcc gtc aac ggc caa gag atg gca   643
Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn Gly Gln Glu Met Ala
                170                 175                 180

agc ttc acc gcc atc cgc gat gcg atc ctc gag ctc cca ggc gaa acg   691
Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu Leu Pro Gly Glu Thr
            185                 190                 195

gca acg ctg acg att gaa cgg gag gga acg ctt ttc gac gtc gac ctc   739
Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu Phe Asp Val Asp Leu
        200                 205                 210

cag gtt gcc tct gtc acc cgt ctc gcc tct gac ggt tca gaa att acc   787
Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp Gly Ser Glu Ile Thr
    215                 220                 225

gtc ggc gcg gtg ggc atg tcg agc ctt cca ccg acc gat gtg tac aaa   835
Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro Thr Asp Val Tyr Lys
230                 235                 240                 245

aaa tac ggc cca atc gag ggt gtg gga gca act gca cgt ttc acc ggc   883
Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr Ala Arg Phe Thr Gly
                250                 255                 260

gac atg atc agc gcc acg tgg gat ggc ctc aaa gcc ttc ccg gcg aaa   931
Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys Ala Phe Pro Ala Lys
            265                 270                 275

atc cca ggg gtc gtc gca tcc atc ttc ggt gca gaa cga gat gta gaa   979
Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala Glu Arg Asp Val Glu
        280                 285                 290

agc ccc atg agt gtg gtg ggc gcc gta cgc atc ggc ggc gaa ttt gtc  1027
Ser Pro Met Ser Val Val Gly Ala Val Arg Ile Gly Gly Glu Phe Val
    295                 300                 305
```

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gaa cgt tcc atg tgg gac atg ttc atg atg atg ctg gcc agc ctg aac   1075
Glu Arg Ser Met Trp Asp Met Phe Met Met Met Leu Ala Ser Leu Asn
310                 315                 320                 325

ttc ttc ctc gcg ctg ttt aac ctc gtg ccg ctg cca cca ctt gat ggc   1123
Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu Pro Pro Leu Asp Gly
                330                 335                 340

gga cac att gcc gtg gtg atc tat gaa aaa atc cgc gac ttc ttc cgc   1171
Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile Arg Asp Phe Phe Arg
            345                 350                 355

aaa ctg cgc gga aaa cca gcg ggc ggc cca gcg gat tac acc aaa cta   1219
Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala Asp Tyr Thr Lys Leu
        360                 365                 370

atg ccc gtc acc gta gct gtc gca gcc ttg ctg atg aca gtg gga ggc   1267
Met Pro Val Thr Val Ala Val Ala Ala Leu Leu Met Thr Val Gly Gly
    375                 380                 385

ctg gtc att gtc gcc gat gtg gtc aat ccc atc cga ctc ttt ggc       1312
Leu Val Ile Val Ala Asp Val Val Asn Pro Ile Arg Leu Phe Gly
390                 395                 400

taacgatacg gaattgaact gcc                                        1335
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<210> 214
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<213> Corynebacterium glutamicum

<400> 214

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Val Ala Ala Tyr Leu Leu Gly Val Val Leu Phe Phe Leu Gly Ile Ala
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Val Thr Ile Ala Leu His Glu Trp Gly His Phe Ile Thr Ala Arg Ile
             20                  25                  30

Phe Gly Met Lys Val Arg Arg Phe Phe Ile Gly Phe Gly Pro Thr Val
         35                  40                  45

Phe Ala Lys Arg Arg Gly Glu Thr Val Tyr Gly Leu Lys Ala Ile Pro
     50                  55                  60

Val Gly Gly Phe Cys Asp Ile Ala Gly Met Thr Ala Gln Asp Glu Leu
 65                  70                  75                  80

Asp Pro Glu Asp Leu Pro Arg Ala Met Tyr Leu Lys Pro Trp Trp Gln
                 85                  90                  95

Arg Ile Ile Val Leu Ser Gly Gly Val Ile Met Asn Leu Ile Val Gly
            100                 105                 110

Phe Leu Val Leu Tyr Gly Val Ala Val Ser Ser Gly Ile Pro Asn Pro
        115                 120                 125

Asp Val Asp Thr Thr Ala Thr Val Asp Thr Val Gln Cys Val Pro Glu
    130                 135                 140

Thr Gln Ile Ser Ala Thr Glu Leu Ser Ser Cys Val Gly Ser Gly Pro
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145 150 155 160

Ala Gly Asp Ala Gly Ile Glu His Gly Asp Lys Ile Leu Ala Val Asn
165 170 175

Gly Gln Glu Met Ala Ser Phe Thr Ala Ile Arg Asp Ala Ile Leu Glu
180 185 190

Leu Pro Gly Glu Thr Ala Thr Leu Thr Ile Glu Arg Glu Gly Thr Leu
195 200 205

Phe Asp Val Asp Leu Gln Val Ala Ser Val Thr Arg Leu Ala Ser Asp
210 215 220

Gly Ser Glu Ile Thr Val Gly Ala Val Gly Met Ser Ser Leu Pro Pro
225 230 235 240

Thr Asp Val Tyr Lys Lys Tyr Gly Pro Ile Glu Gly Val Gly Ala Thr
245 250 255

Ala Arg Phe Thr Gly Asp Met Ile Ser Ala Thr Trp Asp Gly Leu Lys
260 265 270

Ala Phe Pro Ala Lys Ile Pro Gly Val Val Ala Ser Ile Phe Gly Ala
275 280 285

Glu Arg Asp Val Glu Ser Pro Met Ser Val Val Gly Ala Val Arg Ile
290 295 300

Gly Gly Glu Phe Val Glu Arg Ser Met Trp Asp Met Phe Met Met Met
305 310 315 320

Leu Ala Ser Leu Asn Phe Phe Leu Ala Leu Phe Asn Leu Val Pro Leu
325 330 335

Pro Pro Leu Asp Gly Gly His Ile Ala Val Val Ile Tyr Glu Lys Ile
340 345 350

Arg Asp Phe Phe Arg Lys Leu Arg Gly Lys Pro Ala Gly Gly Pro Ala
355 360 365

Asp Tyr Thr Lys Leu Met Pro Val Thr Val Ala Val Ala Ala Leu Leu
370 375 380

Met Thr Val Gly Gly Leu Val Ile Val Ala Asp Val Val Asn Pro Ile
385 390 395 400

Arg Leu Phe Gly

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<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(712)
<223> RXS01223

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aggatgctca tggcaccatc ctaggcgcgc ctgccatagg atg act tcc gtg agt 115
Met Thr Ser Val Ser
1 5

ttt ttg tct aaa atc caa gca ctg ttt gcc ccc aag cct gaa ctt ccc 163
Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro Lys Pro Glu Leu Pro
10 15 20

gcc gcc aaa tgg ctg gtc gtg ggc ctg ggc aac ccc ggc gcc aag tac 211
Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn Pro Gly Ala Lys Tyr
25 30 35

gaa tcc acc cga cac aac gtc ggt tac atg tgc caa gac atg ctt atc 259
Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys Gln Asp Met Leu Ile
40 45 50

gac gcc cac cag cag cag ccc ctc acc ccc gcc acg ggc tac aag gcc 307
Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala Thr Gly Tyr Lys Ala
55 60 65

ctc aca acg cag ctc gca cca ggg gtg ctc gcc gtt cga tcc acc act 355
Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala Val Arg Ser Thr Thr
70 75 80 85

ttt atg aac cac tcc ggc caa ggt gtc gca ccg atc gcc gca gcg ttg 403
Phe Met Asn His Ser Gly Gln Gly Val Ala Pro Ile Ala Ala Ala Leu
90 95 100

ggt atc cca gca gag cgc atc atc gtg atc cac gac gag ctc gat ctg 451
Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His Asp Glu Leu Asp Leu
105 110 115

ccc gct gga aaa gta cgc ctg aaa aag ggc gga aac gaa aac ggt cac 499
Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly Asn Glu Asn Gly His
120 125 130

aac ggc ctg aaa tcc ctc acg gaa gag ctc ggc acc aga gac tac ctg 547
Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly Thr Arg Asp Tyr Leu
135 140 145

cgc gtc cgc atc ggc att tca cga cca cca gca gga atg gcc gtg ccc 595
Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala Gly Met Ala Val Pro
150 155 160 165

gac tac gtt ttg gaa cca gtc gat cac gac caa cca ggc att gaa ctt 643
Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln Pro Gly Ile Glu Leu
170 175 180

gcc gcc gag gca gtg gat ttg ctg ctg gcc cag gga tta tct gct gcg 691
Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln Gly Leu Ser Ala Ala
185 190 195

caa aac gct atc cac agc cgc tagattgcta gagattcccg cac 735
Gln Asn Ala Ile His Ser Arg
200

<210> 216

<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 216
Met Thr Ser Val Ser Phe Leu Ser Lys Ile Gln Ala Leu Phe Ala Pro
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Lys Pro Glu Leu Pro Ala Ala Lys Trp Leu Val Val Gly Leu Gly Asn
20 25 30

Pro Gly Ala Lys Tyr Glu Ser Thr Arg His Asn Val Gly Tyr Met Cys
35 40 45

Gln Asp Met Leu Ile Asp Ala His Gln Gln Gln Pro Leu Thr Pro Ala
50 55 60

Thr Gly Tyr Lys Ala Leu Thr Thr Gln Leu Ala Pro Gly Val Leu Ala
65 70 75 80

Val Arg Ser Thr Thr Phe Met Asn His Ser Gly Gln Gly Val Ala Pro
85 90 95

Ile Ala Ala Ala Leu Gly Ile Pro Ala Glu Arg Ile Ile Val Ile His
100 105 110

Asp Glu Leu Asp Leu Pro Ala Gly Lys Val Arg Leu Lys Lys Gly Gly
115 120 125

Asn Glu Asn Gly His Asn Gly Leu Lys Ser Leu Thr Glu Glu Leu Gly
130 135 140

Thr Arg Asp Tyr Leu Arg Val Arg Ile Gly Ile Ser Arg Pro Pro Ala
145 150 155 160

Gly Met Ala Val Pro Asp Tyr Val Leu Glu Pro Val Asp His Asp Gln
165 170 175

Pro Gly Ile Glu Leu Ala Ala Glu Ala Val Asp Leu Leu Leu Ala Gln
180 185 190

Gly Leu Ser Ala Ala Gln Asn Ala Ile His Ser Arg
195 200

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<211> 1365
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(1342)
<223> RXS01642

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ggaatgctgc gcggtcttga tattggattc ggtggataag atg cgc aga ctc atc 115
Met Arg Arg Leu Ile
1 5

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gcg gtt agc ttg gcc gct ctg ttt atg ttg gct tcc act cca gcg acg   163
Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala Ser Thr Pro Ala Thr
                10                  15                  20

agg gca cag gaa gta gaa gct ctc gct tgc ccc gag gta gcg atc gcc   211
Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro Glu Val Ala Ile Ala
            25                  30                  35

gat cct tcc tcc gca gtt tta gat gaa cac ctt tcg cag tca tta tcc   259
Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu Ser Gln Ser Leu Ser
        40                  45                  50

caa gct cac caa cta gca act ggc gcc ggt gtg atg gtg gca gtc atc   307
Gln Ala His Gln Leu Ala Thr Gly Ala Gly Val Met Val Ala Val Ile
    55                  60                  65

gac acc gga gta tcc ctg cat cca cgt ctg ccc cac tta att ccc ggc   355
Asp Thr Gly Val Ser Leu His Pro Arg Leu Pro His Leu Ile Pro Gly
70                  75                  80                  85

ggt gat ttc gtg ggc gcc cac caa agc ccc gat gtg cca ggt gaa ctt   403
Gly Asp Phe Val Gly Ala His Gln Ser Pro Asp Val Pro Gly Glu Leu
                90                  95                  100

atc gat tgc gac ggc cac ggc acc atc gtc gcc gga atc atc gcc tcc   451
Ile Asp Cys Asp Gly His Gly Thr Ile Val Ala Gly Ile Ile Ala Ser
            105                 110                 115

caa gga aac ccc ggc acc ggc tgg cca tat gac ggc agc tcc gat cct   499
Gln Gly Asn Pro Gly Thr Gly Trp Pro Tyr Asp Gly Ser Ser Asp Pro
        120                 125                 130

tat atc ggt gtc gcc cca gat tcc gga atc atc tcc att aaa caa acc   547
Tyr Ile Gly Val Ala Pro Asp Ser Gly Ile Ile Ser Ile Lys Gln Thr
    135                 140                 145

agc tca tat gtg cgt act cgt gaa gat tcc aac gtc gga acg ctg agc   595
Ser Ser Tyr Val Arg Thr Arg Glu Asp Ser Asn Val Gly Thr Leu Ser
150                 155                 160                 165

acc ctg gcg gaa tcc atc cac cga gct ctc gat tcc ggt gcc cac gtg   643
Thr Leu Ala Glu Ser Ile His Arg Ala Leu Asp Ser Gly Ala His Val
                170                 175                 180

atc aat att tcc gtg gtg tcc tgt ttg ccc caa tca ccc gac gag gcc   691
Ile Asn Ile Ser Val Val Ser Cys Leu Pro Gln Ser Pro Asp Glu Ala
            185                 190                 195

gca tcg ttc cag cct ctg acg gat gct ctt aac aga gca gaa ctt caa   739
Ala Ser Phe Gln Pro Leu Thr Asp Ala Leu Asn Arg Ala Glu Leu Gln
        200                 205                 210

ggg gtg ata gtg gtg gca gca gca gga aac ctc ggg cag gat tgt cca   787
Gly Val Ile Val Val Ala Ala Ala Gly Asn Leu Gly Gln Asp Cys Pro
    215                 220                 225

gtt gga tct acc gtt tat cct gca cat tca gac act gtg ctc tct gtg   835
Val Gly Ser Thr Val Tyr Pro Ala His Ser Asp Thr Val Leu Ser Val
230                 235                 240                 245
```

```
tcg gca cgt ttt gat tct cac acg ctt gca gaa tat tcc atg cct ggc   883
Ser Ala Arg Phe Asp Ser His Thr Leu Ala Glu Tyr Ser Met Pro Gly
                250                 255                 260

aac caa caa atc ctc tct gca cca agc cac att cag gct ggt cta tca   931
Asn Gln Gln Ile Leu Ser Ala Pro Ser His Ile Gln Ala Gly Leu Ser
            265                 270                 275

ccg cgt ggc gac ggc ttc gcc agc cac atg atc acc acc gct ggc gaa   979
Pro Arg Gly Asp Gly Phe Ala Ser His Met Ile Thr Thr Ala Gly Glu
        280                 285                 290

agc ccc ttc gag ggc acc agt ttt gcc gct cca gtt gtc agc gcc aca   1027
Ser Pro Phe Glu Gly Thr Ser Phe Ala Ala Pro Val Val Ser Ala Thr
    295                 300                 305

gct gca ctg ctt cgc cag cat ttt ccc ttt gcc aca ccc tat gaa att   1075
Ala Ala Leu Leu Arg Gln His Phe Pro Phe Ala Thr Pro Tyr Glu Ile
310                 315                 320                 325

cgt gca cga atc ttc aac agc atc gac cct gca aga ggc gct att gat   1123
Arg Ala Arg Ile Phe Asn Ser Ile Asp Pro Ala Arg Gly Ala Ile Asp
                330                 335                 340

ccc tac ctg gca ctt act caa gaa atc tat ccc acc act ccc ctg gtt   1171
Pro Tyr Leu Ala Leu Thr Gln Glu Ile Tyr Pro Thr Thr Pro Leu Val
            345                 350                 355

cat gag atc gca cta agt gtt ccc acg ccg ccg gat gat tct cca cgg   1219
His Glu Ile Ala Leu Ser Val Pro Thr Pro Pro Asp Asp Ser Pro Arg
        360                 365                 370

gag cgg ggc atc cta gtt acc gca atc att gtt ggg ttg ctc gca gtg   1267
Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val Gly Leu Leu Ala Val
    375                 380                 385

tta gct gtg ctg atg gga cta cgc cga att cat cat cac tcg gcc ttt   1315
Leu Ala Val Leu Met Gly Leu Arg Arg Ile His His His Ser Ala Phe
390                 395                 400                 405

caa aaa gct agc tca agt gtt atc act taatctatga ggcaccgttc         1362
Gln Lys Ala Ser Ser Ser Val Ile Thr
                410

aga                                                              1365


<210> 218
<211> 414
<212> PRT
<213> Corynebacterium glutamicum

<400> 218
Met Arg Arg Leu Ile Ala Val Ser Leu Ala Ala Leu Phe Met Leu Ala
  1               5                  10                  15

Ser Thr Pro Ala Thr Arg Ala Gln Glu Val Glu Ala Leu Ala Cys Pro
            20                  25                  30

Glu Val Ala Ile Ala Asp Pro Ser Ser Ala Val Leu Asp Glu His Leu
        35                  40                  45
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Asp Asp Ser Pro Arg Glu Arg Gly Ile Leu Val Thr Ala Ile Ile Val
    370                 375                 380

Gly Leu Leu Ala Val Leu Ala Val Leu Met Gly Leu Arg Arg Ile His
385                 390                 395                 400

His His Ser Ala Phe Gln Lys Ala Ser Ser Ser Val Ile Thr
                405                 410


<210> 219
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01728

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ggaaagtgat tttggcacct gcccgcagtt gaaggaagct atg gca gat gcc gtt   115
                                            Met Ala Asp Ala Val
                                              1               5

gag cgc gag gtc ttc gga tac cca cca gat gct act ggg ttg aat gat   163
Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala Thr Gly Leu Asn Asp
                  10                  15                  20

gcg ttg act gga ttc tac gag cgt cgc tat ggg ttt ggc cca aat ccg   211
Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly Phe Gly Pro Asn Pro
              25                  30                  35

gaa agt gtt ttc gcc att ccg gat gtg gtt cgt ggc ctg aag ctt gcc   259
Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg Gly Leu Lys Leu Ala
          40                  45                  50

att gag cat ttc act aag cct ggt tcg gcg atc att gtg ccg ttg cct   307
Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile Ile Val Pro Leu Pro
      55                  60                  65

gca tac cct cct ttc att gag ttg cct aag gtg act ggt cgt cag gcg   355
Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val Thr Gly Arg Gln Ala
  70                  75                  80                  85

atc tac att gat gcg cat gag tac gat ttg aag gaa att gag aag gcc   403
Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys Glu Ile Glu Lys Ala
                  90                  95                 100

ttc gct gac ggt gcg gga tca ctg ttg ttc tgc aat cca cac aac cca   451
Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys Asn Pro His Asn Pro
              105                 110                 115

ctg ggc acg gtc ttt tct gaa gag tac atc cgc gag ctc acc gat att   499
Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg Glu Leu Thr Asp Ile
          120                 125                 130

gcg gcg aag tac gat gcc cgc atc atc gtc gat gag atc cac gcg cca   547
Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp Glu Ile His Ala Pro
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    135                 140                 145

ctg gtt tat gaa ggc acc cat gtg gtt gct gct ggt gtt tct gag aac   595
Leu Val Tyr Glu Gly Thr His Val Val Ala Ala Gly Val Ser Glu Asn
150                 155                 160                 165

gct gca aac act tgc atc acc atc acc gca act tct aag gcg tgg aac   643
Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr Ser Lys Ala Trp Asn
                170                 175                 180

act gct ggt ttg aag tgt gct cag atc ttc ttc agt aat gaa gcc gat   691
Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe Ser Asn Glu Ala Asp
            185                 190                 195

gtg aag gcc tgg aag aat ttg tcg gat att acc cgt gac ggt gtg tcc   739
Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr Arg Asp Gly Val Ser
        200                 205                 210

atc ctt gga ttg atc gct gcg gag aca gtg tac aac gag ggc gaa gaa   787
Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr Asn Glu Gly Glu Glu
    215                 220                 225

ttc ctt gat gag tca att cag att ctc aag gac aac cgt gac ttt gcg   835
Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp Asn Arg Asp Phe Ala
230                 235                 240                 245

gct gct gaa ctg gaa aag ctt ggc gtg aag gtc tac gca ccg gac tcc   883
Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val Tyr Ala Pro Asp Ser
                250                 255                 260

act tat ttg atg tgg ttg gac ttc gct ggc acc aag atc gaa gag gcg   931
Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr Lys Ile Glu Glu Ala
            265                 270                 275

cct tct aaa att ctt cgt gag gag ggt aag gtc atg ctg aat gat ggc   979
Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val Met Leu Asn Asp Gly
        280                 285                 290

gca gct ttt ggt ggt ttc acc acc tgc gct cgt ctt aat ttt gcg tgt   1027
Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg Leu Asn Phe Ala Cys
    295                 300                 305

tcc aga gag acc ctt gag gag ggg ctg cgc cgt atc gcc agc gtg ttg   1075
Ser Arg Glu Thr Leu Glu Glu Gly Leu Arg Arg Ile Ala Ser Val Leu
310                 315                 320                 325

taaataatga gtaaaaagtc tgt                                        1098


<210> 220
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 220
Met Ala Asp Ala Val Glu Arg Glu Val Phe Gly Tyr Pro Pro Asp Ala
  1               5                  10                  15

Thr Gly Leu Asn Asp Ala Leu Thr Gly Phe Tyr Glu Arg Arg Tyr Gly
             20                  25                  30
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Phe Gly Pro Asn Pro Glu Ser Val Phe Ala Ile Pro Asp Val Val Arg
         35                  40                  45

Gly Leu Lys Leu Ala Ile Glu His Phe Thr Lys Pro Gly Ser Ala Ile
     50                  55                  60

Ile Val Pro Leu Pro Ala Tyr Pro Pro Phe Ile Glu Leu Pro Lys Val
 65                  70                  75                  80

Thr Gly Arg Gln Ala Ile Tyr Ile Asp Ala His Glu Tyr Asp Leu Lys
                 85                  90                  95

Glu Ile Glu Lys Ala Phe Ala Asp Gly Ala Gly Ser Leu Leu Phe Cys
            100                 105                 110

Asn Pro His Asn Pro Leu Gly Thr Val Phe Ser Glu Glu Tyr Ile Arg
        115                 120                 125

Glu Leu Thr Asp Ile Ala Ala Lys Tyr Asp Ala Arg Ile Ile Val Asp
    130                 135                 140

Glu Ile His Ala Pro Leu Val Tyr Glu Gly Thr His Val Val Ala Ala
145                 150                 155                 160

Gly Val Ser Glu Asn Ala Ala Asn Thr Cys Ile Thr Ile Thr Ala Thr
                165                 170                 175

Ser Lys Ala Trp Asn Thr Ala Gly Leu Lys Cys Ala Gln Ile Phe Phe
            180                 185                 190

Ser Asn Glu Ala Asp Val Lys Ala Trp Lys Asn Leu Ser Asp Ile Thr
        195                 200                 205

Arg Asp Gly Val Ser Ile Leu Gly Leu Ile Ala Ala Glu Thr Val Tyr
    210                 215                 220

Asn Glu Gly Glu Glu Phe Leu Asp Glu Ser Ile Gln Ile Leu Lys Asp
225                 230                 235                 240

Asn Arg Asp Phe Ala Ala Ala Glu Leu Glu Lys Leu Gly Val Lys Val
                245                 250                 255

Tyr Ala Pro Asp Ser Thr Tyr Leu Met Trp Leu Asp Phe Ala Gly Thr
            260                 265                 270

Lys Ile Glu Glu Ala Pro Ser Lys Ile Leu Arg Glu Glu Gly Lys Val
        275                 280                 285

Met Leu Asn Asp Gly Ala Ala Phe Gly Gly Phe Thr Thr Cys Ala Arg
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Ile Ala Ser Val Leu
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Met Ser Pro Thr Val
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Leu Pro Ala Thr Gln Ala Asp Phe Pro Lys Ile Val Asp Val Leu Val
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gaa gca ttc gcc aac gat cca gca ttt tta cga tgg atc ccg cag ccg 211
Glu Ala Phe Ala Asn Asp Pro Ala Phe Leu Arg Trp Ile Pro Gln Pro
25 30 35

gac ccc ggt tca gca aag ctt cga gca ctt ttc gaa ctg cag att gag 259
Asp Pro Gly Ser Ala Lys Leu Arg Ala Leu Phe Glu Leu Gln Ile Glu
40 45 50

aag cag tat gca gtg gcg gga aat att gat gtc gcg cgt gat tct gag 307
Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val Ala Arg Asp Ser Glu
55 60 65

gga gaa atc gtc ggc gtc gcg tta tgg gat cgg cca gat ggt aat cac 355
Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg Pro Asp Gly Asn His
70 75 80 85

agt gcc aaa gat caa gca gcg atg ctc ccc cgg ctc gtc tcc att ttc 403
Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg Leu Val Ser Ile Phe
90 95 100

ggg atc aag gct gca cac gtg gcg tgg acg gat ttg agt tcg gct cgt 451
Gly Ile Lys Ala Ala His Val Ala Trp Thr Asp Leu Ser Ser Ala Arg
105 110 115

ttc cac ccc aaa ttc ccc cat tgg tac ctc tac acc gtg gca aca tct 499
Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr Thr Val Ala Thr Ser
120 125 130

agc tct gcc cgt gga acg gat gtt ggc agt gcg ctt ctt aat cac gga 547
Ser Ser Ala Arg Gly Thr Asp Val Gly Ser Ala Leu Leu Asn His Gly
135 140 145

atc gct cgc gcg gct gat gaa gct atc tat ttg gag gcg acg ccg act 595
Ile Ala Arg Ala Ala Asp Glu Ala Ile Tyr Leu Glu Ala Thr Pro Thr
150 155 160 165

cgt gcg gct caa cta tat aac cgt ctg gga ttc gtg ccc ttg ggt tat 643
Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe Val Pro Leu Gly Tyr
170 175 180

atc ccc tca gat gat gat ggc act cct gaa ctg gcg atg tgg aaa ccg 691
Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu Ala Met Trp Lys Pro
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35 40 45

Glu Leu Gln Ile Glu Lys Gln Tyr Ala Val Ala Gly Asn Ile Asp Val
50 55 60

Ala Arg Asp Ser Glu Gly Glu Ile Val Gly Val Ala Leu Trp Asp Arg
65 70 75 80

Pro Asp Gly Asn His Ser Ala Lys Asp Gln Ala Ala Met Leu Pro Arg
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Leu Val Ser Ile Phe Gly Ile Lys Ala Ala His Val Ala Trp Thr Asp
100 105 110

Leu Ser Ser Ala Arg Phe His Pro Lys Phe Pro His Trp Tyr Leu Tyr
115 120 125

Thr Val Ala Thr Ser Ser Ser Ala Arg Gly Thr Asp Val Gly Ser Ala
130 135 140

Leu Leu Asn His Gly Ile Ala Arg Ala Ala Asp Glu Ala Ile Tyr Leu
145 150 155 160

Glu Ala Thr Pro Thr Arg Ala Ala Gln Leu Tyr Asn Arg Leu Gly Phe
165 170 175

Val Pro Leu Gly Tyr Ile Pro Ser Asp Asp Asp Gly Thr Pro Glu Leu
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Ala Met Trp Lys Pro Pro Ala Met Pro Thr Val
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Val Ser Pro Ile Ile
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cgt aaa ttg agt atc ccc gag ttc acc acc aac acc cca gtg ttg gtg 163
Arg Lys Leu Ser Ile Pro Glu Phe Thr Thr Asn Thr Pro Val Leu Val
10 15 20

gat atc tac atc gca gcg atg aac tat gac aaa gca atc agg gat acc 211
Asp Ile Tyr Ile Ala Ala Met Asn Tyr Asp Lys Ala Ile Arg Asp Thr
25 30 35

cgg atc gaa gtc tgg cgg aga aac tcc cag aac ccc gga ttc aca gca 259
Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn Pro Gly Phe Thr Ala
40 45 50

gtg gca gcg ctg atg gat gat cag gtc gtg ggc gtg gcc tat ggc ttc 307
Val Ala Ala Leu Met Asp Asp Gln Val Val Gly Val Ala Tyr Gly Phe
55 60 65

aat ggc agc cca gat cat tgg tgg caa cac caa tta cgc cgg gga ctc 355
Asn Gly Ser Pro Asp His Trp Trp Gln His Gln Leu Arg Arg Gly Leu
70 75 80 85

cga caa caa gga ggc ccg acg gaa gag gaa atc cat atc atc cac aac 403
Arg Gln Gln Gly Gly Pro Thr Glu Glu Glu Ile His Ile Ile His Asn
90 95 100

tac ttt gag gtt gcg gaa gtt cat gtt cag cct ggc ttc caa ggt cac 451
Tyr Phe Glu Val Ala Glu Val His Val Gln Pro Gly Phe Gln Gly His
105 110 115

ggc att ggc cga aag ctg atg cat gaa ctg tta aaa gac aaa caa aac 499
Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu Lys Asp Lys Gln Asn
120 125 130

act ttt gcc att ttg tct aca ccc gag gtc gac gat gag gcg aac cat 547
Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp Asp Glu Ala Asn His
135 140 145

gcg ttt agc ctg tat cgc tct ctc ggc ttc act gac ttg ctc agg cag 595
Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr Asp Leu Leu Arg Gln
150 155 160 165

ttt agg ttt gac ggg gat caa cgg ccg ttt gcc gta ttg atc acc gcc 643
Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala Val Leu Ile Thr Ala
170 175 180

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Leu Pro Leu His Asp Ser
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Ala Ile Arg Asp Thr Arg Ile Glu Val Trp Arg Arg Asn Ser Gln Asn
35 40 45

Pro Gly Phe Thr Ala Val Ala Ala Leu Met Asp Asp Gln Val Val Gly
50 55 60

Val Ala Tyr Gly Phe Asn Gly Ser Pro Asp His Trp Trp Gln His Gln
65 70 75 80

Leu Arg Arg Gly Leu Arg Gln Gln Gly Gly Pro Thr Glu Glu Glu Ile
85 90 95

His Ile Ile His Asn Tyr Phe Glu Val Ala Glu Val His Val Gln Pro
100 105 110

Gly Phe Gln Gly His Gly Ile Gly Arg Lys Leu Met His Glu Leu Leu
115 120 125

Lys Asp Lys Gln Asn Thr Phe Ala Ile Leu Ser Thr Pro Glu Val Asp
130 135 140

Asp Glu Ala Asn His Ala Phe Ser Leu Tyr Arg Ser Leu Gly Phe Thr
145 150 155 160

Asp Leu Leu Arg Gln Phe Arg Phe Asp Gly Asp Gln Arg Pro Phe Ala
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Val Leu Ile Thr Ala Leu Pro Leu His Asp Ser
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Leu Trp Asp Val Leu
1 5

gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc 163
Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
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cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct 211

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Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
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gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att   259
Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
        40                  45                  50

cgc atg ccg tct ggt acg cgt gac ctt tac atc gct att ttg gcc act   307
Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
    55                  60                  65

ctc gct gct ggt gct gct tac gtg cca gtt gat gca gat gat cct gaa   355
Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp Ala Asp Asp Pro Glu
70                  75                  80                  85

gag cgc gcc gag atg gtg ttt ggt gaa gca aat att aat gcg ctt ttc   403
Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn Ile Asn Ala Leu Phe
                90                  95                  100

gac gcc acc ggc ttc cat atg ctt cgc ccg acc gcg ggc ggc gat acc   451
Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr Ala Gly Gly Asp Thr
            105                 110                 115

cgt aga cca cgc ttg gat gat acg gcg tgg att atc ttt act tcc ggt   499
Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly
        120                 125                 130

tcc acc ggc aag cct aag ggt gtg gct gtg tcc cac cgt tca gct gcg   547
Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser His Arg Ser Ala Ala
    135                 140                 145

gct ttc gtg gat gcc gaa gca caa atg ttc ctt gtc gat cac cct tcc   595
Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu Val Asp His Pro Ser
150                 155                 160                 165

ggc ccc ctt ggc cca gaa gac cga gtc ctt gcg gga ttg tct gta gcc   643
Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala Gly Leu Ser Val Ala
                170                 175                 180

ttt gac gca tct tgt gag gaa atg tgg ttg gcc tgg ggc cac ggc gcc   691
Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala Trp Gly His Gly Ala
            185                 190                 195

tgc ttg gtg cca gca cca cgc tcc cta gtc cgt tcc ggt atg gac ttg   739
Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg Ser Gly Met Asp Leu
        200                 205                 210

ggc cca tgg ctg att cgc cgc gac atc agt gtc gtc tcc acc gtc cca   787
Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val Val Ser Thr Val Pro
    215                 220                 225

act ctg gct ggt ctg tgg cca gca gaa gca ttg tca cag gtc cgc ttg   835
Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu Ser Gln Val Arg Leu
230                 235                 240                 245

ctc atc gtc ggc ggc gag gct tgc tcg cag gag ctc gtt gaa cgc tta   883
Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu Leu Val Glu Arg Leu
                250                 255                 260

tcg acg cct gac cgc gag gtg tgg aac act tac ggc ccc acc gaa gca   931
Ser Thr Pro Asp Arg Glu Val Trp Asn Thr Tyr Gly Pro Thr Glu Ala
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            265                 270                 275

acg gtg gtt gcc tgt ggc act caa ctc tat gct ggt cag cca gtg ggc   979
Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala Gly Gln Pro Val Gly
        280                 285                 290

att ggt ttg cca ctt gct ggt tgg gat ctt gtt gtt gtc gac gat gcc   1027
Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val Val Val Asp Asp Ala
    295                 300                 305

ggc gaa cct gtc gga atc ggc gag gtc ggc gaa ttg gtc atc ggt ggt   1075
Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu Leu Val Ile Gly Gly
310                 315                 320                 325

gtg ggt ctt gca cgc tac ctt gat cca gaa aaa gac cgc gag aag tat   1123
Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys Asp Arg Glu Lys Tyr
                330                 335                 340

gcg cca ctg aag tct gtt ggt tgg acc cgc gct tat cgt tcc ggt gac   1171
Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala Tyr Arg Ser Gly Asp
            345                 350                 355

cac gtt cgt ctg gaa gaa gat ggc ctc tac ttt gtg ggc cgc gtt gat   1219
His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe Val Gly Arg Val Asp
        360                 365                 370

gat cag gtg aaa atc ggc ggt cga cgc atc gag ctc ggt gaa gtt gat   1267
Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu Leu Gly Glu Val Asp
    375                 380                 385

gcc aat gtg gca gcg ctt tcc aac gtt cgt tcc tcc gca gtg gtt gtt   1315
Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser Ser Ala Val Val Val
390                 395                 400                 405

cag acc act ggt gcg gat caa aaa gtt ctg gtt gca tac gtt tct ttg   1363
Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val Ala Tyr Val Ser Leu
                410                 415                 420

gaa gat gct gca gct gga ttt gat cac aac gtc gcg act gcc cga ctc   1411
Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val Ala Thr Ala Arg Leu
            425                 430                 435

acc gaa acc atg cct gct gct ttg gtt ccg cgc att cac gtg atg gat   1459
Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg Ile His Val Met Asp
        440                 445                 450

gat ctg cct gtc acc acc tcc ggc aag gtt gat aag aag tct ttg ccg   1507
Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp Lys Lys Ser Leu Pro
    455                 460                 465

tgg cct ctt cct ggc acc gtg gtg gaa gct aat gac ctc agc gca acg   1555
Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn Asp Leu Ser Ala Thr
470                 475                 480                 485

gaa gcg tgg att gct cag gaa tgg gtc gat atc ctc ggc act tct gtg   1603
Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val
                490                 495                 500

agc agc aaa gac gcc gac ttc ttc tcc ctt ggc ggt acc tct ctc gcg   1651
Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala
            505                 510                 515
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gct gcg act ttg gtt ggc cgg gta cgc gca aag gtt ccc acc gct gcg   1699
Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala
        520                 525                 530

gtg cgt gat ctt tac gat cac cct cgc ttg gag aaa ttc gcc gag cgt   1747
Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu Lys Phe Ala Glu Arg
    535                 540                 545

gtc gag gct atc gcc gcc gac act ggc att tct ttg gag gcg cca aac   1795
Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn
550                 555                 560                 565

cag gtg gag gag cgc gtc gtc aag cct gtt tct ttt ggc act cgt gtg   1843
Gln Val Glu Glu Arg Val Val Lys Pro Val Ser Phe Gly Thr Arg Val
                570                 575                 580

atg cag acc ctc atc cag att ccg atc atg acg ctg caa gca gca cag   1891
Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr Leu Gln Ala Ala Gln
            585                 590                 595

tgg att gca tgg ttg ctg ttg ggc aac aac atc atg gca gcg ctt gat   1939
Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile Met Ala Ala Leu Asp
        600                 605                 610

ttc gat tgg gct gtt cat gtc tcc tgg tgg ctt gtc atc ggc atg att   1987
Phe Asp Trp Ala Val His Val Ser Trp Trp Leu Val Ile Gly Met Ile
    615                 620                 625

ttg gtg ttc gct acc ccg att ggt cgc ttg ccg atc ggc ggt tgg ggc   2035
Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro Ile Gly Gly Trp Gly
630                 635                 640                 645

gcc cgc atc atc acc cgt ggc ata act cct ggc tcc tac cct cgt ggc   2083
Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly Ser Tyr Pro Arg Gly
                650                 655                 660

ggt tcc act cac ctg cgc att tgg tcc gcc gag cgc ctt gct gat gcc   2131
Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu Arg Leu Ala Asp Ala
            665                 670                 675

tct ggc tct cgc aat att tct ggc gca acc tgg gtg aac tac ttc gcg   2179
Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala
        680                 685                 690

cgt tcc ctg ggt gtg aag atg ggc aag ggc gtg gat ctt cac tcc ctg   2227
Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu
    695                 700                 705

cca cca atc act ggc ctt ttg acc ttg ggc aac aat gtt tcc atc gag   2275
Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn Asn Val Ser Ile Glu
710                 715                 720                 725

caa gaa gtt gac ctt cgt ggc tac tgg ctc gac ggc gat atc ctg cgt   2323
Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg
                730                 735                 740

gta ggc acc att gag gtc cat gac aac gct cgc atc ggc gct cgt tcc   2371
Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser
            745                 750                 755
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acc ctg ctt ccc ggc acc gtg gtg ggc acc ggc gct cac ctg ctg cct   2419
Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly Ala His Leu Leu Pro
        760                 765                 770

ggt tca aca gtg act ggt gat aag acc atc aag cct ggt tct cgt tgg   2467
Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys Pro Gly Ser Arg Trp
    775                 780                 785

gct ggc tcc cct gca caa aag gtg ggt cgt gca aag cac cgg ttc cca   2515
Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala Lys His Arg Phe Pro
790                 795                 800                 805

acc tcc cat cct cca cgc agg tcc cgg tgg gtt ccg gtg ttc ggc gcg   2563
Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala
                810                 815                 820

acc tcc atc gtg ttg tcg ctg ctg cca ctt cag gct ctc gct att ggc   2611
Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly
            825                 830                 835

gct gct atc acc ttg tgg ctg gcc acg att agc ccg ctt cca ctg atc   2659
Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile
        840                 845                 850

tgg ggt gtg ctg gtt ttt gct acc gtc ggc gcg ttg gct gcg ttc ttt   2707
Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala Leu Ala Ala Phe Phe
    855                 860                 865

gct tac acc gtg acc atc tgg gtg ctt gtc cgt ttg atc cag atc ggc   2755
Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg Leu Ile Gln Ile Gly
870                 875                 880                 885

atc aag ggc ggc acc gca cca gtg agg tcc cgt ctt ggt tgg cag gtc   2803
Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val
                890                 895                 900

tgg gca gtt caa cgc ctc atg gac gat gcc cgc acc tat ctc ttc ccg   2851
Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro
            905                 910                 915

ctc tac gca tcc caa ctg acc cca ctg tgg ttc cgc agc ttg ggc gcg   2899
Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe Arg Ser Leu Gly Ala
        920                 925                 930

aag atc ggc aag gat gtt gag atc tcc acc gcg gtg atg gtt cct aaa   2947
Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys
    935                 940                 945

ctg gct gat atc cgc gaa ggc gca ttc ctg gcc gat gac acc ctc atc   2995
Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala Asp Asp Thr Leu Ile
950                 955                 960                 965

ggt ggc tat gag ctg ggt aat ggt tgg ctg ctc agt ggt gaa acc cgc   3043
Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu Ser Gly Glu Thr Arg
                970                 975                 980

gtg ggt aag cgt tcc ttc att ggt aac tct ggc atc gca gga cct gag   3091
Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly Ile Ala Gly Pro Glu
            985                 990                 995

cgc aag ctc gct aag aac tcc ctg gtt gca gtg ctc tcc tcc acc ccg   3139
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Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val Leu Ser Ser Thr Pro
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aag aag gct aag gcc aac tcc aac tgg tgg ggt tcc cct cca gag cgc   3187
Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly Ser Pro Pro Glu Arg
    1015                1020                1025

atg cgt cgt gtc act gtc gaa gtt gat gag ggc gaa gca aag acc tac   3235
Met Arg Arg Val Thr Val Glu Val Asp Glu Gly Glu Ala Lys Thr Tyr
1030                1035                1040                1045

agc cct ggc ttt ggt gtg aag ttt gca cgt ggc gcg gtg gaa acc gca   3283
Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly Ala Val Glu Thr Ala
                1050                1055                1060

cgt ctg ctt gct cca ata acc tct ggt gtg ttg gct gcg ctg tca ctg   3331
Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu Ala Ala Leu Ser Leu
            1065                1070                1075

ctg ctc atg cag tac ctg ctc act gag ttc aac atg tgg atc acc tgg   3379
Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn Met Trp Ile Thr Trp
        1080                1085                1090

ttg ctt ggc gga ctg atc ctc atg acg gtt ggt gtg ctc gcc atg ggc   3427
Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly Val Leu Ala Met Gly
    1095                1100                1105

att acg gtt gtg atg aag tgg gtt tgc gtc ggc aag cat aag ccg tct   3475
Ile Thr Val Val Met Lys Trp Val Cys Val Gly Lys His Lys Pro Ser
1110                1115                1120                1125

gag cac cct ctc ttc agc cgc ttt gtg tgg ctg aat gag ctg caa gat   3523
Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu Asn Glu Leu Gln Asp
                1130                1135                1140

gcg ttc gtg gaa tcc gtg gct ggc cca tgg ttc ctc gtg ccc aac ctg   3571
Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe Leu Val Pro Asn Leu
            1145                1150                1155

ggc acc ggc gcg ctg aac gcc ggc atg agc gcg ctt ggc gca cac atc   3619
Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile
        1160                1165                1170

ggc cgt ggc gca tgg atc gaa tcc tac tgg ctg ccg gaa acc gac ctc   3667
Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu Pro Glu Thr Asp Leu
    1175                1180                1185

tgc tac atc ggc aag ggc gca acc gtg ggc cct ggc gtg gtc gtg cag   3715
Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln
1190                1195                1200                1205

acc cac ctc ttc cag gac cgc gtg atg agc cta gat acg gtg acc gtc   3763
Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val
                1210                1215                1220

gct gac ggc gcc acc cta gcg gac cac tcc gtt gcc ctt cct gct tcg   3811
Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser
            1225                1230                1235

ctt atc gac gcc tcc gcc acc atc ggc cca ggc tcg ctg gtg atg cgc   3859
Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg
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1240 1245 1250

ggc gac aag gta cca gcg cat acc cgc tgg caa ggc aac cca att gag 3907
Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu
1255 1260 1265

ccg tgg agc aac tct taaataacaa caatcagccg gat 3945
Pro Trp Ser Asn Ser
1270

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Ala Ile Asp Asp Gly Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu
20 25 30

Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly
35 40 45

Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
50 55 60

Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
65 70 75 80

Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn
85 90 95

Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr
100 105 110

Ala Gly Gly Asp Thr Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile
115 120 125

Ile Phe Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser
130 135 140

His Arg Ser Ala Ala Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu
145 150 155 160

Val Asp His Pro Ser Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala
165 170 175

Gly Leu Ser Val Ala Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala
180 185 190

Trp Gly His Gly Ala Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg
195 200 205

Ser Gly Met Asp Leu Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val
210 215 220

Val Ser Thr Val Pro Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu
225 230 235 240

Ser Gln Val Arg Leu Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu
245 250 255

Leu Val Glu Arg Leu Ser Thr Pro Asp Arg Glu Val Trp Asn Thr Tyr
260 265 270

Gly Pro Thr Glu Ala Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala
275 280 285

Gly Gln Pro Val Gly Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val
290 295 300

Val Val Asp Asp Ala Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu
305 310 315 320

Leu Val Ile Gly Gly Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys
325 330 335

Asp Arg Glu Lys Tyr Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala
340 345 350

Tyr Arg Ser Gly Asp His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe
355 360 365

Val Gly Arg Val Asp Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu
370 375 380

Leu Gly Glu Val Asp Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser
385 390 395 400

Ser Ala Val Val Val Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val
405 410 415

Ala Tyr Val Ser Leu Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val
420 425 430

Ala Thr Ala Arg Leu Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg
435 440 445

Ile His Val Met Asp Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp
450 455 460

Lys Lys Ser Leu Pro Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn
465 470 475 480

Asp Leu Ser Ala Thr Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile
485 490 495

Leu Gly Thr Ser Val Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly
500 505 510

Gly Thr Ser Leu Ala Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys
515 520 525

Val Pro Thr Ala Ala Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu
530 535 540

Lys Phe Ala Glu Arg Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser
545 550 555 560

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Leu Glu Ala Pro Asn Gln Val Glu Glu Arg Val Val Lys Pro Val Ser
                565                 570                 575

Phe Gly Thr Arg Val Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr
            580                 585                 590

Leu Gln Ala Ala Gln Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile
        595                 600                 605

Met Ala Ala Leu Asp Phe Asp Trp Ala Val His Val Ser Trp Trp Leu
    610                 615                 620

Val Ile Gly Met Ile Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro
625                 630                 635                 640

Ile Gly Gly Trp Gly Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly
                645                 650                 655

Ser Tyr Pro Arg Gly Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu
            660                 665                 670

Arg Leu Ala Asp Ala Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp
        675                 680                 685

Val Asn Tyr Phe Ala Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val
    690                 695                 700

Asp Leu His Ser Leu Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn
705                 710                 715                 720

Asn Val Ser Ile Glu Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp
                725                 730                 735

Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
            740                 745                 750

Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly
        755                 760                 765

Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys
    770                 775                 780

Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala
785                 790                 795                 800

Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val
                805                 810                 815

Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln
            820                 825                 830

Ala Leu Ala Ile Gly Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser
        835                 840                 845

Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala
    850                 855                 860

Leu Ala Ala Phe Phe Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg
865                 870                 875                 880

Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg
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Confidential - Pending

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                885                 890                 895

Leu Gly Trp Gln Val Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg
            900                 905                 910

Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe
        915                 920                 925

Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala
    930                 935                 940

Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala
945                 950                 955                 960

Asp Asp Thr Leu Ile Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu
                965                 970                 975

Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly
            980                 985                 990

Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val
        995                 1000                1005

Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly
    1010                1015                1020

Ser Pro Pro Glu Arg Met Arg Arg Val Thr Val Glu Val Asp Glu Gly
1025                1030                1035                1040

Glu Ala Lys Thr Tyr Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly
                1045                1050                1055

Ala Val Glu Thr Ala Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu
            1060                1065                1070

Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn
        1075                1080                1085

Met Trp Ile Thr Trp Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly
    1090                1095                1100

Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly
1105                1110                1115                1120

Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu
                1125                1130                1135

Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe
            1140                1145                1150

Leu Val Pro Asn Leu Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala
        1155                1160                1165

Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu
    1170                1175                1180

Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro
1185                1190                1195                1200

Gly Val Val Val Gln Thr His Leu Phe Gln Asp Arg Val Met Ser Leu
                1205                1210                1215
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Asp Thr Val Thr Val Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val
            1220                1225                1230

Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly
        1235                1240                1245

Ser Leu Val Met Arg Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln
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Gly Asn Pro Ile Glu Pro Trp Ser Asn Ser
1265                1270
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acagttcctg agatccgccc aggcgccccc gaagcgtact ttg tgg gac gtc tta   115
                                          Leu Trp Asp Val Leu
                                            1               5

gaa tcc gtc gcc tct act tat cct gag gca gca gct att gac gat ggc   163
Glu Ser Val Ala Ser Thr Tyr Pro Glu Ala Ala Ala Ile Asp Asp Gly
                10                  15                  20

cag gtg ttg acc tac gca gag ttg atg gaa gaa gtc acc gcg ttg gct   211
Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu Val Thr Ala Leu Ala
            25                  30                  35

gat tcc att cat gca cag ggc att cgc cgt ggt gat cgc atc ggt att   259
Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly Asp Arg Ile Gly Ile
        40                  45                  50

cgc atg ccg tct ggt acg cgt gac ctt tac atc gct att ttg gcc act   307
Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile Ala Ile Leu Ala Thr
    55                  60                  65

ctc gct gct ggt gct gct tac gtg cca gtt gat gca gat gat cct gaa   355
Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp Ala Asp Asp Pro Glu
70                  75                  80                  85

gag cgc gcc gag atg gtg ttt ggt gaa gca aat att aat gcg ctt ttc   403
Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn Ile Asn Ala Leu Phe
                90                  95                  100

gac gcc acc ggc ttc cat atg ctt cgc ccg acc gcg ggc ggc gat acc   451
Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr Ala Gly Gly Asp Thr
            105                 110                 115

cgt aga cca cgc ttg gat gat acg gcg tgg att atc ttt act tcc ggt   499
Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile Ile Phe Thr Ser Gly
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        120                 125                 130

tcc acc ggc aag cct aag ggt gtg gct gtg tcc cac cgt tca gct gcg   547
Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser His Arg Ser Ala Ala
    135                 140                 145

gct ttc gtg gat gcc gaa gca caa atg ttc ctt gtc gat cac cct tcc   595
Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu Val Asp His Pro Ser
150                 155                 160                 165

ggc ccc ctt ggc cca gaa gac cga gtc ctt gcg gga ttg tct gta gcc   643
Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala Gly Leu Ser Val Ala
                170                 175                 180

ttt gac gca tct tgt gag gaa atg tgg ttg gcc tgg ggc cac ggc gcc   691
Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala Trp Gly His Gly Ala
            185                 190                 195

tgc ttg gtg cca gca cca cgc tcc cta gtc cgt tcc ggt atg gac ttg   739
Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg Ser Gly Met Asp Leu
        200                 205                 210

ggc cca tgg ctg att cgc cgc gac atc agt gtc gtc tcc acc gtc cca   787
Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val Val Ser Thr Val Pro
    215                 220                 225

act ctg gct ggt ctg tgg cca gca gaa gca ttg tca cag gtc cgc ttg   835
Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu Ser Gln Val Arg Leu
230                 235                 240                 245

ctc atc gtc ggc ggc gag gct tgc tcg cag gag ctc gtt gaa cgc tta   883
Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu Leu Val Glu Arg Leu
                250                 255                 260

tcg acg cct gac cgc gag gtg tgg aac act tac ggc ccc acc gaa gca   931
Ser Thr Pro Asp Arg Glu Val Trp Asn Thr Tyr Gly Pro Thr Glu Ala
            265                 270                 275

acg gtg gtt gcc tgt ggc act caa ctc tat gct ggt cag cca gtg ggc   979
Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala Gly Gln Pro Val Gly
        280                 285                 290

att ggt ttg cca ctt gct ggt tgg gat ctt gtt gtt gtc gac gat gcc   1027
Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val Val Val Asp Asp Ala
    295                 300                 305

ggc gaa cct gtc gga atc ggc gag gtc ggc gaa ttg gtc atc ggt ggt   1075
Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu Leu Val Ile Gly Gly
310                 315                 320                 325

gtg ggt ctt gca cgc tac ctt gat cca gaa aaa gac cgc gag aag tat   1123
Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys Asp Arg Glu Lys Tyr
                330                 335                 340

gcg cca ctg aag tct gtt ggt tgg acc cgc gct tat cgt tcc ggt gac   1171
Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala Tyr Arg Ser Gly Asp
            345                 350                 355

cac gtt cgt ctg gaa gaa gat ggc ctc tac ttt gtg ggc cgc gtt gat   1219
His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe Val Gly Arg Val Asp
        360                 365                 370
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gat cag gtg aaa atc ggc ggt cga cgc atc gag ctc ggt gaa gtt gat   1267
Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu Leu Gly Glu Val Asp
    375                 380                 385

gcc aat gtg gca gcg ctt tcc aac gtt cgt tcc tcc gca gtg gtt gtt   1315
Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser Ser Ala Val Val Val
390                 395                 400                 405

cag acc act ggt gcg gat caa aaa gtt ctg gtt gca tac gtt tct ttg   1363
Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val Ala Tyr Val Ser Leu
                410                 415                 420

gaa gat gct gca gct gga ttt gat cac aac gtc gcg act gcc cga ctc   1411
Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val Ala Thr Ala Arg Leu
            425                 430                 435

acc gaa acc atg cct gct gct ttg gtt ccg cgc att cac gtg atg gat   1459
Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg Ile His Val Met Asp
        440                 445                 450

gat ctg cct gtc acc acc tcc ggc aag gtt gat aag aag tct ttg ccg   1507
Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp Lys Lys Ser Leu Pro
    455                 460                 465

tgg cct ctt cct ggc acc gtg gtg gaa gct aat gac ctc agc gca acg   1555
Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn Asp Leu Ser Ala Thr
470                 475                 480                 485

gaa gcg tgg att gct cag gaa tgg gtc gat atc ctc ggc act tct gtg   1603
Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile Leu Gly Thr Ser Val
                490                 495                 500

agc agc aaa gac gcc gac ttc ttc tcc ctt ggc ggt acc tct ctc gcg   1651
Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly Gly Thr Ser Leu Ala
            505                 510                 515

gct gcg act ttg gtt ggc cgg gta cgc gca aag gtt ccc acc gct gcg   1699
Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys Val Pro Thr Ala Ala
        520                 525                 530

gtg cgt gat ctt tac gat cac cct cgc ttg gag aaa ttc gcc gag cgt   1747
Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu Lys Phe Ala Glu Arg
    535                 540                 545

gtc gag gct atc gcc gcc gac act ggc att tct ttg gag gcg cca aac   1795
Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser Leu Glu Ala Pro Asn
550                 555                 560                 565

cag gtg gag gag cgc gtc gtc aag cct gtt tct ttt ggc act cgt gtg   1843
Gln Val Glu Glu Arg Val Val Lys Pro Val Ser Phe Gly Thr Arg Val
                570                 575                 580

atg cag acc ctc atc cag att ccg atc atg acg ctg caa gca gca cag   1891
Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr Leu Gln Ala Ala Gln
            585                 590                 595

tgg att gca tgg ttg ctg ttg ggc aac aac atc atg gca gcg ctt gat   1939
Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile Met Ala Ala Leu Asp
        600                 605                 610
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ttc gat tgg gct gtt cat gtc tcc tgg tgg ctt gtc atc ggc atg att   1987
Phe Asp Trp Ala Val His Val Ser Trp Trp Leu Val Ile Gly Met Ile
    615                 620                 625

ttg gtg ttc gct acc ccg att ggt cgc ttg ccg atc ggc ggt tgg ggc   2035
Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro Ile Gly Gly Trp Gly
630                 635                 640                 645

gcc cgc atc atc acc cgt ggc ata act cct ggc tcc tac cct cgt ggc   2083
Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly Ser Tyr Pro Arg Gly
                650                 655                 660

ggt tcc act cac ctg cgc att tgg tcc gcc gag cgc ctt gct gat gcc   2131
Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu Arg Leu Ala Asp Ala
            665                 670                 675

tct ggc tct cgc aat att tct ggc gca acc tgg gtg aac tac ttc gcg   2179
Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp Val Asn Tyr Phe Ala
        680                 685                 690

cgt tcc ctg ggt gtg aag atg ggc aag ggc gtg gat ctt cac tcc ctg   2227
Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val Asp Leu His Ser Leu
    695                 700                 705

cca cca atc act ggc ctt ttg acc ttg ggc aac aat gtt tcc atc gag   2275
Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn Asn Val Ser Ile Glu
710                 715                 720                 725

caa gaa gtt gac ctt cgt ggc tac tgg ctc gac ggc gat atc ctg cgt   2323
Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp Gly Asp Ile Leu Arg
                730                 735                 740

gta ggc acc att gag gtc cat gac aac gct cgc atc ggc gct cgt tcc   2371
Val Gly Thr Ile Glu Val His Asp Asn Ala Arg Ile Gly Ala Arg Ser
            745                 750                 755

acc ctg ctt ccc ggc acc gtg gtg ggc acc ggc gct cac ctg ctg cct   2419
Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly Ala His Leu Leu Pro
        760                 765                 770

ggt tca aca gtg act ggt gat aag acc atc aag cct ggt tct cgt tgg   2467
Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys Pro Gly Ser Arg Trp
    775                 780                 785

gct ggc tcc cct gca caa aag gtg ggt cgt gca aag cac cgg ttc cca   2515
Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala Lys His Arg Phe Pro
790                 795                 800                 805

acc tcc cat cct cca cgc agg tcc cgg tgg gtt ccg gtg ttc ggc gcg   2563
Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val Pro Val Phe Gly Ala
                810                 815                 820

acc tcc atc gtg ttg tcg ctg ctg cca ctt cag gct ctc gct att ggc   2611
Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln Ala Leu Ala Ile Gly
            825                 830                 835

gct gct atc acc ttg tgg ctg gcc acg att agc ccg ctt cca ctg atc   2659
Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser Pro Leu Pro Leu Ile
        840                 845                 850

tgg ggt gtg ctg gtt ttt gct acc gtc ggc gcg ttg gct gcg ttc ttt   2707
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Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala Leu Ala Ala Phe Phe
    855                 860                 865

gct tac acc gtg acc atc tgg gtg ctt gtc cgt ttg atc cag atc ggc   2755
Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg Leu Ile Gln Ile Gly
870                 875                 880                 885

atc aag ggc ggc acc gca cca gtg agg tcc cgt ctt ggt tgg cag gtc   2803
Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg Leu Gly Trp Gln Val
                890                 895                 900

tgg gca gtt caa cgc ctc atg gac gat gcc cgc acc tat ctc ttc ccg   2851
Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg Thr Tyr Leu Phe Pro
            905                 910                 915

ctc tac gca tcc caa ctg acc cca ctg tgg ttc cgc agc ttg ggc gcg   2899
Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe Arg Ser Leu Gly Ala
        920                 925                 930

aag atc ggc aag gat gtt gag atc tcc acc gcg gtg atg gtt cct aaa   2947
Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala Val Met Val Pro Lys
    935                 940                 945

ctg gct gat atc cgc gaa ggc gca ttc ctg gcc gat gac acc ctc atc   2995
Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala Asp Asp Thr Leu Ile
950                 955                 960                 965

ggt ggc tat gag ctg ggt aat ggt tgg ctg ctc agt ggt gaa acc cgc   3043
Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu Ser Gly Glu Thr Arg
                970                 975                 980

gtg ggt aag cgt tcc ttc att ggt aac tct ggc atc gca gga cct gag   3091
Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly Ile Ala Gly Pro Glu
            985                 990                 995

cgc aag ctc gct aag aac tcc ctg gtt gca gtg ctc tcc tcc acc ccg   3139
Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val Leu Ser Ser Thr Pro
        1000                1005                1010

aag aag gct aag gcc aac tcc aac tgg tgg ggt tcc cct cca gag cgc   3187
Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly Ser Pro Pro Glu Arg
    1015                1020                1025

atg cgt cgt gtc act gtc gaa gtt gat gag ggc gaa gca aag acc tac   3235
Met Arg Arg Val Thr Val Glu Val Asp Glu Gly Glu Ala Lys Thr Tyr
1030                1035                1040                1045

agc cct ggc ttt ggt gtg aag ttt gca cgt ggc gcg gtg gaa acc gca   3283
Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly Ala Val Glu Thr Ala
                1050                1055                1060

cgt ctg ctt gct cca ata acc tct ggt gtg ttg gct gcg ctg tca ctg   3331
Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu Ala Ala Leu Ser Leu
            1065                1070                1075

ctg ctc atg cag tac ctg ctc act gag ttc aac atg tgg atc acc tgg   3379
Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn Met Trp Ile Thr Trp
        1080                1085                1090

ttg ctt ggc gga ctg atc ctc atg acg gtt ggt gtg ctc gcc atg ggc   3427
Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly Val Leu Ala Met Gly
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    1095                1100                1105

att acg gtt gtg atg aag tgg gtt tgc gtc ggc aag cat aag ccg tct   3475
Ile Thr Val Val Met Lys Trp Val Cys Val Gly Lys His Lys Pro Ser
1110                1115                1120                1125

gag cac cct ctc ttc agc cgc ttt gtg tgg ctg aat gag ctg caa gat   3523
Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu Asn Glu Leu Gln Asp
                1130                1135                1140

gcg ttc gtg gaa tcc gtg gct ggc cca tgg ttc ctc gtg ccc aac ctg   3571
Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe Leu Val Pro Asn Leu
            1145                1150                1155

ggc acc ggc gcg ctg aac gcc ggc atg agc gcg ctt ggc gca cac atc   3619
Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala Leu Gly Ala His Ile
        1160                1165                1170

ggc cgt ggc gca tgg atc gaa tcc tac tgg ctg ccg gaa acc gac ctc   3667
Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu Pro Glu Thr Asp Leu
    1175                1180                1185

tgc tac atc ggc aag ggc gca acc gtg ggc cct ggc gtg gtc gtg cag   3715
Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro Gly Val Val Val Gln
1190                1195                1200                1205

acc cac ctc ttc cag gac cgc gtg atg agc cta gat acg gtg acc gtc   3763
Thr His Leu Phe Gln Asp Arg Val Met Ser Leu Asp Thr Val Thr Val
                1210                1215                1220

gct gac ggc gcc acc cta gcg gac cac tcc gtt gcc ctt cct gct tcg   3811
Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val Ala Leu Pro Ala Ser
            1225                1230                1235

ctt atc gac gcc tcc gcc acc atc ggc cca ggc tcg ctg gtg atg cgc   3859
Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly Ser Leu Val Met Arg
        1240                1245                1250

ggc gac aag gta cca gcg cat acc cgc tgg caa ggc aac cca att gag   3907
Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln Gly Asn Pro Ile Glu
    1255                1260                1265

ccg tgg agc aac tct taaataacaa caatcagccg gat                    3945
Pro Trp Ser Asn Ser
1270
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Ala Ile Asp Asp Gly Gln Val Leu Thr Tyr Ala Glu Leu Met Glu Glu
             20                  25                  30

Val Thr Ala Leu Ala Asp Ser Ile His Ala Gln Gly Ile Arg Arg Gly
         35                  40                  45
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Asp Arg Ile Gly Ile Arg Met Pro Ser Gly Thr Arg Asp Leu Tyr Ile
     50                  55                  60

Ala Ile Leu Ala Thr Leu Ala Ala Gly Ala Ala Tyr Val Pro Val Asp
 65                  70                  75                  80

Ala Asp Asp Pro Glu Glu Arg Ala Glu Met Val Phe Gly Glu Ala Asn
                 85                  90                  95

Ile Asn Ala Leu Phe Asp Ala Thr Gly Phe His Met Leu Arg Pro Thr
            100                 105                 110

Ala Gly Gly Asp Thr Arg Arg Pro Arg Leu Asp Asp Thr Ala Trp Ile
        115                 120                 125

Ile Phe Thr Ser Gly Ser Thr Gly Lys Pro Lys Gly Val Ala Val Ser
    130                 135                 140

His Arg Ser Ala Ala Ala Phe Val Asp Ala Glu Ala Gln Met Phe Leu
145                 150                 155                 160

Val Asp His Pro Ser Gly Pro Leu Gly Pro Glu Asp Arg Val Leu Ala
                165                 170                 175

Gly Leu Ser Val Ala Phe Asp Ala Ser Cys Glu Glu Met Trp Leu Ala
            180                 185                 190

Trp Gly His Gly Ala Cys Leu Val Pro Ala Pro Arg Ser Leu Val Arg
        195                 200                 205

Ser Gly Met Asp Leu Gly Pro Trp Leu Ile Arg Arg Asp Ile Ser Val
    210                 215                 220

Val Ser Thr Val Pro Thr Leu Ala Gly Leu Trp Pro Ala Glu Ala Leu
225                 230                 235                 240

Ser Gln Val Arg Leu Leu Ile Val Gly Gly Glu Ala Cys Ser Gln Glu
                245                 250                 255

Leu Val Glu Arg Leu Ser Thr Pro Asp Arg Glu Val Trp Asn Thr Tyr
            260                 265                 270

Gly Pro Thr Glu Ala Thr Val Val Ala Cys Gly Thr Gln Leu Tyr Ala
        275                 280                 285

Gly Gln Pro Val Gly Ile Gly Leu Pro Leu Ala Gly Trp Asp Leu Val
    290                 295                 300

Val Val Asp Asp Ala Gly Glu Pro Val Gly Ile Gly Glu Val Gly Glu
305                 310                 315                 320

Leu Val Ile Gly Gly Val Gly Leu Ala Arg Tyr Leu Asp Pro Glu Lys
                325                 330                 335

Asp Arg Glu Lys Tyr Ala Pro Leu Lys Ser Val Gly Trp Thr Arg Ala
            340                 345                 350

Tyr Arg Ser Gly Asp His Val Arg Leu Glu Glu Asp Gly Leu Tyr Phe
        355                 360                 365
```

```
Val Gly Arg Val Asp Asp Gln Val Lys Ile Gly Gly Arg Arg Ile Glu
    370                 375                 380

Leu Gly Glu Val Asp Ala Asn Val Ala Ala Leu Ser Asn Val Arg Ser
385                 390                 395                 400

Ser Ala Val Val Val Gln Thr Thr Gly Ala Asp Gln Lys Val Leu Val
                405                 410                 415

Ala Tyr Val Ser Leu Glu Asp Ala Ala Ala Gly Phe Asp His Asn Val
            420                 425                 430

Ala Thr Ala Arg Leu Thr Glu Thr Met Pro Ala Ala Leu Val Pro Arg
        435                 440                 445

Ile His Val Met Asp Asp Leu Pro Val Thr Thr Ser Gly Lys Val Asp
    450                 455                 460

Lys Lys Ser Leu Pro Trp Pro Leu Pro Gly Thr Val Val Glu Ala Asn
465                 470                 475                 480

Asp Leu Ser Ala Thr Glu Ala Trp Ile Ala Gln Glu Trp Val Asp Ile
                485                 490                 495

Leu Gly Thr Ser Val Ser Ser Lys Asp Ala Asp Phe Phe Ser Leu Gly
            500                 505                 510

Gly Thr Ser Leu Ala Ala Ala Thr Leu Val Gly Arg Val Arg Ala Lys
        515                 520                 525

Val Pro Thr Ala Ala Val Arg Asp Leu Tyr Asp His Pro Arg Leu Glu
    530                 535                 540

Lys Phe Ala Glu Arg Val Glu Ala Ile Ala Ala Asp Thr Gly Ile Ser
545                 550                 555                 560

Leu Glu Ala Pro Asn Gln Val Glu Glu Arg Val Val Lys Pro Val Ser
                565                 570                 575

Phe Gly Thr Arg Val Met Gln Thr Leu Ile Gln Ile Pro Ile Met Thr
            580                 585                 590

Leu Gln Ala Ala Gln Trp Ile Ala Trp Leu Leu Leu Gly Asn Asn Ile
        595                 600                 605

Met Ala Ala Leu Asp Phe Asp Trp Ala Val His Val Ser Trp Trp Leu
    610                 615                 620

Val Ile Gly Met Ile Leu Val Phe Ala Thr Pro Ile Gly Arg Leu Pro
625                 630                 635                 640

Ile Gly Gly Trp Gly Ala Arg Ile Ile Thr Arg Gly Ile Thr Pro Gly
                645                 650                 655

Ser Tyr Pro Arg Gly Gly Ser Thr His Leu Arg Ile Trp Ser Ala Glu
            660                 665                 670

Arg Leu Ala Asp Ala Ser Gly Ser Arg Asn Ile Ser Gly Ala Thr Trp
        675                 680                 685

Val Asn Tyr Phe Ala Arg Ser Leu Gly Val Lys Met Gly Lys Gly Val
```

```
    690                 695                 700

Asp Leu His Ser Leu Pro Pro Ile Thr Gly Leu Leu Thr Leu Gly Asn
705                 710                 715                 720

Asn Val Ser Ile Glu Gln Glu Val Asp Leu Arg Gly Tyr Trp Leu Asp
                725                 730                 735

Gly Asp Ile Leu Arg Val Gly Thr Ile Glu Val His Asp Asn Ala Arg
            740                 745                 750

Ile Gly Ala Arg Ser Thr Leu Leu Pro Gly Thr Val Val Gly Thr Gly
        755                 760                 765

Ala His Leu Leu Pro Gly Ser Thr Val Thr Gly Asp Lys Thr Ile Lys
    770                 775                 780

Pro Gly Ser Arg Trp Ala Gly Ser Pro Ala Gln Lys Val Gly Arg Ala
785                 790                 795                 800

Lys His Arg Phe Pro Thr Ser His Pro Pro Arg Arg Ser Arg Trp Val
                805                 810                 815

Pro Val Phe Gly Ala Thr Ser Ile Val Leu Ser Leu Leu Pro Leu Gln
            820                 825                 830

Ala Leu Ala Ile Gly Ala Ala Ile Thr Leu Trp Leu Ala Thr Ile Ser
        835                 840                 845

Pro Leu Pro Leu Ile Trp Gly Val Leu Val Phe Ala Thr Val Gly Ala
    850                 855                 860

Leu Ala Ala Phe Phe Ala Tyr Thr Val Thr Ile Trp Val Leu Val Arg
865                 870                 875                 880

Leu Ile Gln Ile Gly Ile Lys Gly Gly Thr Ala Pro Val Arg Ser Arg
                885                 890                 895

Leu Gly Trp Gln Val Trp Ala Val Gln Arg Leu Met Asp Asp Ala Arg
            900                 905                 910

Thr Tyr Leu Phe Pro Leu Tyr Ala Ser Gln Leu Thr Pro Leu Trp Phe
        915                 920                 925

Arg Ser Leu Gly Ala Lys Ile Gly Lys Asp Val Glu Ile Ser Thr Ala
    930                 935                 940

Val Met Val Pro Lys Leu Ala Asp Ile Arg Glu Gly Ala Phe Leu Ala
945                 950                 955                 960

Asp Asp Thr Leu Ile Gly Gly Tyr Glu Leu Gly Asn Gly Trp Leu Leu
                965                 970                 975

Ser Gly Glu Thr Arg Val Gly Lys Arg Ser Phe Ile Gly Asn Ser Gly
            980                 985                 990

Ile Ala Gly Pro Glu Arg Lys Leu Ala Lys Asn Ser Leu Val Ala Val
        995                 1000                1005

Leu Ser Ser Thr Pro Lys Lys Ala Lys Ala Asn Ser Asn Trp Trp Gly
    1010                1015                1020
```

Substitute Sheet

```
Ser Pro Pro Glu Arg Met Arg Arg Val Thr Val Glu Val Asp Glu Gly
1025                1030                1035                1040

Glu Ala Lys Thr Tyr Ser Pro Gly Phe Gly Val Lys Phe Ala Arg Gly
                1045                1050                1055

Ala Val Glu Thr Ala Arg Leu Leu Ala Pro Ile Thr Ser Gly Val Leu
            1060                1065                1070

Ala Ala Leu Ser Leu Leu Leu Met Gln Tyr Leu Leu Thr Glu Phe Asn
        1075                1080                1085

Met Trp Ile Thr Trp Leu Leu Gly Gly Leu Ile Leu Met Thr Val Gly
    1090                1095                1100

Val Leu Ala Met Gly Ile Thr Val Val Met Lys Trp Val Cys Val Gly
1105                1110                1115                1120

Lys His Lys Pro Ser Glu His Pro Leu Phe Ser Arg Phe Val Trp Leu
                1125                1130                1135

Asn Glu Leu Gln Asp Ala Phe Val Glu Ser Val Ala Gly Pro Trp Phe
            1140                1145                1150

Leu Val Pro Asn Leu Gly Thr Gly Ala Leu Asn Ala Gly Met Ser Ala
        1155                1160                1165

Leu Gly Ala His Ile Gly Arg Gly Ala Trp Ile Glu Ser Tyr Trp Leu
    1170                1175                1180

Pro Glu Thr Asp Leu Cys Tyr Ile Gly Lys Gly Ala Thr Val Gly Pro
1185                1190                1195                1200

Gly Val Val Val Gln Thr His Leu Phe Gln Asp Arg Val Met Ser Leu
                1205                1210                1215

Asp Thr Val Thr Val Ala Asp Gly Ala Thr Leu Ala Asp His Ser Val
            1220                1225                1230

Ala Leu Pro Ala Ser Leu Ile Asp Ala Ser Ala Thr Ile Gly Pro Gly
        1235                1240                1245

Ser Leu Val Met Arg Gly Asp Lys Val Pro Ala His Thr Arg Trp Gln
    1250                1255                1260

Gly Asn Pro Ile Glu Pro Trp Ser Asn Ser
1265                1270


<210> 229
<211> 2025
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(2002)
<223> RXN00787

<400> 229
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ccagcccgcc caataaataa tttctctctt ctaattgcgg agcctcatat attgagtacg 60

gtattttgaa acaccttcag ccccctttt aggagccaca gtg tct cag cct ctc   115
                                          Val Ser Gln Pro Leu
                                            1               5

agc aag cgt ctc agc ata cga aaa gca ctc gcc agc gcc ttc ata gtt   163
Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val
                10                  15                  20

gcg ctg gcg ttt tcg ctt tcc cca gta gcc aaa gcc caa gcc aat gaa   211
Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu
            25                  30                  35

act ccg acg atg atc gtg ttg gac aat tca ggc tcc atg aca gct caa   259
Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly Ser Met Thr Ala Gln
        40                  45                  50

gat gcc ggc gga cag acc cgt atc gat gca gca aaa caa gcc tcc act   307
Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala Lys Gln Ala Ser Thr
    55                  60                  65

cag tta att aat gac atc tcc gac cgc acc gac gta ggt ctg acc tac   355
Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp Val Gly Leu Thr Tyr
70                  75                  80                  85

tac ggc gga aac acc ggc gaa aca gaa gca gac gtt gag atg gga tgc   403
Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp Val Glu Met Gly Cys
                90                  95                  100

caa gac gtc acc atc ctt ggc ggc ccc tcc cga gga aat gca gac acc   451
Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg Gly Asn Ala Asp Thr
            105                 110                 115

tta att gac acg atc aac agc ctg cag cct cga ggc ttc acc ccc atc   499
Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg Gly Phe Thr Pro Ile
        120                 125                 130

ggc aaa gca ctc acc gat acc gcc gcc gag ctc ccc gaa ggc gga aac   547
Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu Pro Glu Gly Gly Asn
    135                 140                 145

att gtg ttg gtc tcc gat ggc atc gcc aac tgc acc cca ccg gat gtc   595
Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys Thr Pro Pro Asp Val
150                 155                 160                 165

tgc gaa gta gcc caa gaa ctg gct caa agt gga atc aac ctg gtt atc   643
Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly Ile Asn Leu Val Ile
                170                 175                 180

aac acc atc gga cta aat gtt gat cca gca gcg cgc gaa gaa ctg gag   691
Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala Arg Glu Glu Leu Glu
            185                 190                 195

tgc atc gct gga gtc ggt ggt ggc act tac gcg gat gct tcc gac gcg   739
Cys Ile Ala Gly Val Gly Gly Gly Thr Tyr Ala Asp Ala Ser Asp Ala
        200                 205                 210

cag agc ctt acc gat gcg ctg aca cga gcc gcc agt agg caa tac aac   787
Gln Ser Leu Thr Asp Ala Leu Thr Arg Ala Ala Ser Arg Gln Tyr Asn
    215                 220                 225
```

```
tct tac acc tcc gat gtg aca aaa att gat ggg gca tcg gaa caa agc   835
Ser Tyr Thr Ser Asp Val Thr Lys Ile Asp Gly Ala Ser Glu Gln Ser
230                 235                 240                 245

gca gcc gta gaa att gat gag gat aca gaa cta ttc ctc acc gac ctg   883
Ala Ala Val Glu Ile Asp Glu Asp Thr Glu Leu Phe Leu Thr Asp Leu
                250                 255                 260

cca caa gaa tcc cgc ttt tgg aaa atc cct gta gag cca ggt gaa acc   931
Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro Val Glu Pro Gly Glu Thr
            265                 270                 275

atc tca gtt tct gcc aac aca gtt acc gac cca aca gta ctc acc atg   979
Ile Ser Val Ser Ala Asn Thr Val Thr Asp Pro Thr Val Leu Thr Met
        280                 285                 290

ggg caa ggc gga atc aag ctt gaa gcc caa ctc cat act gaa gag gct   1027
Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln Leu His Thr Glu Glu Ala
    295                 300                 305

cca caa tac ggc ctg cgt ggt cgg tgc act cgg gtc tca ttt gat aat   1075
Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg Val Ser Phe Asp Asn
310                 315                 320                 325

ttc aag ccc ggc ctt ggt gta cgc gga atc caa aac gcg tcc gtt gca   1123
Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln Asn Ala Ser Val Ala
                330                 335                 340

tca aaa gaa gtg ggc acc aac aac tgt gac acc gat gcc atc tac ctc   1171
Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr Asp Ala Ile Tyr Leu
            345                 350                 355

gaa att tct aga agc gga gat tac ctc aac ggg cag gac att cca acg   1219
Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly Gln Asp Ile Pro Thr
        360                 365                 370

gaa atc acc atc gag cgc ttc gga aaa gta gat gaa tca aca atc gga   1267
Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp Glu Ser Thr Ile Gly
    375                 380                 385

aat gtc aca gag gaa cat agc tcc gtc gat ctt acc gag gct gca gca   1315
Asn Val Thr Glu Glu His Ser Ser Val Asp Leu Thr Glu Ala Ala Ala
390                 395                 400                 405

tca gag gca cac cct gtc aca cct ggc cag tgg ttc aca tcg gcc gct   1363
Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp Phe Thr Ser Ala Ala
                410                 415                 420

gat cta gat ccc gca ggt gag aaa gtc tcc tcc atc atc gtt cca gga   1411
Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser Ile Ile Val Pro Gly
            425                 430                 435

gaa acc cac ttc tat gcg ctg cct gtc gac tac ggc caa gaa ctg cgc   1459
Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr Gly Gln Glu Leu Arg
        440                 445                 450

gca gct gta gaa aca act ttt gac caa atc gac agt tcc gcg ctt ggc   1507
Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp Ser Ser Ala Leu Gly
    455                 460                 465
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acg cat ctt tat atc caa gcg ttc agc cca aac cgg gca gag ata gag   1555
Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn Arg Ala Glu Ile Glu
470                 475                 480                 485

ctc acc aat aga gat acg tca tat gcg gac gac aac ggg ctc aaa act   1603
Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp Asn Gly Leu Lys Thr
                490                 495                 500

ttt gga ttc ttc acc cca gtg agt gca gca aat ttg ttc gag aaa agt   1651
Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn Leu Phe Glu Lys Ser
            505                 510                 515

tct caa ggc ata tcg cta agg agc cca tgg caa ggt ggc acc caa tac   1699
Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln Gly Gly Thr Gln Tyr
        520                 525                 530

ctc gca gtg aca tac cta cca agt ggt caa gat gaa gat gta tcc gca   1747
Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp Glu Asp Val Ser Ala
    535                 540                 545

act gat cag ctg ccc aca ttg gaa tat gaa ctc gtg gca gaa gcg ttt   1795
Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu Val Ala Glu Ala Phe
550                 555                 560                 565

gga gac cct gtt gac cca ccg gtt ttc gct tca ttg acg gga gca acc   1843
Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser Leu Thr Gly Ala Thr
                570                 575                 580

cca agc acc tcc acc ccc cca tca gat gtt gcg gaa gat gaa caa atc   1891
Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala Glu Asp Glu Gln Ile
            585                 590                 595

tcc gag gca aca gaa gaa gac tca agc agt ttc ccc atc gtg tgg att   1939
Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe Pro Ile Val Trp Ile
        600                 605                 610

ggg ctg ggt gtc att ggc tta ggc ata atc att ggt ttg atc ttt gcg   1987
Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile Gly Leu Ile Phe Ala
    615                 620                 625

ctg aga aga aag aat taagccctaa aagataaaga gtc                    2025
Leu Arg Arg Lys Asn
630
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<210> 230
<211> 634
<212> PRT
<213> Corynebacterium glutamicum

<400> 230

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Val Ser Gln Pro Leu Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala
  1               5                  10                  15

Ser Ala Phe Ile Val Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys
             20                  25                  30

Ala Gln Ala Asn Glu Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly
         35                  40                  45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
```

50 55 60

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
85 90 95

Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
115 120 125

Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
130 135 140

Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
145 150 155 160

Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
165 170 175

Ile Asn Leu Val Ile Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala
180 185 190

Arg Glu Glu Leu Glu Cys Ile Ala Gly Val Gly Gly Gly Thr Tyr Ala
195 200 205

Asp Ala Ser Asp Ala Gln Ser Leu Thr Asp Ala Leu Thr Arg Ala Ala
210 215 220

Ser Arg Gln Tyr Asn Ser Tyr Thr Ser Asp Val Thr Lys Ile Asp Gly
225 230 235 240

Ala Ser Glu Gln Ser Ala Ala Val Glu Ile Asp Glu Asp Thr Glu Leu
245 250 255

Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro Val
260 265 270

Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp Pro
275 280 285

Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln Leu
290 295 300

His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr Arg
305 310 315 320

Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile Gln
325 330 335

Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp Thr
340 345 350

Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn Gly
355 360 365

Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val Asp
370 375 380

```
Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp Leu
385                 390                 395                 400

Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln Trp
                405                 410                 415

Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser Ser
            420                 425                 430

Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp Tyr
        435                 440                 445

Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile Asp
    450                 455                 460

Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro Asn
465                 470                 475                 480

Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp Asp
                485                 490                 495

Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala Asn
            500                 505                 510

Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp Gln
        515                 520                 525

Gly Gly Thr Gln Tyr Leu Ala Val Thr Tyr Leu Pro Ser Gly Gln Asp
    530                 535                 540

Glu Asp Val Ser Ala Thr Asp Gln Leu Pro Thr Leu Glu Tyr Glu Leu
545                 550                 555                 560

Val Ala Glu Ala Phe Gly Asp Pro Val Asp Pro Pro Val Phe Ala Ser
                565                 570                 575

Leu Thr Gly Ala Thr Pro Ser Thr Ser Thr Pro Pro Ser Asp Val Ala
            580                 585                 590

Glu Asp Glu Gln Ile Ser Glu Ala Thr Glu Glu Asp Ser Ser Ser Phe
        595                 600                 605

Pro Ile Val Trp Ile Gly Leu Gly Val Ile Gly Leu Gly Ile Ile Ile
    610                 615                 620

Gly Leu Ile Phe Ala Leu Arg Arg Lys Asn
625                 630
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<210> 231
<211> 694
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(694)
<223> FRXA00787

<400> 231

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ccagcccgcc caataaataa tttctctctt ctaattgcgg agcctcatat attgagtacg 60

gtattttgaa acaccttcag ccccctttt aggagccaca gtg tct cag cct ctc   115
                                          Val Ser Gln Pro Leu
                                            1               5

agc aag cgt ctc agc ata cga aaa gca ctc gcc agc gcc ttc ata gtt   163
Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala Ser Ala Phe Ile Val
                 10                  15                  20

gcg ctg gcg ttt tcg ctt tcc cca gta gcc aaa gcc caa gcc aat gaa   211
Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys Ala Gln Ala Asn Glu
             25                  30                  35

act ccg acg atg atc gtg ttg gac aat tca ggc tcc atg aca gct caa   259
Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly Ser Met Thr Ala Gln
         40                  45                  50

gat gcc ggc gga cag acc cgt atc gat gca gca aaa caa gcc tcc act   307
Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala Lys Gln Ala Ser Thr
     55                  60                  65

cag tta att aat gac atc tcc gac cgc acc gac gta ggt ctg acc tac   355
Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp Val Gly Leu Thr Tyr
 70                  75                  80                  85

tac ggc gga aac acc ggc gaa aca gaa gca gac gtt gag atg gga tgc   403
Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp Val Glu Met Gly Cys
                 90                  95                 100

caa gac gtc acc atc ctt ggc ggc ccc tcc cga gga aat gca gac acc   451
Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg Gly Asn Ala Asp Thr
            105                 110                 115

tta att gac acg atc aac agc ctg cag cct cga ggc ttc acc ccc atc   499
Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg Gly Phe Thr Pro Ile
        120                 125                 130

ggc aaa gca ctc acc gat acc gcc gcc gag ctc ccc gaa ggc gga aac   547
Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu Pro Glu Gly Gly Asn
    135                 140                 145

att gtg ttg gtc tcc gat ggc atc gcc aac tgc acc cca ccg gat gtc   595
Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys Thr Pro Pro Asp Val
150                 155                 160                 165

tgc gaa gta gcc caa gaa ctg gct caa agt gga atc aac ctg gtt atc   643
Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly Ile Asn Leu Val Ile
                170                 175                 180

aac acc atc gga cta aat gtt gat cca gca gcg cgc gaa gaa ctg gag   691
Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala Arg Glu Glu Leu Glu
            185                 190                 195

tgc                                                              694
Cys
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CONFIDENTIAL

<210> 232
<211> 198

<212> PRT
<213> Corynebacterium glutamicum

<400> 232
Val Ser Gln Pro Leu Ser Lys Arg Leu Ser Ile Arg Lys Ala Leu Ala
1 5 10 15

Ser Ala Phe Ile Val Ala Leu Ala Phe Ser Leu Ser Pro Val Ala Lys
20 25 30

Ala Gln Ala Asn Glu Thr Pro Thr Met Ile Val Leu Asp Asn Ser Gly
35 40 45

Ser Met Thr Ala Gln Asp Ala Gly Gly Gln Thr Arg Ile Asp Ala Ala
50 55 60

Lys Gln Ala Ser Thr Gln Leu Ile Asn Asp Ile Ser Asp Arg Thr Asp
65 70 75 80

Val Gly Leu Thr Tyr Tyr Gly Gly Asn Thr Gly Glu Thr Glu Ala Asp
85 90 95

Val Glu Met Gly Cys Gln Asp Val Thr Ile Leu Gly Gly Pro Ser Arg
100 105 110

Gly Asn Ala Asp Thr Leu Ile Asp Thr Ile Asn Ser Leu Gln Pro Arg
115 120 125

Gly Phe Thr Pro Ile Gly Lys Ala Leu Thr Asp Thr Ala Ala Glu Leu
130 135 140

Pro Glu Gly Gly Asn Ile Val Leu Val Ser Asp Gly Ile Ala Asn Cys
145 150 155 160

Thr Pro Pro Asp Val Cys Glu Val Ala Gln Glu Leu Ala Gln Ser Gly
165 170 175

Ile Asn Leu Val Ile Asn Thr Ile Gly Leu Asn Val Asp Pro Ala Ala
180 185 190

Arg Glu Glu Leu Glu Cys
195

<210> 233
<211> 828
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(828)
<223> FRXA00791

<400> 233
cta ttc ctc acc gac ctg cca caa gaa tcc cgc ttt tgg aaa atc cct 48
Leu Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro
1 5 10 15

gta gag cca ggt gaa acc atc tca gtt tct gcc aac aca gtt acc gac 96
Val Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp

```
                20                  25                  30

cca aca gta ctc acc atg ggg caa ggc gga atc aag ctt gaa gcc caa   144
Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
         35                  40                  45

ctc cat act gaa gag gct cca caa tac ggc ctg cgt ggt cgg tgc act   192
Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr
     50                  55                  60

cgg gtc tca ttt gat aat ttc aag ccc ggc ctt ggt gta cgc gga atc   240
Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile
 65                  70                  75                  80

caa aac gcg tcc gtt gca tca aaa gaa gtg ggc acc aac aac tgt gac   288
Gln Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp
                 85                  90                  95

acc gat gcc atc tac ctc gaa att tct aga agc gga gat tac ctc aac   336
Thr Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn
            100                 105                 110

ggg cag gac att cca acg gaa atc acc atc gag cgc ttc gga aaa gta   384
Gly Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val
        115                 120                 125

gat gaa tca aca atc gga aat gtc aca gag gaa cat agc tcc gtc gat   432
Asp Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp
    130                 135                 140

ctt acc gag gct gca gca tca gag gca cac cct gtc aca cct ggc cag   480
Leu Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln
145                 150                 155                 160

tgg ttc aca tcg gcc gct gat cta gat ccc gca ggt gag aaa gtc tcc   528
Trp Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser
                165                 170                 175

tcc atc atc gtt cca gga gaa acc cac ttc tat gcg ctg cct gtc gac   576
Ser Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp
            180                 185                 190

tac ggc caa gaa ctg cgc gca gct gta gaa aca act ttt gac caa atc   624
Tyr Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile
        195                 200                 205

gac agt tcc gcg ctt ggc acg cat ctt tat atc caa gcg ttc agc cca   672
Asp Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro
    210                 215                 220

aac cgg gca gag ata gag ctc acc aat aga gat acg tca tat gcg gac   720
Asn Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp
225                 230                 235                 240

gac aac ggg ctc aaa act ttt gga ttc ttc acc cca gtg agt gca gca   768
Asp Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala
                245                 250                 255

aat ttg ttc gag aaa agt tct caa ggc ata tcg cta agg agc cca tgg   816
Asn Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp
            260                 265                 270
```

caa ggt ggc acc 828
Gln Gly Gly Thr
275

<210> 234
<211> 276
<212> PRT
<213> Corynebacterium glutamicum

<400> 234
Leu Phe Leu Thr Asp Leu Pro Gln Glu Ser Arg Phe Trp Lys Ile Pro
1 5 10 15

Val Glu Pro Gly Glu Thr Ile Ser Val Ser Ala Asn Thr Val Thr Asp
20 25 30

Pro Thr Val Leu Thr Met Gly Gln Gly Gly Ile Lys Leu Glu Ala Gln
35 40 45

Leu His Thr Glu Glu Ala Pro Gln Tyr Gly Leu Arg Gly Arg Cys Thr
50 55 60

Arg Val Ser Phe Asp Asn Phe Lys Pro Gly Leu Gly Val Arg Gly Ile
65 70 75 80

Gln Asn Ala Ser Val Ala Ser Lys Glu Val Gly Thr Asn Asn Cys Asp
85 90 95

Thr Asp Ala Ile Tyr Leu Glu Ile Ser Arg Ser Gly Asp Tyr Leu Asn
100 105 110

Gly Gln Asp Ile Pro Thr Glu Ile Thr Ile Glu Arg Phe Gly Lys Val
115 120 125

Asp Glu Ser Thr Ile Gly Asn Val Thr Glu Glu His Ser Ser Val Asp
130 135 140

Leu Thr Glu Ala Ala Ala Ser Glu Ala His Pro Val Thr Pro Gly Gln
145 150 155 160

Trp Phe Thr Ser Ala Ala Asp Leu Asp Pro Ala Gly Glu Lys Val Ser
165 170 175

Ser Ile Ile Val Pro Gly Glu Thr His Phe Tyr Ala Leu Pro Val Asp
180 185 190

Tyr Gly Gln Glu Leu Arg Ala Ala Val Glu Thr Thr Phe Asp Gln Ile
195 200 205

Asp Ser Ser Ala Leu Gly Thr His Leu Tyr Ile Gln Ala Phe Ser Pro
210 215 220

Asn Arg Ala Glu Ile Glu Leu Thr Asn Arg Asp Thr Ser Tyr Ala Asp
225 230 235 240

Asp Asn Gly Leu Lys Thr Phe Gly Phe Phe Thr Pro Val Ser Ala Ala
245 250 255

Asn Leu Phe Glu Lys Ser Ser Gln Gly Ile Ser Leu Arg Ser Pro Trp

```
            260                 265                 270

Gln Gly Gly Thr
        275


<210> 235
<211> 1626
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1603)
<223> RXA01057

<400> 235
aactaatggg caggctgagc agcttaaaca acacatcgat agcctccaac cgcggggcta 60

tacgccgatt ggtgaatccc tgcgcaaggc tgcagcagaa ttg cct gaa ggc caa   115
                                          Leu Pro Glu Gly Gln
                                            1               5

tct ggc acc atc gta ttg gtc tct gat ggc att gca acg tgt acg ccc   163
Ser Gly Thr Ile Val Leu Val Ser Asp Gly Ile Ala Thr Cys Thr Pro
                10                  15                  20

cct cca gtg tgt gag gtt gct gca gaa cta gcc gac cag ggt gtt gat   211
Pro Pro Val Cys Glu Val Ala Ala Glu Leu Ala Asp Gln Gly Val Asp
            25                  30                  35

ctg gtg att aac act gtt gga ttc aac gtc gat gag tct gct cgc gcg   259
Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp Glu Ser Ala Arg Ala
        40                  45                  50

gaa ctg gag tgc att gcg cag gct gga aac ggt act tat gca gat gcg   307
Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly Thr Tyr Ala Asp Ala
    55                  60                  65

agc gat gcg gat tcg ctt gtg gca gaa ctg aag cga gct gcc acc cgc   355
Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys Arg Ala Ala Thr Arg
70                  75                  80                  85

acg gca gtg ggc tat gaa tca gac ctg gaa caa atc gat ggc aac agc   403
Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln Ile Asp Gly Asn Ser
                90                  95                  100

agc caa aca agc ctg acc cca att cca gat gat gtg gaa ttg ttc aaa   451
Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp Val Glu Leu Phe Lys
            105                 110                 115

gcc gat ctt cca gca cta gat aat aaa gac ggc gaa gta act cag tac   499
Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly Glu Val Thr Gln Tyr
        120                 125                 130

tgg tcc att ccc gtt gaa gat tat gaa cgt gtg cag gta acc acc tcg   547
Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val Gln Val Thr Thr Ser
    135                 140                 145

tat gtt gcg cca gtg act ttt gga ctc ggg aac gac tac ctg agc att   595
Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn Asp Tyr Leu Ser Ile
```

```
150                 155                 160                 165

agg aat gaa ctg ctt ttc gga gat gaa caa gat caa acc tgt cat cgt   643
Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp Gln Thr Cys His Arg
                170                 175                 180

tcg atc agc aat gat caa att ctt gat aat tac ggt gcg cgg cct ttg   691
Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr Gly Ala Arg Pro Leu
            185                 190                 195

gtt gcc agt gtg gag tca gat gtg att gga gat aag tgc gat acc gat   739
Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp Lys Cys Asp Thr Asp
        200                 205                 210

gaa ctg gtt ctc gca atc acc aga agc cag cct ttc aat tgg gaa gaa   787
Glu Leu Val Leu Ala Ile Thr Arg Ser Gln Pro Phe Asn Trp Glu Glu
    215                 220                 225

gaa tta cct gtt gag atc gtg gta aag cgc ctt aat cac gcg gat acg   835
Glu Leu Pro Val Glu Ile Val Val Lys Arg Leu Asn His Ala Asp Thr
230                 235                 240                 245

tca ggg ctt cca ctc ggt gat caa cag cgt gaa atc cca gat ctc gac   883
Ser Gly Leu Pro Leu Gly Asp Gln Gln Arg Glu Ile Pro Asp Leu Asp
                250                 255                 260

gtg gcc gca gta caa aca tgg gca ccc acc act ggc gga tct tgg ttt   931
Val Ala Ala Val Gln Thr Trp Ala Pro Thr Thr Gly Gly Ser Trp Phe
            265                 270                 275

acc aac gct acg gag cta act cca ggt gaa ggt gtt gaa gca gag atc   979
Thr Asn Ala Thr Glu Leu Thr Pro Gly Glu Gly Val Glu Ala Glu Ile
        280                 285                 290

gta cct ggt gaa aat cac gtt tat cgc ctg cct atg gca act ggt cag  1027
Val Pro Gly Glu Asn His Val Tyr Arg Leu Pro Met Ala Thr Gly Gln
    295                 300                 305

cag ctg cat ggc ttt gtg gaa gtt gta gaa aac acg gca cca gat gat  1075
Gln Leu His Gly Phe Val Glu Val Val Glu Asn Thr Ala Pro Asp Asp
310                 315                 320                 325

cct ggc gtg acg gac aaa ttg ggt gtt gca gtg tat tcg cca aca cga  1123
Pro Gly Val Thr Asp Lys Leu Gly Val Ala Val Tyr Ser Pro Thr Arg
                330                 335                 340

cag gac gcc gga gtt gat atg tgg acg gat atc gct cca cgt gag ggc  1171
Gln Asp Ala Gly Val Asp Met Trp Thr Asp Ile Ala Pro Arg Glu Gly
            345                 350                 355

acc agt gag tat ttt gca gcg cca gtt gca ctg act tat ctg aat atg  1219
Thr Ser Glu Tyr Phe Ala Ala Pro Val Ala Leu Thr Tyr Leu Asn Met
        360                 365                 370

ttc cct gct gaa ggc gga ttt ggc act act tct aag gcc acc agc acg  1267
Phe Pro Ala Glu Gly Gly Phe Gly Thr Thr Ser Lys Ala Thr Ser Thr
    375                 380                 385

ttt acg ttt gaa ggc gat tac tac ctc gtt gtg cac tat gac gat ctc  1315
Phe Thr Phe Glu Gly Asp Tyr Tyr Leu Val Val His Tyr Asp Asp Leu
390                 395                 400                 405
```

```
agt ggc agt aca atc aga gat gcc agc aac cag cag tct ttt ccc ctt   1363
Ser Gly Ser Thr Ile Arg Asp Ala Ser Asn Gln Gln Ser Phe Pro Leu
                410                 415                 420

cgt tat cgc tta gca gcg gat gct ttt ggt gat gca gag cca ggc cca   1411
Arg Tyr Arg Leu Ala Ala Asp Ala Phe Gly Asp Ala Glu Pro Gly Pro
            425                 430                 435

gtg ttt gaa aag gtt tct gca acc acc tca gaa tcc tct agc cca agc   1459
Val Phe Glu Lys Val Ser Ala Thr Thr Ser Glu Ser Ser Ser Pro Ser
        440                 445                 450

act caa cca gat gag cca gct caa aat acc gca act gag gaa agc agc   1507
Thr Gln Pro Asp Glu Pro Ala Gln Asn Thr Ala Thr Glu Glu Ser Ser
    455                 460                 465

act gga atc tcc ccg ctc att gtt ggc gct atc gtc gca ctc att ttg   1555
Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile Val Ala Leu Ile Leu
470                 475                 480                 485

gcg ttc gct gcg ttt gcc agc tgg cta gtt ttg aaa ggc cgc aag aaa   1603
Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu Lys Gly Arg Lys Lys
                490                 495                 500

taaccccata ggaatttcca aac                                        1626
```

<210> 236
<211> 501
<212> PRT
<213> Corynebacterium glutamicum

<400> 236

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Leu Pro Glu Gly Gln Ser Gly Thr Ile Val Leu Val Ser Asp Gly Ile
  1               5                  10                  15

Ala Thr Cys Thr Pro Pro Pro Val Cys Glu Val Ala Ala Glu Leu Ala
             20                  25                  30

Asp Gln Gly Val Asp Leu Val Ile Asn Thr Val Gly Phe Asn Val Asp
         35                  40                  45

Glu Ser Ala Arg Ala Glu Leu Glu Cys Ile Ala Gln Ala Gly Asn Gly
     50                  55                  60

Thr Tyr Ala Asp Ala Ser Asp Ala Asp Ser Leu Val Ala Glu Leu Lys
 65                  70                  75                  80

Arg Ala Ala Thr Arg Thr Ala Val Gly Tyr Glu Ser Asp Leu Glu Gln
                 85                  90                  95

Ile Asp Gly Asn Ser Ser Gln Thr Ser Leu Thr Pro Ile Pro Asp Asp
            100                 105                 110

Val Glu Leu Phe Lys Ala Asp Leu Pro Ala Leu Asp Asn Lys Asp Gly
        115                 120                 125

Glu Val Thr Gln Tyr Trp Ser Ile Pro Val Glu Asp Tyr Glu Arg Val
    130                 135                 140
```

```
Gln Val Thr Thr Ser Tyr Val Ala Pro Val Thr Phe Gly Leu Gly Asn
145                 150                 155                 160

Asp Tyr Leu Ser Ile Arg Asn Glu Leu Leu Phe Gly Asp Glu Gln Asp
                165                 170                 175

Gln Thr Cys His Arg Ser Ile Ser Asn Asp Gln Ile Leu Asp Asn Tyr
            180                 185                 190

Gly Ala Arg Pro Leu Val Ala Ser Val Glu Ser Asp Val Ile Gly Asp
        195                 200                 205

Lys Cys Asp Thr Asp Glu Leu Val Leu Ala Ile Thr Arg Ser Gln Pro
    210                 215                 220

Phe Asn Trp Glu Glu Glu Leu Pro Val Glu Ile Val Val Lys Arg Leu
225                 230                 235                 240

Asn His Ala Asp Thr Ser Gly Leu Pro Leu Gly Asp Gln Gln Arg Glu
                245                 250                 255

Ile Pro Asp Leu Asp Val Ala Ala Val Gln Thr Trp Ala Pro Thr Thr
            260                 265                 270

Gly Gly Ser Trp Phe Thr Asn Ala Thr Glu Leu Thr Pro Gly Glu Gly
        275                 280                 285

Val Glu Ala Glu Ile Val Pro Gly Glu Asn His Val Tyr Arg Leu Pro
    290                 295                 300

Met Ala Thr Gly Gln Gln Leu His Gly Phe Val Glu Val Val Glu Asn
305                 310                 315                 320

Thr Ala Pro Asp Asp Pro Gly Val Thr Asp Lys Leu Gly Val Ala Val
                325                 330                 335

Tyr Ser Pro Thr Arg Gln Asp Ala Gly Val Asp Met Trp Thr Asp Ile
            340                 345                 350

Ala Pro Arg Glu Gly Thr Ser Glu Tyr Phe Ala Ala Pro Val Ala Leu
        355                 360                 365

Thr Tyr Leu Asn Met Phe Pro Ala Glu Gly Gly Phe Gly Thr Thr Ser
    370                 375                 380

Lys Ala Thr Ser Thr Phe Thr Phe Glu Gly Asp Tyr Tyr Leu Val Val
385                 390                 395                 400

His Tyr Asp Asp Leu Ser Gly Ser Thr Ile Arg Asp Ala Ser Asn Gln
                405                 410                 415

Gln Ser Phe Pro Leu Arg Tyr Arg Leu Ala Ala Asp Ala Phe Gly Asp
            420                 425                 430

Ala Glu Pro Gly Pro Val Phe Glu Lys Val Ser Ala Thr Thr Ser Glu
        435                 440                 445

Ser Ser Ser Pro Ser Thr Gln Pro Asp Glu Pro Ala Gln Asn Thr Ala
    450                 455                 460

Thr Glu Glu Ser Ser Thr Gly Ile Ser Pro Leu Ile Val Gly Ala Ile
```

```
465                 470                 475                 480

Val Ala Leu Ile Leu Ala Phe Ala Ala Phe Ala Ser Trp Leu Val Leu
                485                 490                 495

Lys Gly Arg Lys Lys
            500
```

<210> 237
<211> 225
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(202)
<223> RXA01055

<400> 237

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agaatgaagt gggtgggttc ccggcccggt cactccggat gggcgtccgt tgattgggca 60

gaccaaggcg gagaacattt acgttgccgg tggtcacggc atg tgg ggt gtg gtg   115
                                            Met Trp Gly Val Val
                                              1               5

ctg ggc cct gcc acc ggt aag tat ttg gcg gag ctg atg gct acg ggc   163
Leu Gly Pro Ala Thr Gly Lys Tyr Leu Ala Glu Leu Met Ala Thr Gly
                10                  15                  20

aac acc aac ccg atc atc aag ccg ttc gat ccg ctg cgt taactgccca    212
Asn Thr Asn Pro Ile Ile Lys Pro Phe Asp Pro Leu Arg
            25                  30

ataattggtt gaa                                                   225
```

<210> 238
<211> 34
<212> PRT
<213> Corynebacterium glutamicum

<400> 238

```
Met Trp Gly Val Val Leu Gly Pro Ala Thr Gly Lys Tyr Leu Ala Glu
  1               5                  10                  15

Leu Met Ala Thr Gly Asn Thr Asn Pro Ile Ile Lys Pro Phe Asp Pro
            20                  25                  30

Leu Arg
```

<210> 239
<211> 1023
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1000)

<223> RXA01056

<400> 239

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caagaaataa ccccatagga atttccaaac caatacattt aagtacgaac tcatgaatac 60

tgggggcact aggagtccac cccaccctca ggagggtttc atg agt tcg tct gga   115
                                            Met Ser Ser Ser Gly
                                              1               5

aaa gtc att gtt gtt gga gcc ggc ata gtg ggt ctt gcc acc gcc tgg   163
Lys Val Ile Val Val Gly Ala Gly Ile Val Gly Leu Ala Thr Ala Trp
                 10                  15                  20

cat tta cag gag cac ggg ttc gag gtg agc gtc ctt gat cgg gat ggt   211
His Leu Gln Glu His Gly Phe Glu Val Ser Val Leu Asp Arg Asp Gly
             25                  30                  35

gtc gct gca ggt tct tcg tgg ggt aat gct ggt tgg tta gcg ccg gcg   259
Val Ala Ala Gly Ser Ser Trp Gly Asn Ala Gly Trp Leu Ala Pro Ala
         40                  45                  50

aaa act att ccg ttg tcg gag ccg ggg ctg tgg acg tat ggt ccg aaa   307
Lys Thr Ile Pro Leu Ser Glu Pro Gly Leu Trp Thr Tyr Gly Pro Lys
     55                  60                  65

gag ctg ttc aat ccg gtg tcg ccg atg cat atg cca ctt cgt gtg gat   355
Glu Leu Phe Asn Pro Val Ser Pro Met His Met Pro Leu Arg Val Asp
 70                  75                  80                  85

ccc aaa ctg tgg ctt ttc ttg gcg caa ttt atg gcg cag gct ttt caa   403
Pro Lys Leu Trp Leu Phe Leu Ala Gln Phe Met Ala Gln Ala Phe Gln
                 90                  95                 100

cgc aag tgg gat tcc acg atg gcg gac ctc acg gag atc gat aag gtc   451
Arg Lys Trp Asp Ser Thr Met Ala Asp Leu Thr Glu Ile Asp Lys Val
            105                 110                 115

gcg ctc gaa gct ttt gat gaa ctg tcg atc ggt ggc gtg gaa ggc ctc   499
Ala Leu Glu Ala Phe Asp Glu Leu Ser Ile Gly Gly Val Glu Gly Leu
        120                 125                 130

acc cat gaa ggt cca ttt gtt att ggt ttt gag gaa gag cgc caa tcg   547
Thr His Glu Gly Pro Phe Val Ile Gly Phe Glu Glu Glu Arg Gln Ser
    135                 140                 145

gcg ggt ttc cgt aag gaa att gat ggc gtg agc agg cac ggc cag aaa   595
Ala Gly Phe Arg Lys Glu Ile Asp Gly Val Ser Arg His Gly Gln Lys
150                 155                 160                 165

gtg gag atg tct cga ctg gag aat cca caa gag ttg gcg ccg atg ctg   643
Val Glu Met Ser Arg Leu Glu Asn Pro Gln Glu Leu Ala Pro Met Leu
                170                 175                 180

aat gag caa att cag gtg gct tac cgt ttg gaa ggc cag cgt ttc atc   691
Asn Glu Gln Ile Gln Val Ala Tyr Arg Leu Glu Gly Gln Arg Phe Ile
            185                 190                 195

gag ccg ggt cca tac gtg cag tca ttg gcg gat gct gtg gtg aag cgt   739
Glu Pro Gly Pro Tyr Val Gln Ser Leu Ala Asp Ala Val Val Lys Arg
        200                 205                 210
```

```
ggt ggc gtg atc cgc gcc ggg gca gaa gtt gtg cat gtg gcg aag ggt   787
Gly Gly Val Ile Arg Ala Gly Ala Glu Val Val His Val Ala Lys Gly
    215                 220                 225

gat cgt ccc gcg gtc att ttg gcg gat ggt agc cgt gaa gaa gcg gac   835
Asp Arg Pro Ala Val Ile Leu Ala Asp Gly Ser Arg Glu Glu Ala Asp
230                 235                 240                 245

aag gtg gtt gtg gca acg ggt gcc tgg ctg ccg ggt cta acg cgt gaa   883
Lys Val Val Val Ala Thr Gly Ala Trp Leu Pro Gly Leu Thr Arg Glu
                250                 255                 260

tac ggt gtg aaa act ctt gtt cag gct ggt cgt ggc tat tcc ttc tct   931
Tyr Gly Val Lys Thr Leu Val Gln Ala Gly Arg Gly Tyr Ser Phe Ser
            265                 270                 275

gtg gca acg gat att cct gcc aag cat tct gtg tac ctt ccc cac cac   979
Val Ala Thr Asp Ile Pro Ala Lys His Ser Val Tyr Leu Pro His His
        280                 285                 290

cgg cat ggc ctg cac gcc gta tgagggccgt ttccgcattg cgg            1023
Arg His Gly Leu His Ala Val
    295                 300
```

Sequence Listing

<210> 240
<211> 300
<212> PRT
<213> Corynebacterium glutamicum

<400> 240

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Met Ser Ser Ser Gly Lys Val Ile Val Val Gly Ala Gly Ile Val Gly
  1               5                  10                  15

Leu Ala Thr Ala Trp His Leu Gln Glu His Gly Phe Glu Val Ser Val
             20                  25                  30

Leu Asp Arg Asp Gly Val Ala Ala Gly Ser Ser Trp Gly Asn Ala Gly
         35                  40                  45

Trp Leu Ala Pro Ala Lys Thr Ile Pro Leu Ser Glu Pro Gly Leu Trp
     50                  55                  60

Thr Tyr Gly Pro Lys Glu Leu Phe Asn Pro Val Ser Pro Met His Met
 65                  70                  75                  80

Pro Leu Arg Val Asp Pro Lys Leu Trp Leu Phe Leu Ala Gln Phe Met
                 85                  90                  95

Ala Gln Ala Phe Gln Arg Lys Trp Asp Ser Thr Met Ala Asp Leu Thr
            100                 105                 110

Glu Ile Asp Lys Val Ala Leu Glu Ala Phe Asp Glu Leu Ser Ile Gly
        115                 120                 125

Gly Val Glu Gly Leu Thr His Glu Gly Pro Phe Val Ile Gly Phe Glu
    130                 135                 140

Glu Glu Arg Gln Ser Ala Gly Phe Arg Lys Glu Ile Asp Gly Val Ser
145                 150                 155                 160
```

```
Arg His Gly Gln Lys Val Glu Met Ser Arg Leu Glu Asn Pro Gln Glu
                165                 170                 175

Leu Ala Pro Met Leu Asn Glu Gln Ile Gln Val Ala Tyr Arg Leu Glu
            180                 185                 190

Gly Gln Arg Phe Ile Glu Pro Gly Pro Tyr Val Gln Ser Leu Ala Asp
        195                 200                 205

Ala Val Val Lys Arg Gly Gly Val Ile Arg Ala Gly Ala Glu Val Val
    210                 215                 220

His Val Ala Lys Gly Asp Arg Pro Ala Val Ile Leu Ala Asp Gly Ser
225                 230                 235                 240

Arg Glu Glu Ala Asp Lys Val Val Val Ala Thr Gly Ala Trp Leu Pro
                245                 250                 255

Gly Leu Thr Arg Glu Tyr Gly Val Lys Thr Leu Val Gln Ala Gly Arg
            260                 265                 270

Gly Tyr Ser Phe Ser Val Ala Thr Asp Ile Pro Ala Lys His Ser Val
        275                 280                 285

Tyr Leu Pro His His Arg His Gly Leu His Ala Val
    290                 295                 300
```

SEQUENCE LISTING

<210> 241
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXN02021

<400> 241

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ttgggtcgcc gaggagatct aatcctggtt tgagttcaga gttcacaggt ttaagcctac 60

aaaccttagt taaaacatga tggaagcggt cgattaaaaa atg agt gaa aac att   115
                                            Met Ser Glu Asn Ile
                                              1               5

cgc gga gcc caa gca gtt gga atc gca aat atc gcc atg gac ggg acc   163
Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile Ala Met Asp Gly Thr
                10                  15                  20

atc ctg gac acg tgg tac cca gaa ccc caa att ttc aac ccg gat cag   211
Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile Phe Asn Pro Asp Gln
            25                  30                  35

tgg gct gaa cgc tac cca ttg gaa gtg ggc acc aca cgc ctc gga gca   259
Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr Thr Arg Leu Gly Ala
        40                  45                  50

aac gaa ctc acc cca cgg atg ctg cag ttg gta aaa ctg gac caa gat   307
Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val Lys Leu Asp Gln Asp
    55                  60                  65
```

```
cgc ctc gtc gaa cag gta gca gtc cgc acc gtt atc ccc gat ctg tct   355
Arg Leu Val Glu Gln Val Ala Val Arg Thr Val Ile Pro Asp Leu Ser
 70                  75                  80                  85

caa cct cca gta gac gcg cac gat gtt tac ctg cgc ctc cac ctg ctt   403
Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu Arg Leu His Leu Leu
                 90                  95                 100

tcc cac cgg ctg gtc cgc ccc cac gaa atg cac atg caa aac acc ttg   451
Ser His Arg Leu Val Arg Pro His Glu Met His Met Gln Asn Thr Leu
            105                 110                 115

gag ctg ctg tcc gac gtg gtg tgg aca aac aag ggc cct tgc ctt cct   499
Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys Gly Pro Cys Leu Pro
        120                 125                 130

gaa aac ttt gag tgg gtg cgt ggt gct ctg cgg tcc cgc gga ctc atc   547
Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg Ser Arg Gly Leu Ile
    135                 140                 145

cac gtc tac tgt gtg gac cgt ctt ccc cgc atg gtc gac tat gtg gtt   595
His Val Tyr Cys Val Asp Arg Leu Pro Arg Met Val Asp Tyr Val Val
150                 155                 160                 165

ccc cct gga gtc cgc atc tcc gaa gca gaa cgc gtg cgc cta ggt gca   643
Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg Val Arg Leu Gly Ala
                170                 175                 180

tac ctt gct ccg ggt acc tct gtg ctg cgt gaa ggt ttc gtg tct ttc   691
Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu Gly Phe Val Ser Phe
            185                 190                 195

aac tcc ggc acc ttg ggt gcc gca aag gtg gaa ggc cgc ctg agt tcc   739
Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu Gly Arg Leu Ser Ser
        200                 205                 210

ggt gtg gtc atc ggt gaa ggt tcc gag att gga ctg tct tct act att   787
Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly Leu Ser Ser Thr Ile
    215                 220                 225

cag tcc ccg aga gat gaa cag cgc cgc cgt ttg ccg ttg agc atc ggc   835
Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu Pro Leu Ser Ile Gly
230                 235                 240                 245

caa aac tgc aac ttt ggt gtc agc tcc gga atc atc gga gtc agt ctg   883
Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile Ile Gly Val Ser Leu
                250                 255                 260

gga gac aat tgc gac atc gga aat aac att gtc ttg gat gga gat acc   931
Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val Leu Asp Gly Asp Thr
            265                 270                 275

ccc att tgg ttc gca gcc gat gag gag tta cgc act atc gac tcc atc   979
Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg Thr Ile Asp Ser Ile
        280                 285                 290

gaa ggc caa gca aat tgg tca atc aag cgt gaa tcc ggc ttc cat gag   1027
Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu Ser Gly Phe His Glu
    295                 300                 305

cca gtt gcc cgc ctc aaa gct tgacccattt tcataaccag tgc            1071
```

```
Pro Val Ala Arg Leu Lys Ala
310                 315
```

<210> 242
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 242

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Met Ser Glu Asn Ile Arg Gly Ala Gln Ala Val Gly Ile Ala Asn Ile
  1               5                  10                  15

Ala Met Asp Gly Thr Ile Leu Asp Thr Trp Tyr Pro Glu Pro Gln Ile
            20                  25                  30

Phe Asn Pro Asp Gln Trp Ala Glu Arg Tyr Pro Leu Glu Val Gly Thr
        35                  40                  45

Thr Arg Leu Gly Ala Asn Glu Leu Thr Pro Arg Met Leu Gln Leu Val
    50                  55                  60

Lys Leu Asp Gln Asp Arg Leu Val Glu Gln Val Ala Val Arg Thr Val
65                  70                  75                  80

Ile Pro Asp Leu Ser Gln Pro Pro Val Asp Ala His Asp Val Tyr Leu
                85                  90                  95

Arg Leu His Leu Leu Ser His Arg Leu Val Arg Pro His Glu Met His
            100                 105                 110

Met Gln Asn Thr Leu Glu Leu Leu Ser Asp Val Val Trp Thr Asn Lys
        115                 120                 125

Gly Pro Cys Leu Pro Glu Asn Phe Glu Trp Val Arg Gly Ala Leu Arg
    130                 135                 140

Ser Arg Gly Leu Ile His Val Tyr Cys Val Asp Arg Leu Pro Arg Met
145                 150                 155                 160

Val Asp Tyr Val Val Pro Pro Gly Val Arg Ile Ser Glu Ala Glu Arg
                165                 170                 175

Val Arg Leu Gly Ala Tyr Leu Ala Pro Gly Thr Ser Val Leu Arg Glu
            180                 185                 190

Gly Phe Val Ser Phe Asn Ser Gly Thr Leu Gly Ala Ala Lys Val Glu
        195                 200                 205

Gly Arg Leu Ser Ser Gly Val Val Ile Gly Glu Gly Ser Glu Ile Gly
    210                 215                 220

Leu Ser Ser Thr Ile Gln Ser Pro Arg Asp Glu Gln Arg Arg Arg Leu
225                 230                 235                 240

Pro Leu Ser Ile Gly Gln Asn Cys Asn Phe Gly Val Ser Ser Gly Ile
                245                 250                 255

Ile Gly Val Ser Leu Gly Asp Asn Cys Asp Ile Gly Asn Asn Ile Val
            260                 265                 270
```

```
Leu Asp Gly Asp Thr Pro Ile Trp Phe Ala Ala Asp Glu Glu Leu Arg
        275                 280                 285

Thr Ile Asp Ser Ile Glu Gly Gln Ala Asn Trp Ser Ile Lys Arg Glu
    290                 295                 300

Ser Gly Phe His Glu Pro Val Ala Arg Leu Lys Ala
305                 310                 315
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<210> 243
<211> 771
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(748)
<223> RXS00949

<400> 243

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gctcaaggat ccttcctggg caaaccaagc agccctcgca ctaggtgcgg aacccaggta 60

tgttcaccaa tacgactacg tactttaaag gagagttgac atg aag gtt ttc atc   115
                                            Met Lys Val Phe Ile
                                              1               5

atc ggc gct gcg ggt ggc atc ggc aat cga ctt tcc agc ctg ctt cac   163
Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu Ser Ser Leu Leu His
                10                  15                  20

gcc agg gga gat gca gtt agc ggc atg cac cgc aat ctt gag cag gcc   211
Ala Arg Gly Asp Ala Val Ser Gly Met His Arg Asn Leu Glu Gln Ala
            25                  30                  35

tca aaa atc aca gac act ggg gca act gcc gta ctc ggg gat ctc atc   259
Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val Leu Gly Asp Leu Ile
        40                  45                  50

cac aac agc acg gag gag ctt gcg gag ctt ttc cgc ggt cac gat gcc   307
His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe Arg Gly His Asp Ala
    55                  60                  65

atc gta ttt tct gca ggc gcc cac gga aca ggg caa gaa aat acc acg   355
Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly Gln Glu Asn Thr Thr
70                  75                  80                  85

ctt atc gac ggc gcc ggc ctc cgt aaa gcc gcc gac gct gcc agc gcg   403
Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala Asp Ala Ala Ser Ala
                90                  95                  100

gcc aac gtt tca cgc ttc atc ttg gtc tct gcg ttt ccg gaa tcc tcc   451
Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala Phe Pro Glu Ser Ser
            105                 110                 115

cgc ggg gag aac acc acc gag aac ttt gag cac tat atg aag gtg aag   499
Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His Tyr Met Lys Val Lys
        120                 125                 130

aag tcc gcc gat gtc tac ctc agt cac act gac cta gac tgg gtt att   547
Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp Leu Asp Trp Val Ile
```

```
    135                 140                 145

gtc cga cca ggc gtg ctt caa gat gag gca ggg gat ggt tta gtc act   595
Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly Asp Gly Leu Val Thr
150                 155                 160                 165

gct ggc tta gcg att aat tac ggc aat gtt gct cgc gat aat gtc gca   643
Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala Arg Asp Asn Val Ala
                170                 175                 180

gcg ttc att gat gaa gct ctg cat caa ccg cag ttg tca aag atc att   691
Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln Leu Ser Lys Ile Ile
            185                 190                 195

gtt gaa ctc acc gac ggt tca act ccg gtg gcg gaa gcc gta gaa cgc   739
Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala Glu Ala Val Glu Arg
        200                 205                 210

ctc atc aag taaagacgaa aagagggaga atg                            771
Leu Ile Lys
    215
```

Sequence Listing

<210> 244
<211> 216
<212> PRT
<213> Corynebacterium glutamicum

<400> 244

```
Met Lys Val Phe Ile Ile Gly Ala Ala Gly Gly Ile Gly Asn Arg Leu
  1               5                  10                  15

Ser Ser Leu Leu His Ala Arg Gly Asp Ala Val Ser Gly Met His Arg
             20                  25                  30

Asn Leu Glu Gln Ala Ser Lys Ile Thr Asp Thr Gly Ala Thr Ala Val
         35                  40                  45

Leu Gly Asp Leu Ile His Asn Ser Thr Glu Glu Leu Ala Glu Leu Phe
     50                  55                  60

Arg Gly His Asp Ala Ile Val Phe Ser Ala Gly Ala His Gly Thr Gly
 65                  70                  75                  80

Gln Glu Asn Thr Thr Leu Ile Asp Gly Ala Gly Leu Arg Lys Ala Ala
                 85                  90                  95

Asp Ala Ala Ser Ala Ala Asn Val Ser Arg Phe Ile Leu Val Ser Ala
            100                 105                 110

Phe Pro Glu Ser Ser Arg Gly Glu Asn Thr Thr Glu Asn Phe Glu His
        115                 120                 125

Tyr Met Lys Val Lys Lys Ser Ala Asp Val Tyr Leu Ser His Thr Asp
    130                 135                 140

Leu Asp Trp Val Ile Val Arg Pro Gly Val Leu Gln Asp Glu Ala Gly
145                 150                 155                 160

Asp Gly Leu Val Thr Ala Gly Leu Ala Ile Asn Tyr Gly Asn Val Ala
                165                 170                 175
```

Arg Asp Asn Val Ala Ala Phe Ile Asp Glu Ala Leu His Gln Pro Gln
180 185 190

Leu Ser Lys Ile Ile Val Glu Leu Thr Asp Gly Ser Thr Pro Val Ala
195 200 205

Glu Ala Val Glu Arg Leu Ile Lys
210 215

<210> 245
<211> 594
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(571)
<223> RXS00004

<400> 245
ttgcactgtc atgactgtat cccgcgaaga agtgtccctg ccgagccgaa ctctgaacaa 60

tgccttccgg aagtattttc caattcccga tgtagggtca gtg ctg act caa ttg 115
Val Leu Thr Gln Leu
1 5

att gaa tca tcg att ttc gac aac gtt gcg agc agg gag tcc tct gaa 163
Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser Arg Glu Ser Ser Glu
10 15 20

ttt ctc ggc cat gct gcc atc gat cta ctt gct ggc ctt gtc tat gaa 211
Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala Gly Leu Val Tyr Glu
25 30 35

aaa gcc act ccc tat gct cca gat gaa gca ctt aga gtg gca gtt tat 259
Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu Arg Val Ala Val Tyr
40 45 50

ggc tat att cgg gag aac ctt gga tcc tca caa ctt acg gtc gca gct 307
Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln Leu Thr Val Ala Ala
55 60 65

gta gcc ggg gcg cat aga atc gcg gtt cgt acg ttg cat cga tta ttt 355
Val Ala Gly Ala His Arg Ile Ala Val Arg Thr Leu His Arg Leu Phe
70 75 80 85

gaa ggc gaa gca tac gga gta gcg gaa tta atc cga cac ctc cga tta 403
Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile Arg His Leu Arg Leu
90 95 100

gag gca gta tat gaa gac ctt cgg gat cct cgc ctc cag aac ctg acc 451
Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg Leu Gln Asn Leu Thr
105 110 115

att ttg gct atc ggc atg cgc cac ggc att tcc agc caa gct cat tta 499
Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser Ser Gln Ala His Leu
120 125 130

aca aga ctg ttt cgc gct aaa tat ggg gta ccg ccg gca gag ttt cgc 547

```
Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro Pro Ala Glu Phe Arg
    135                 140                 145

cga ggg tat att aat agc gct gct tgagggcacc gcaagcgtgg cgc          594
Arg Gly Tyr Ile Asn Ser Ala Ala
150                 155


<210> 246
<211> 157
<212> PRT
<213> Corynebacterium glutamicum

<400> 246
Val Leu Thr Gln Leu Ile Glu Ser Ser Ile Phe Asp Asn Val Ala Ser
  1               5                  10                  15

Arg Glu Ser Ser Glu Phe Leu Gly His Ala Ala Ile Asp Leu Leu Ala
             20                  25                  30

Gly Leu Val Tyr Glu Lys Ala Thr Pro Tyr Ala Pro Asp Glu Ala Leu
         35                  40                  45

Arg Val Ala Val Tyr Gly Tyr Ile Arg Glu Asn Leu Gly Ser Ser Gln
     50                  55                  60

Leu Thr Val Ala Ala Val Ala Gly Ala His Arg Ile Ala Val Arg Thr
 65                  70                  75                  80

Leu His Arg Leu Phe Glu Gly Glu Ala Tyr Gly Val Ala Glu Leu Ile
                 85                  90                  95

Arg His Leu Arg Leu Glu Ala Val Tyr Glu Asp Leu Arg Asp Pro Arg
            100                 105                 110

Leu Gln Asn Leu Thr Ile Leu Ala Ile Gly Met Arg His Gly Ile Ser
        115                 120                 125

Ser Gln Ala His Leu Thr Arg Leu Phe Arg Ala Lys Tyr Gly Val Pro
    130                 135                 140

Pro Ala Glu Phe Arg Arg Gly Tyr Ile Asn Ser Ala Ala
145                 150                 155


<210> 247
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> RXS00166

<400> 247
ggcgtttagc gatcttcaac atcgagcaac cagcgccagc gcttttaccc aaggcagcac 60

gacttatcac gatgtccgac ctggatatcc ggctgaggcc gtg gag tta gcc cgt   115
                                              Val Glu Leu Ala Arg
                                                1               5
```

```
ggg ttt ggc cga gtc ctg gat gtc ggt gca ggt acc gga aaa cta acc   163
Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly Thr Gly Lys Leu Thr
                10                  15                  20

agt gag cta aca gct gat cag gtc cta gcc ctt gat cca agc atg gac   211
Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu Asp Pro Ser Met Asp
            25                  30                  35

atg ttg cgg gtg ttt cgc tcc gcg ctt ccg gcg gtt ccc tgc tgg caa   259
Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala Val Pro Cys Trp Gln
        40                  45                  50

gcg aca gca gaa cac aca gga ata cgt gac aac gcg gtt gat ctg att   307
Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn Ala Val Asp Leu Ile
    55                  60                  65

acg tgc gca caa acg tgg cat tgg gtt gac gtg acg gct gcc tca gcg   355
Thr Cys Ala Gln Thr Trp His Trp Val Asp Val Thr Ala Ala Ser Ala
70                  75                  80                  85

gaa ttt gat cgg gtg att gca cct gag ggt gca gtc ctg ctc gtg tgg   403
Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala Val Leu Leu Val Trp
                90                  95                  100

aat aac ctg gac acc tcc atc gcg tgg gta cac cga ctc agt cgc att   451
Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His Arg Leu Ser Arg Ile
            105                 110                 115

atg cat gcc ggc gat gta ctc aag ccg gga ttc acc cca gaa acc gca   499
Met His Ala Gly Asp Val Leu Lys Pro Gly Phe Thr Pro Glu Thr Ala
        120                 125                 130

gct ccc tgg ata att gat cga gaa att cgc acc acg tgg aat cag cac   547
Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr Thr Trp Asn Gln His
    135                 140                 145

ctc acc cct gaa gaa atc atc cag ctc gct cac acg agg tcc tac tgg   595
Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His Thr Arg Ser Tyr Trp
150                 155                 160                 165

tta aac gcg tca gag aaa atc aaa gag cgt gtt gat cag aac ctt cag   643
Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val Asp Gln Asn Leu Gln
                170                 175                 180

tgg tat ctc tac gag cat ttg ggt ttc agt ccc gac aat cca gtg gaa   691
Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro Asp Asn Pro Val Glu
            185                 190                 195

ctt ccc tat cgc tgt gat gca ttt tta ctt tca cgt tcc ggt acc ctg   739
Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser Arg Ser Gly Thr Leu
        200                 205                 210

gca ggc aga tct tcc aat ctt taggagccct cgccatgtac ctg             783
Ala Gly Arg Ser Ser Asn Leu
    215                 220
```

<210> 248
<211> 220
<212> PRT

<213> Corynebacterium glutamicum

<400> 248

```
Val Glu Leu Ala Arg Gly Phe Gly Arg Val Leu Asp Val Gly Ala Gly
 1               5                  10                  15

Thr Gly Lys Leu Thr Ser Glu Leu Thr Ala Asp Gln Val Leu Ala Leu
            20                  25                  30

Asp Pro Ser Met Asp Met Leu Arg Val Phe Arg Ser Ala Leu Pro Ala
        35                  40                  45

Val Pro Cys Trp Gln Ala Thr Ala Glu His Thr Gly Ile Arg Asp Asn
    50                  55                  60

Ala Val Asp Leu Ile Thr Cys Ala Gln Thr Trp His Trp Val Asp Val
65                  70                  75                  80

Thr Ala Ala Ser Ala Glu Phe Asp Arg Val Ile Ala Pro Glu Gly Ala
                85                  90                  95

Val Leu Leu Val Trp Asn Asn Leu Asp Thr Ser Ile Ala Trp Val His
            100                 105                 110

Arg Leu Ser Arg Ile Met His Ala Gly Asp Val Leu Lys Pro Gly Phe
        115                 120                 125

Thr Pro Glu Thr Ala Ala Pro Trp Ile Ile Asp Arg Glu Ile Arg Thr
    130                 135                 140

Thr Trp Asn Gln His Leu Thr Pro Glu Glu Ile Ile Gln Leu Ala His
145                 150                 155                 160

Thr Arg Ser Tyr Trp Leu Asn Ala Ser Glu Lys Ile Lys Glu Arg Val
                165                 170                 175

Asp Gln Asn Leu Gln Trp Tyr Leu Tyr Glu His Leu Gly Phe Ser Pro
            180                 185                 190

Asp Asn Pro Val Glu Leu Pro Tyr Arg Cys Asp Ala Phe Leu Leu Ser
        195                 200                 205

Arg Ser Gly Thr Leu Ala Gly Arg Ser Ser Asn Leu
    210                 215                 220
```

<210> 249
<211> 1134
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1111)
<223> RXS00288

<400> 249

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ggcgtgctaa aaaagcacgt caaatacaga atcggcagat tacatcgctg agcagagaaa 60

acacgggcat gaaacgtacc caagggctaa catcgggggc atg agc gcg caa atg   115
                                               Met Ser Ala Gln Met
```

```
                                                    1               5

gat acc cct gat ccc act atg tct gct gtt gca atg tta gat tcc atc   163
Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala Met Leu Asp Ser Ile
                10                  15                  20

cct tct gat caa cca gat ttc ctg atc gat gta gaa gta gat cga cca   211
Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val Glu Val Asp Arg Pro
            25                  30                  35

act ccc gga cca cat gat ctg cta gtc cac att gag gcg gtc tca att   259
Thr Pro Gly Pro His Asp Leu Leu Val His Ile Glu Ala Val Ser Ile
        40                  45                  50

aac cct gtt gat acc aag gta cgc atg cgg gcc ggg aag caa aag cat   307
Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala Gly Lys Gln Lys His
    55                  60                  65

cct aaa att tta ggt ttt gat gct gca ggt gag gtg gtg gct gtt gga   355
Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu Val Val Ala Val Gly
70                  75                  80                  85

tcg cag gtc acg ctc ttc aat gtt ggt gac aaa gtg ttc tac gca gga   403
Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys Val Phe Tyr Ala Gly
                90                  95                  100

tcc aat cag cgt cca gga agt aac gca gag tac cag gtg gtg gat gaa   451
Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr Gln Val Val Asp Glu
            105                 110                 115

cgg ctg gtg ggt cac gca cca caa agc ttg ggg gca cac gac gcc gct   499
Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly Ala His Asp Ala Ala
        120                 125                 130

gct ctc cca ctt gtc gcg ctc act gca tgg gag tca ctt ttt gac cga   547
Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu Ser Leu Phe Asp Arg
    135                 140                 145

ttg gga gta act cag tca act act gga aca ctg ttg gtc ttg ggc ggt   595
Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu Leu Val Leu Gly Gly
150                 155                 160                 165

tca gga ggt gtg cct tca gct ctt att caa ctt gct cga gct ctc act   643
Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu Ala Arg Ala Leu Thr
                170                 175                 180

ggt ctg aaa gta gtg gca aca gct tct cgc cct gaa tca caa gaa tgg   691
Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro Glu Ser Gln Glu Trp
            185                 190                 195

gtg aca aag ctc ggt gct cat gag gtg att gat cac tcc aag gat ttg   739
Val Thr Lys Leu Gly Ala His Glu Val Ile Asp His Ser Lys Asp Leu
        200                 205                 210

agt gag caa atc tcc gac gtg gat ttt gtt ttc agc tcg tgg act act   787
Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe Ser Ser Trp Thr Thr
    215                 220                 225

ggg cgt gaa gta gag ctc gcc acg ttg atg aaa ccc cag tcc cac cta   835
Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys Pro Gln Ser His Leu
230                 235                 240                 245
```

```
gtg ctc atc gat gat cca gtg gat ccc aat ttg ggc gct ttt aag caa   883
Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu Gly Ala Phe Lys Gln
                250                 255                 260

aaa gcg atc gct ttg cac tgg gag ttc atg ttt acc cgc gct atg ttc   931
Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe Thr Arg Ala Met Phe
            265                 270                 275

aac act cct gat atg ggt gaa caa ggg aaa att ctg aat aag atc gcc   979
Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile Leu Asn Lys Ile Ala
        280                 285                 290

gac atg gtt gat cgg ggt cag ttt gag tcc gtg aca gca acg gtg ctg   1027
Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val Thr Ala Thr Val Leu
    295                 300                 305

gat ggg ctc aac gct gca aac atc atg gag ggg cac cgg ctc gtt gag   1075
Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly His Arg Leu Val Glu
310                 315                 320                 325

cag ggt aaa acc tca gga aaa att gtt gtg agg gta taaagaggac        1121
Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg Val
                330                 335

ttgaaaaatg cac                                                   1134


<210> 250
<211> 337
<212> PRT
<213> Corynebacterium glutamicum

<400> 250
Met Ser Ala Gln Met Asp Thr Pro Asp Pro Thr Met Ser Ala Val Ala
  1               5                  10                  15

Met Leu Asp Ser Ile Pro Ser Asp Gln Pro Asp Phe Leu Ile Asp Val
             20                  25                  30

Glu Val Asp Arg Pro Thr Pro Gly Pro His Asp Leu Leu Val His Ile
         35                  40                  45

Glu Ala Val Ser Ile Asn Pro Val Asp Thr Lys Val Arg Met Arg Ala
     50                  55                  60

Gly Lys Gln Lys His Pro Lys Ile Leu Gly Phe Asp Ala Ala Gly Glu
 65                  70                  75                  80

Val Val Ala Val Gly Ser Gln Val Thr Leu Phe Asn Val Gly Asp Lys
                 85                  90                  95

Val Phe Tyr Ala Gly Ser Asn Gln Arg Pro Gly Ser Asn Ala Glu Tyr
            100                 105                 110

Gln Val Val Asp Glu Arg Leu Val Gly His Ala Pro Gln Ser Leu Gly
        115                 120                 125

Ala His Asp Ala Ala Ala Leu Pro Leu Val Ala Leu Thr Ala Trp Glu
    130                 135                 140
```

```
Ser Leu Phe Asp Arg Leu Gly Val Thr Gln Ser Thr Thr Gly Thr Leu
145                 150                 155                 160

Leu Val Leu Gly Gly Ser Gly Gly Val Pro Ser Ala Leu Ile Gln Leu
                165                 170                 175

Ala Arg Ala Leu Thr Gly Leu Lys Val Val Ala Thr Ala Ser Arg Pro
            180                 185                 190

Glu Ser Gln Glu Trp Val Thr Lys Leu Gly Ala His Glu Val Ile Asp
        195                 200                 205

His Ser Lys Asp Leu Ser Glu Gln Ile Ser Asp Val Asp Phe Val Phe
    210                 215                 220

Ser Ser Trp Thr Thr Gly Arg Glu Val Glu Leu Ala Thr Leu Met Lys
225                 230                 235                 240

Pro Gln Ser His Leu Val Leu Ile Asp Asp Pro Val Asp Pro Asn Leu
                245                 250                 255

Gly Ala Phe Lys Gln Lys Ala Ile Ala Leu His Trp Glu Phe Met Phe
            260                 265                 270

Thr Arg Ala Met Phe Asn Thr Pro Asp Met Gly Glu Gln Gly Lys Ile
        275                 280                 285

Leu Asn Lys Ile Ala Asp Met Val Asp Arg Gly Gln Phe Glu Ser Val
    290                 295                 300

Thr Ala Thr Val Leu Asp Gly Leu Asn Ala Ala Asn Ile Met Glu Gly
305                 310                 315                 320

His Arg Leu Val Glu Gln Gly Lys Thr Ser Gly Lys Ile Val Val Arg
                325                 330                 335

Val
```

Sequence Listing

<210> 251
<211> 1347
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1324)
<223> RXS01114

<400> 251
ttcggtggaa gatatccgca agctggtgct gccgcagctt ttagaaacgg ctcaagcaat 60

ttcgacagat ctctctgcac tctaaattaa ggatcaaaaa atg aac cct caa gat 115
Met Asn Pro Gln Asp
1 5

att gtc atc tgt tcc cca ttg cgc acc cca gtt ggt gct tac cgc gga 163
Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val Gly Ala Tyr Gly Gly
10 15 20

```
tcc ttc acc ggc gtc cct gtt gaa gaa ttg gcc acc acc gtg atc aac   211
Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala Thr Thr Val Ile Asn
             25                  30                  35

gcg atc gtt gag gca acc ggc atc acc ggc gac gat gtg gac gat ctg   259
Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp Asp Val Asp Asp Leu
         40                  45                  50

atc ctc ggc cag gca tcc ccc aac ggt gcg gct cca gca ctg ggc cgt   307
Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala Pro Ala Leu Gly Arg
     55                  60                  65

gtt gtt gct cta gat tcc aag ctt ggc caa aac gtt cca ggc atg cag   355
Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn Val Pro Gly Met Gln
 70                  75                  80                  85

ctt gat cgc cgc tgt ggt tcc ggc ctg cag gca atc gtc acc gct gct   403
Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala Ile Val Thr Ala Ala
                 90                  95                 100

gca cac gtt gca tcc ggc gct gct gat ctg atc atc gca ggt ggc gca   451
Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile Ile Ala Gly Gly Ala
            105                 110                 115

gaa tcc atg agc cgc gtt gag tac acc gtg tcc ggc gat atc cgt tgg   499
Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser Gly Asp Ile Arg Trp
        120                 125                 130

ggt gtc aag ggc ggc gac atg cag ctt cgt gac cgc ctt gca gaa gca   547
Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp Arg Leu Ala Glu Ala
    135                 140                 145

cgc gaa acc gct ggc gga cgc aac cac ccg atc cct ggt ggc atg atc   595
Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile Pro Gly Gly Met Ile
150                 155                 160                 165

gag acc gct gag aac ctg cgt cgc gaa tac ggc atc tcc cgc gag gag   643
Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly Ile Ser Arg Glu Glu
                170                 175                 180

cag gac aag atc tcc gca gcg tcc cag cag cgt tgg ggc aag gct gct   691
Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg Trp Gly Lys Ala Ala
            185                 190                 195

gat gcg ggg ctt ttc gac gac gag atc gtg cca gtc acc gtc cct gcc   739
Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro Val Thr Val Pro Ala
        200                 205                 210

aag aag cgc ggc cag gag cca acc atc gtt tct cga gac gag cat ggt   787
Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser Arg Asp Glu His Gly
    215                 220                 225

cga cca gga aca acc gtc gaa aag ctt gct gct ttg cgc ccc atc atg   835
Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala Leu Arg Pro Ile Met
230                 235                 240                 245

ggc cgc cag gat gcg gaa gca acc gtc acc gct ggc aac gcg tcc ggc   883
Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala Gly Asn Ala Ser Gly
                250                 255                 260

caa aat gat ggc gct gct gcc gtc atc gtg acc act cgc gcc aag gcc   931
```

```
Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr Thr Arg Ala Lys Ala
            265                 270                 275

gag gag aag ggc ctg cgc cca gtc atg cgt ttg gct ggc tgg tct gtg   979
Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu Ala Gly Trp Ser Val
        280                 285                 290

gct gct gtt ccc cca gag acc atg ggt att gga cct gtt cct gcc acc   1027
Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly Pro Val Pro Ala Thr
    295                 300                 305

aag aag gtc ctg gat cgt ttg ggc ctt acc ctg gag gac atc ggc gcg   1075
Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu Glu Asp Ile Gly Ala
310                 315                 320                 325

atc gaa ctc aac gaa gct ttc gca gct cag gca ctg tct gtg ctg aag   1123
Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala Leu Ser Val Leu Lys
                330                 335                 340

gaa tgg aac att tct tgg gaa gat gag cgc gtc aac cca ctg ggt tcc   1171
Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val Asn Pro Leu Gly Ser
            345                 350                 355

ggt att tcc atg gga cac cca gtc ggt gcc acc ggt gct cgc atg gca   1219
Gly Ile Ser Met Gly His Pro Val Gly Ala Thr Gly Ala Arg Met Ala
        360                 365                 370

gta acc ttg gct cac cgc atg cag cgt gaa aac act cag tac gga ctg   1267
Val Thr Leu Ala His Arg Met Gln Arg Glu Asn Thr Gln Tyr Gly Leu
    375                 380                 385

gcc acc atg tgc atc ggt ggc ggc cag ggt ctt gca gct gtc ttt gaa   1315
Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu Ala Ala Val Phe Glu
390                 395                 400                 405

aag gag aac taaaaatggc tattttgcac agc                            1347
Lys Glu Asn
```

09509425.1-090105

<210> 252
<211> 408
<212> PRT
<213> Corynebacterium glutamicum

<400> 252

```
Met Asn Pro Gln Asp Ile Val Ile Cys Ser Pro Leu Arg Thr Pro Val
  1               5                  10                  15

Gly Ala Tyr Gly Gly Ser Phe Thr Gly Val Pro Val Glu Glu Leu Ala
            20                  25                  30

Thr Thr Val Ile Asn Ala Ile Val Glu Ala Thr Gly Ile Thr Gly Asp
        35                  40                  45

Asp Val Asp Asp Leu Ile Leu Gly Gln Ala Ser Pro Asn Gly Ala Ala
    50                  55                  60

Pro Ala Leu Gly Arg Val Val Ala Leu Asp Ser Lys Leu Gly Gln Asn
65                  70                  75                  80
```

Val Pro Gly Met Gln Leu Asp Arg Arg Cys Gly Ser Gly Leu Gln Ala
85 90 95

Ile Val Thr Ala Ala Ala His Val Ala Ser Gly Ala Ala Asp Leu Ile
100 105 110

Ile Ala Gly Gly Ala Glu Ser Met Ser Arg Val Glu Tyr Thr Val Ser
115 120 125

Gly Asp Ile Arg Trp Gly Val Lys Gly Gly Asp Met Gln Leu Arg Asp
130 135 140

Arg Leu Ala Glu Ala Arg Glu Thr Ala Gly Gly Arg Asn His Pro Ile
145 150 155 160

Pro Gly Gly Met Ile Glu Thr Ala Glu Asn Leu Arg Arg Glu Tyr Gly
165 170 175

Ile Ser Arg Glu Glu Gln Asp Lys Ile Ser Ala Ala Ser Gln Gln Arg
180 185 190

Trp Gly Lys Ala Ala Asp Ala Gly Leu Phe Asp Asp Glu Ile Val Pro
195 200 205

Val Thr Val Pro Ala Lys Lys Arg Gly Gln Glu Pro Thr Ile Val Ser
210 215 220

Arg Asp Glu His Gly Arg Pro Gly Thr Thr Val Glu Lys Leu Ala Ala
225 230 235 240

Leu Arg Pro Ile Met Gly Arg Gln Asp Ala Glu Ala Thr Val Thr Ala
245 250 255

Gly Asn Ala Ser Gly Gln Asn Asp Gly Ala Ala Ala Val Ile Val Thr
260 265 270

Thr Arg Ala Lys Ala Glu Glu Lys Gly Leu Arg Pro Val Met Arg Leu
275 280 285

Ala Gly Trp Ser Val Ala Ala Val Pro Pro Glu Thr Met Gly Ile Gly
290 295 300

Pro Val Pro Ala Thr Lys Lys Val Leu Asp Arg Leu Gly Leu Thr Leu
305 310 315 320

Glu Asp Ile Gly Ala Ile Glu Leu Asn Glu Ala Phe Ala Ala Gln Ala
325 330 335

Leu Ser Val Leu Lys Glu Trp Asn Ile Ser Trp Glu Asp Glu Arg Val
340 345 350

Asn Pro Leu Gly Ser Gly Ile Ser Met Gly His Pro Val Gly Ala Thr
355 360 365

Gly Ala Arg Met Ala Val Thr Leu Ala His Arg Met Gln Arg Glu Asn
370 375 380

Thr Gln Tyr Gly Leu Ala Thr Met Cys Ile Gly Gly Gly Gln Gly Leu
385 390 395 400

Ala Ala Val Phe Glu Lys Glu Asn

405

<210> 253
<211> 554
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(531)
<223> RXS01205

<400> 253

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gta tcg gcc tat ccg ccg gcc atc atc gca gcg gct ctc gta gga att   48
Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
  1               5                  10                  15

tgc gcg gga gtt ttg ccc cat aat ttt gaa ccc tcg cga ata ttt atg   96
Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
             20                  25                  30

ggc gat tcc ggc tcc atg ctc atc ggc ctg ctg ttg gct gca gca tcg   144
Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser
         35                  40                  45

acc tca gcg tca gga aaa atc aac atg agc ctg tat ggc gca gct gat   192
Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp
     50                  55                  60

ttt atc gca ttg atc tca ccc atc atc gtt gtt ctc gcc gcc gtg gcc   240
Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala
 65                  70                  75                  80

atc cca ctg ctc gac ctc gtg atg gca gtg gtt agg cgc gtg ggc agg   288
Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg
                 85                  90                  95

gga gca tca ccc ttt tcc ccg gac aaa atg cat ctg cac cac cga ctg   336
Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu
            100                 105                 110

ctg tcc atc gga cac acc cat agg cgc gtg gtc cta gtg ctc tac acc   384
Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr
        115                 120                 125

tgg gcg agc gcc gtg gca ttc ggc gca gtg agc ttc tcc gtc gtt ccg   432
Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro
    130                 135                 140

cca ctg ttt gcc acc gga tcg agc atc tgt ggc atc ctc atc gcc gtc   480
Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val
145                 150                 155                 160

gct gtc aca gcc gtg cca gtg atg aaa agc cgg cga gcc gcc aaa ctt   528
Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu
                165                 170                 175

gat taagtgattg tcactttgga ttg                                    554
Asp
```

<210> 254
<211> 177
<212> PRT
<213> Corynebacterium glutamicum

<400> 254

```
Val Ser Ala Tyr Pro Pro Ala Ile Ile Ala Ala Ala Leu Val Gly Ile
  1               5                  10                  15

Cys Ala Gly Val Leu Pro His Asn Phe Glu Pro Ser Arg Ile Phe Met
             20                  25                  30

Gly Asp Ser Gly Ser Met Leu Ile Gly Leu Leu Leu Ala Ala Ala Ser
         35                  40                  45

Thr Ser Ala Ser Gly Lys Ile Asn Met Ser Leu Tyr Gly Ala Ala Asp
     50                  55                  60

Phe Ile Ala Leu Ile Ser Pro Ile Ile Val Val Leu Ala Ala Val Ala
 65                  70                  75                  80

Ile Pro Leu Leu Asp Leu Val Met Ala Val Val Arg Arg Val Gly Arg
                 85                  90                  95

Gly Ala Ser Pro Phe Ser Pro Asp Lys Met His Leu His His Arg Leu
            100                 105                 110

Leu Ser Ile Gly His Thr His Arg Arg Val Val Leu Val Leu Tyr Thr
        115                 120                 125

Trp Ala Ser Ala Val Ala Phe Gly Ala Val Ser Phe Ser Val Val Pro
    130                 135                 140

Pro Leu Phe Ala Thr Gly Ser Ser Ile Cys Gly Ile Leu Ile Ala Val
145                 150                 155                 160

Ala Val Thr Ala Val Pro Val Met Lys Ser Arg Arg Ala Ala Lys Leu
                165                 170                 175

Asp
```

<210> 255
<211> 564
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(541)
<223> RXS01269

<400> 255

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gattatctct gcgccgattc agctggcaat agcagcagtt gtattgagag ctcatggtcg 60

tccgattcta tttcgtcaac cacgacctgg gaaagacggt gtg gta ttt gag atg   115
                                              Val Val Phe Glu Met
                                                1               5
```

```
att aag ttt cga acc atg ctt gaa cca gat gaa aaa cat gta act gat   163
Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu Lys His Val Thr Asp
                10                  15                  20

gaa cag cgt cta act aaa gtt gga aag ctt ctg cgg gaa acg agt tta   211
Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu Arg Glu Thr Ser Leu
            25                  30                  35

gat gag tta cct aca ctc tgg aat gta ttt aaa ggt gat atg agc ctt   259
Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys Gly Asp Met Ser Leu
        40                  45                  50

gta ggg cct cga cct ttg ctt gtt agc tat ctg gaa cat tac tct tct   307
Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu Glu His Tyr Ser Ser
    55                  60                  65

gaa caa gct cga cgc cat gaa gtt cgt cct ggg att act ggt ttg gct   355
Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly Ile Thr Gly Leu Ala
70                  75                  80                  85

cag gtg aat ggc cgt aat caa act act tgg gat gaa cga ctt aag ttg   403
Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp Glu Arg Leu Lys Leu
                90                  95                  100

gat gtc gaa tat gtg gat cgc tgt agt ttg aaa cta gat ttc aaa ata   451
Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys Leu Asp Phe Lys Ile
            105                 110                 115

tta atc gcc act gta aaa aca gtt ctt tct aaa aag ggc att agt aat   499
Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys Lys Gly Ile Ser Asn
        120                 125                 130

gaa ggt cat gtc acg atg cca tcc ttc att gaa gaa aga aaa           541
Glu Gly His Val Thr Met Pro Ser Phe Ile Glu Glu Arg Lys
    135                 140                 145

tagcaggtaa aaattttact ttc                                        564
```

<210> 256
<211> 147
<212> PRT
<213> Corynebacterium glutamicum

<400> 256

```
Val Val Phe Glu Met Ile Lys Phe Arg Thr Met Leu Glu Pro Asp Glu
  1               5                  10                  15

Lys His Val Thr Asp Glu Gln Arg Leu Thr Lys Val Gly Lys Leu Leu
            20                  25                  30

Arg Glu Thr Ser Leu Asp Glu Leu Pro Thr Leu Trp Asn Val Phe Lys
        35                  40                  45

Gly Asp Met Ser Leu Val Gly Pro Arg Pro Leu Leu Val Ser Tyr Leu
    50                  55                  60

Glu His Tyr Ser Ser Glu Gln Ala Arg Arg His Glu Val Arg Pro Gly
65                  70                  75                  80
```

```
Ile Thr Gly Leu Ala Gln Val Asn Gly Arg Asn Gln Thr Thr Trp Asp
                 85                  90                  95

Glu Arg Leu Lys Leu Asp Val Glu Tyr Val Asp Arg Cys Ser Leu Lys
            100                 105                 110

Leu Asp Phe Lys Ile Leu Ile Ala Thr Val Lys Thr Val Leu Ser Lys
        115                 120                 125

Lys Gly Ile Ser Asn Glu Gly His Val Thr Met Pro Ser Phe Ile Glu
    130                 135                 140

Glu Arg Lys
145
```

<210> 257
<211> 510
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(487)
<223> RXS01421

<400> 257

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ttgatgcacg tgcagaaatc gtcggcggtc cgtggcaccc atctgttaag ggagactcgg 60

ttactgcagg gatcctgcga gatcgagtaa acgcctaaag atg acg tcg aaa agc   115
                                        Met Thr Ser Lys Ser
                                          1               5

att agc ggc aag cgc ccg aat ctg ccg tcg ctc act gga gcg cgg tgg   163
Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu Thr Gly Ala Arg Trp
                10                  15                  20

ctc gcg gcg ctc gct gtt tat ttt ttg cat gcg ttg gtg ttt ttg tcg   211
Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala Leu Val Phe Leu Ser
            25                  30                  35

gtg tat ccg ttc cag cag tcg gaa ctg ttt gcc aca atc cat aaa ttt   259
Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala Thr Ile His Lys Phe
        40                  45                  50

gtc ccc atg cag ctg ggt tca gct ggt gta acc ttc ttc ttt atc ttg   307
Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr Phe Phe Phe Ile Leu
    55                  60                  65

tcc gga ttt ttg atc tat tgg tca aat agc cag ctc aag ggc atg aag   355
Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln Leu Lys Gly Met Lys
70                  75                  80                  85

aat gtg ctg tat tac tgc aag cgc cgc atc acc aag att tat ccc atg   403
Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr Lys Ile Tyr Pro Met
                90                  95                  100

cac ttg att gcg ttg ccg atg ttt att gag gcg tcg gcg aag ttc acg   451
His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala Ser Ala Lys Phe Thr
            105                 110                 115
```

act aca ggc att acc tgg gtg ctg att ttg cgc gag taaagctgtg 497
Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg Glu
120 125

gctgcggaat gcg 510

<210> 258
<211> 129
<212> PRT
<213> Corynebacterium glutamicum

<400> 258
Met Thr Ser Lys Ser Ile Ser Gly Lys Arg Pro Asn Leu Pro Ser Leu
1 5 10 15

Thr Gly Ala Arg Trp Leu Ala Ala Leu Ala Val Tyr Phe Leu His Ala
20 25 30

Leu Val Phe Leu Ser Val Tyr Pro Phe Gln Gln Ser Glu Leu Phe Ala
35 40 45

Thr Ile His Lys Phe Val Pro Met Gln Leu Gly Ser Ala Gly Val Thr
50 55 60

Phe Phe Phe Ile Leu Ser Gly Phe Leu Ile Tyr Trp Ser Asn Ser Gln
65 70 75 80

Leu Lys Gly Met Lys Asn Val Leu Tyr Tyr Cys Lys Arg Arg Ile Thr
85 90 95

Lys Ile Tyr Pro Met His Leu Ile Ala Leu Pro Met Phe Ile Glu Ala
100 105 110

Ser Ala Lys Phe Thr Thr Thr Gly Ile Thr Trp Val Leu Ile Leu Arg
115 120 125

Glu

<210> 259
<211> 774
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(751)
<223> RXS01491

<400> 259
aacggtgtga aacacattga agtgtcgttg ggttatccgc gcgaatggga gcattggtct 60

gggcagcatg tgtggccata tccagtgatg gaggtggaca atg ctg gat gag tct 115
Met Leu Asp Glu Ser
1 5

ttg ttt cca aat tcg gca aag ttt tct ttc att aaa act ggc gat gct 163
Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile Lys Thr Gly Asp Ala
10 15 20

```
gtt aat tta gac cat ttc cat cag ttg cat ccg ttg gaa aag gca ctg   211
Val Asn Leu Asp His Phe His Gln Leu His Pro Leu Glu Lys Ala Leu
            25                  30                  35

gta gcg cac tcg gtt gat att aga aaa gca gag ttt gga gat gcc agg   259
Val Ala His Ser Val Asp Ile Arg Lys Ala Glu Phe Gly Asp Ala Arg
        40                  45                  50

tgg tgt gca cat cag gca ctc caa gct ttg gga cga gat agc ggt gat   307
Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly Arg Asp Ser Gly Asp
    55                  60                  65

ccc att ttg cgt ggg gaa cga gga atg cca ttg tgg cct tct tcg gtg   355
Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu Trp Pro Ser Ser Val
70                  75                  80                  85

tct ggt tca ttg acc cac act gac gga ttc cga gct gct gtt gtg gcg   403
Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg Ala Ala Val Val Ala
                90                  95                  100

cca cga ttg ttg gtg cgt tct atg gga ttg gat gcc gaa cct gcg gag   451
Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp Ala Glu Pro Ala Glu
            105                 110                 115

ccg ttg ccc aag gat gtt ttg ggt tca atc gct cgg gtg ggg gag att   499
Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala Arg Val Gly Glu Ile
        120                 125                 130

cct caa ctt aag cgc ttg gag gaa caa ggt gtg cac tgc gcg gat cgc   547
Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val His Cys Ala Asp Arg
    135                 140                 145

ctg ctg ttt tgt gcc aag gaa gca aca tac aaa gcg tgg ttc ccg ctg   595
Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys Ala Trp Phe Pro Leu
150                 155                 160                 165

acg cat agg tgg ctt ggt ttt gaa caa gct gag atc gac ttg cgt gat   643
Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu Ile Asp Leu Arg Asp
                170                 175                 180

gat ggc act ttt gtg tcc tat ttg ctg gtt cga cca act cca gtg ccg   691
Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg Pro Thr Pro Val Pro
            185                 190                 195

ttt att tca ggt aaa tgg gta ctg cgt gat ggt tat gtc ata gct gcg   739
Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly Tyr Val Ile Ala Ala
        200                 205                 210

act gca gtg act tgaactggat ggagaggata cct                        774
Thr Ala Val Thr
    215
```

<210> 260
<211> 217
<212> PRT
<213> Corynebacterium glutamicum

<400> 260
Met Leu Asp Glu Ser Leu Phe Pro Asn Ser Ala Lys Phe Ser Phe Ile

```
  1               5                  10                  15

Lys Thr Gly Asp Ala Val Asn Leu Asp His Phe His Gln Leu His Pro
            20                  25                  30

Leu Glu Lys Ala Leu Val Ala His Ser Val Asp Ile Arg Lys Ala Glu
        35                  40                  45

Phe Gly Asp Ala Arg Trp Cys Ala His Gln Ala Leu Gln Ala Leu Gly
    50                  55                  60

Arg Asp Ser Gly Asp Pro Ile Leu Arg Gly Glu Arg Gly Met Pro Leu
65                  70                  75                  80

Trp Pro Ser Ser Val Ser Gly Ser Leu Thr His Thr Asp Gly Phe Arg
                85                  90                  95

Ala Ala Val Val Ala Pro Arg Leu Leu Val Arg Ser Met Gly Leu Asp
            100                 105                 110

Ala Glu Pro Ala Glu Pro Leu Pro Lys Asp Val Leu Gly Ser Ile Ala
        115                 120                 125

Arg Val Gly Glu Ile Pro Gln Leu Lys Arg Leu Glu Glu Gln Gly Val
    130                 135                 140

His Cys Ala Asp Arg Leu Leu Phe Cys Ala Lys Glu Ala Thr Tyr Lys
145                 150                 155                 160

Ala Trp Phe Pro Leu Thr His Arg Trp Leu Gly Phe Glu Gln Ala Glu
                165                 170                 175

Ile Asp Leu Arg Asp Asp Gly Thr Phe Val Ser Tyr Leu Leu Val Arg
            180                 185                 190

Pro Thr Pro Val Pro Phe Ile Ser Gly Lys Trp Val Leu Arg Asp Gly
        195                 200                 205

Tyr Val Ile Ala Ala Thr Ala Val Thr
    210                 215
```

<210> 261
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXS01572

<400> 261

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ctgctgtgcg caggcatcac cacctactcc ccaatcgctc gctggaacgt taaagaaggc 60

gacaaagtag cagtcatggg cctcggcggg actcggacac atg ggt gtc cag atc   115
                                                Met Gly Val Gln Ile
                                                  1               5

gct gca gcc aag ggt gct gag gtt acc gtt ctg tcc cgt tcc ctg cgc   163
Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu Ser Arg Ser Leu Arg
```

```
                10                  15                  20

aag gca gaa ctt gcc aag gaa ctc ggc gca gct cgc acg ctt gcg act   211
Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala Arg Thr Leu Ala Thr
            25                  30                  35

tct gat gag gat ttc ttc acc gaa cac gcc ggt gaa ttc gac ttc atc   259
Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly Glu Phe Asp Phe Ile
        40                  45                  50

ctc aac acc att agc gca tcc atc cca gtc gac aag tac ctg agc ctt   307
Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp Lys Tyr Leu Ser Leu
    55                  60                  65

ctc aag cca cac ggt gtc atg gct gtt gtc ggt ctg cca cca gag aag   355
Leu Lys Pro His Gly Val Met Ala Val Val Gly Leu Pro Pro Glu Lys
70                  75                  80                  85

cag cca ctg agc ttc ggt gcg ctc atc ggc ggc gga aaa gtc ctc acc   403
Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly Gly Lys Val Leu Thr
                90                  95                  100

gga tcc aac att ggc ggc atc cct gaa acc cag gaa atg ctc gac ttc   451
Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln Glu Met Leu Asp Phe
            105                 110                 115

tgt gca aaa cac ggc ctc ggt gcg atg atc gaa act gtc ggc gtc aac   499
Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu Thr Val Gly Val Asn
        120                 125                 130

gat gtt gat gca gcc tac gac cgt gtt gtt gcc ggc gac gtt cag ttc   547
Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala Gly Asp Val Gln Phe
    135                 140                 145

cgc gtt gtc att gat act gct tcg ttt gct gag gtt gag gcg gtt       592
Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu Val Glu Ala Val
150                 155                 160

taggtttact gaagttcaga ctt                                        615
```

<210> 262
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 262

```
Met Gly Val Gln Ile Ala Ala Ala Lys Gly Ala Glu Val Thr Val Leu
  1               5                  10                  15

Ser Arg Ser Leu Arg Lys Ala Glu Leu Ala Lys Glu Leu Gly Ala Ala
            20                  25                  30

Arg Thr Leu Ala Thr Ser Asp Glu Asp Phe Phe Thr Glu His Ala Gly
        35                  40                  45

Glu Phe Asp Phe Ile Leu Asn Thr Ile Ser Ala Ser Ile Pro Val Asp
    50                  55                  60

Lys Tyr Leu Ser Leu Leu Lys Pro His Gly Val Met Ala Val Val Gly
65                  70                  75                  80
```

```
Leu Pro Pro Glu Lys Gln Pro Leu Ser Phe Gly Ala Leu Ile Gly Gly
                85                  90                  95

Gly Lys Val Leu Thr Gly Ser Asn Ile Gly Gly Ile Pro Glu Thr Gln
            100                 105                 110

Glu Met Leu Asp Phe Cys Ala Lys His Gly Leu Gly Ala Met Ile Glu
        115                 120                 125

Thr Val Gly Val Asn Asp Val Asp Ala Ala Tyr Asp Arg Val Val Ala
    130                 135                 140

Gly Asp Val Gln Phe Arg Val Val Ile Asp Thr Ala Ser Phe Ala Glu
145                 150                 155                 160

Val Glu Ala Val
```

<210> 263
<211> 876
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(853)
<223> RXS02453

<400> 263

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aaccaacaaa ggtcatctca accggcttaa gaaaattctg ccagctttct gctgattgaa 60

tcgtgccagc tcagggcata tctcacctaa agtaaacacc atg aaa tca atc ttc   115
                                            Met Lys Ser Ile Phe
                                              1               5

att tcc ggt gcg gcg aac gga att ggc aaa gct gtg gcg ttg aaa ttt   163
Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala Val Ala Leu Lys Phe
                10                  15                  20

ctt cac gaa ggt tgg ctc gtt gga gcc tac gac ctc gcg gaa atc acc   211
Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp Leu Ala Glu Ile Thr
            25                  30                  35

tac tca cac ccc aat ctt cgc tgg ggc tac ctc aat gtt cga cag tcc   259
Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu Asn Val Arg Gln Ser
        40                  45                  50

gag tcg tgg gac aaa gcc cta gaa gac ttt gcg acg cac acc gga ggc   307
Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala Thr His Thr Gly Gly
    55                  60                  65

acc atc gat gtg gtg gac aat aat gcc ggc gta att att gag gga ccg   355
Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val Ile Ile Glu Gly Pro
70                  75                  80                  85

ctg cag gac gca gag gag ggg agc gtc gac aag ctt ctt gca atc aac   403
Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys Leu Leu Ala Ile Asn
                90                  95                  100
```

```
gtc aat ggc gtg act ctt ggt gcc cgc gcc gct cat cct tat ttg gcg   451
Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala His Pro Tyr Leu Ala
            105                 110                 115

cgc acg ccg ggc gcc cag ttg tta aac atg tcc tcg gcg tcg gcg gtg   499
Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser Ser Ala Ser Ala Val
        120                 125                 130

tac ggg cag ccc cag atc gcg gtg tat tcg gct tcg aag ttt tac gtc   547
Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala Ser Lys Phe Tyr Val
    135                 140                 145

gca ggt ctt act gag gcg ctg aat ttg gag tgg cgg aaa gac gat att   595
Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp Arg Lys Asp Asp Ile
150                 155                 160                 165

cgc gtg gtc gat gtt tgg cct ttg tgg gcg aaa acc gat ttg gtg aac   643
Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys Thr Asp Leu Val Asn
                170                 175                 180

ggc gtg aag gct aag tca ctg aag cgt ttg ggt gtc cgg atc act ccg   691
Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly Val Arg Ile Thr Pro
            185                 190                 195

gaa cag gtg gca cag gcg gta tgg gat gcg gtg cat ccg aaa tct cgg   739
Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val His Pro Lys Ser Arg
        200                 205                 210

tgg gcg aag gga aag gtg cat cac ggg gtg tca aag ttg gat aag gcg   787
Trp Ala Lys Gly Lys Val His His Gly Val Ser Lys Leu Asp Lys Ala
    215                 220                 225

ctg tat ctc atg aaa tct ctg tcg cct gat cgg gta gcg atg tgt ttt   835
Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg Val Ala Met Cys Phe
230                 235                 240                 245

gcg cga cta atc gcc gga taaatgaatt gattatttta ggc                876
Ala Arg Leu Ile Ala Gly
                250
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<210> 264
<211> 251
<212> PRT
<213> Corynebacterium glutamicum

<400> 264

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Met Lys Ser Ile Phe Ile Ser Gly Ala Ala Asn Gly Ile Gly Lys Ala
  1               5                  10                  15

Val Ala Leu Lys Phe Leu His Glu Gly Trp Leu Val Gly Ala Tyr Asp
             20                  25                  30

Leu Ala Glu Ile Thr Tyr Ser His Pro Asn Leu Arg Trp Gly Tyr Leu
         35                  40                  45

Asn Val Arg Gln Ser Glu Ser Trp Asp Lys Ala Leu Glu Asp Phe Ala
     50                  55                  60

Thr His Thr Gly Gly Thr Ile Asp Val Val Asp Asn Asn Ala Gly Val
 65                  70                  75                  80
```

```
Ile Ile Glu Gly Pro Leu Gln Asp Ala Glu Glu Gly Ser Val Asp Lys
                85                  90                  95

Leu Leu Ala Ile Asn Val Asn Gly Val Thr Leu Gly Ala Arg Ala Ala
            100                 105                 110

His Pro Tyr Leu Ala Arg Thr Pro Gly Ala Gln Leu Leu Asn Met Ser
        115                 120                 125

Ser Ala Ser Ala Val Tyr Gly Gln Pro Gln Ile Ala Val Tyr Ser Ala
    130                 135                 140

Ser Lys Phe Tyr Val Ala Gly Leu Thr Glu Ala Leu Asn Leu Glu Trp
145                 150                 155                 160

Arg Lys Asp Asp Ile Arg Val Val Asp Val Trp Pro Leu Trp Ala Lys
                165                 170                 175

Thr Asp Leu Val Asn Gly Val Lys Ala Lys Ser Leu Lys Arg Leu Gly
            180                 185                 190

Val Arg Ile Thr Pro Glu Gln Val Ala Gln Ala Val Trp Asp Ala Val
        195                 200                 205

His Pro Lys Ser Arg Trp Ala Lys Gly Lys Val His His Gly Val Ser
    210                 215                 220

Lys Leu Asp Lys Ala Leu Tyr Leu Met Lys Ser Leu Ser Pro Asp Arg
225                 230                 235                 240

Val Ala Met Cys Phe Ala Arg Leu Ile Ala Gly
                245                 250
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<210> 265
<211> 897
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(874)
<223> RXS02474

<400> 265
tgctggtcta ttgtggcgac cgagggcctt tgaaggttcg acaaactgta taaggccttg 60

aatcttgaga atttattttg aggaagcaag aggaagtgtc atg agc aaa gtt gca 115
                                    Met Ser Lys Val Ala
                                      1   5

atg gtt acc ggt ggt gca caa ggc atc ggt cgt gga att tca gag aag 163
Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg Gly Ile Ser Glu Lys
                  10   15   20

ctg gca gca gat ggt ttc gat att gcc gta gcc gac ctg cca caa cag 211
Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala Asp Leu Pro Gln Gln
              25   30   35

gaa gaa caa gct gca gag acc atc aag ttg att gaa gct gca ggt caa 259

```
Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile Glu Ala Ala Gly Gln
         40                  45                  50

aag gct gta ttc gtt gga tta gat gtc acc gat aag gct aat ttc gac   307
Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp Lys Ala Asn Phe Asp
     55                  60                  65

agt gca att gat gag gca gca gag aaa ctt ggc ggc ttc gat gtg cta   355
Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly Gly Phe Asp Val Leu
 70                  75                  80                  85

gta aac aac gcc ggc atc gca caa att aag cca ctt ctg gaa gtc acc   403
Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro Leu Leu Glu Val Thr
                 90                  95                 100

gaa gaa gac cta aag cag atc tac tcc gtg aac gtt ttt agc gta ttt   451
Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn Val Phe Ser Val Phe
            105                 110                 115

ttt ggt att caa gca gca tcc cga aag ttc gat gag ctt ggc gta aaa   499
Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp Glu Leu Gly Val Lys
        120                 125                 130

ggc aag atc atc aac gct gca tca atc gct gct atc caa ggt ttc cca   547
Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala Ile Gln Gly Phe Pro
    135                 140                 145

atc ttg agc gcc tac tcc acc acc aaa ttc gcg gtt cgt ggc ctc acc   595
Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala Val Arg Gly Leu Thr
150                 155                 160                 165

cag gct gct gcg caa gaa ctc gca ccc aag ggt cac acc gtg aat gcc   643
Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly His Thr Val Asn Ala
                170                 175                 180

tac gca cct ggc atc gtg ggc acc gga atg tgg gag caa atc gat gcc   691
Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp Glu Gln Ile Asp Ala
            185                 190                 195

gag ctt tcc aag atc aac ggc aag cca atc ggt gag aac ttc aag gag   739
Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly Glu Asn Phe Lys Glu
        200                 205                 210

tac tcc tcc tca atc gca ttg ggc cga cca tca gta cct gag gat gta   787
Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser Val Pro Glu Asp Val
    215                 220                 225

gcc ggt ctg gtt tcg ttc ctg gct tct gaa aac tcc aac tac atc acc   835
Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn Ser Asn Tyr Ile Thr
230                 235                 240                 245

gga cag gtc atg ctt gtc gac ggc ggc atg ctc tac aac taggggttgc    884
Gly Gln Val Met Leu Val Asp Gly Gly Met Leu Tyr Asn
                250                 255

tttcccgcac tca                                                   897


<210> 266
<211> 258
<212> PRT
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<213> Corynebacterium glutamicum

<400> 266

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Met Ser Lys Val Ala Met Val Thr Gly Gly Ala Gln Gly Ile Gly Arg
  1               5                  10                  15

Gly Ile Ser Glu Lys Leu Ala Ala Asp Gly Phe Asp Ile Ala Val Ala
             20                  25                  30

Asp Leu Pro Gln Gln Glu Glu Gln Ala Ala Glu Thr Ile Lys Leu Ile
         35                  40                  45

Glu Ala Ala Gly Gln Lys Ala Val Phe Val Gly Leu Asp Val Thr Asp
     50                  55                  60

Lys Ala Asn Phe Asp Ser Ala Ile Asp Glu Ala Ala Glu Lys Leu Gly
 65                  70                  75                  80

Gly Phe Asp Val Leu Val Asn Asn Ala Gly Ile Ala Gln Ile Lys Pro
                 85                  90                  95

Leu Leu Glu Val Thr Glu Glu Asp Leu Lys Gln Ile Tyr Ser Val Asn
            100                 105                 110

Val Phe Ser Val Phe Phe Gly Ile Gln Ala Ala Ser Arg Lys Phe Asp
        115                 120                 125

Glu Leu Gly Val Lys Gly Lys Ile Ile Asn Ala Ala Ser Ile Ala Ala
    130                 135                 140

Ile Gln Gly Phe Pro Ile Leu Ser Ala Tyr Ser Thr Thr Lys Phe Ala
145                 150                 155                 160

Val Arg Gly Leu Thr Gln Ala Ala Ala Gln Glu Leu Ala Pro Lys Gly
                165                 170                 175

His Thr Val Asn Ala Tyr Ala Pro Gly Ile Val Gly Thr Gly Met Trp
            180                 185                 190

Glu Gln Ile Asp Ala Glu Leu Ser Lys Ile Asn Gly Lys Pro Ile Gly
        195                 200                 205

Glu Asn Phe Lys Glu Tyr Ser Ser Ser Ile Ala Leu Gly Arg Pro Ser
    210                 215                 220

Val Pro Glu Asp Val Ala Gly Leu Val Ser Phe Leu Ala Ser Glu Asn
225                 230                 235                 240

Ser Asn Tyr Ile Thr Gly Gln Val Met Leu Val Asp Gly Gly Met Leu
                245                 250                 255

Tyr Asn
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<210> 267
<211> 1224
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1201)
<223> RXS02485

<400> 267
cggtggtcag tgcttggtgc accttgccga cgggctgatt gatcgtaatg gtgttttctg 60

tacgcgttgc catgaggata agactaccgt tagtggggtg ttg gat tca tcg cta 115
Leu Asp Ser Ser Leu
1 5

gcc cag gaa atc gcc gcg atc gac ggc gtc gaa ctc gat tcg gaa gtc 163
Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu Leu Asp Ser Glu Val
10 15 20

act ttc gcc gat ctg acg acc ctc cgc atc ggc gga aaa ccc cgc agc 211
Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly Gly Lys Pro Arg Ser
25 30 35

gcc gta cgt tgc cag acc acg gag gcg ctg gtc agc gcc ata aaa ttg 259
Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val Ser Ala Ile Lys Leu
40 45 50

ctt gac gac gcc tcc ctc ccc ctc ctc att gtc ggc ggc ggg tcc aat 307
Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val Gly Gly Gly Ser Asn
55 60 65

ctc gtc gtg gcc gac ggc gat ctg gat gtt att gcc gtc atc atc gaa 355
Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile Ala Val Ile Ile Glu
70 75 80 85

acc gac gac gtc tcc atc aac ctc acc gac ggt ctc ctc acc gcc gat 403
Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly Leu Leu Thr Ala Asp
90 95 100

gca ggc gct gtt tgg gac gat gtt gtc cac ctt tcg gtg gat gcc ggc 451
Ala Gly Ala Val Trp Asp Asp Val Val His Leu Ser Val Asp Ala Gly
105 110 115

ctc ggt gga att gaa tgc ctc tcc gga atc ccc ggc tcc gcc ggc gcc 499
Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro Gly Ser Ala Gly Ala
120 125 130

acc cca gtc caa aac gtg ggc gcc tac ggc acg gaa gtt tcc gat gta 547
Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr Glu Val Ser Asp Val
135 140 145

ctc acc cgc gtc cag ctt ctc gac cgc acc acc cac caa gtc tcc tgg 595
Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr His Gln Val Ser Trp
150 155 160 165

gtc gac gcc tcc gaa ctc gac ctc tct tac cga tac tcc aat ctc aaa 643
Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg Tyr Ser Asn Leu Lys
170 175 180

ttc acc aac cgc gca gtc gtc ttg gcg atc gaa ctc cag ctc ctc acc 691
Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu Leu Gln Leu Leu Thr
185 190 195

gac gga ttg tcc gcg ccg cta cgt ttt ggt gaa ttg gga cgt cga tta 739
Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu Leu Gly Arg Arg Leu

```
        200                 205                 210

gcg atc tcc gag gcc gaa ccc cac cca cgt cgc ccc gtc cgc atg gtc   787
Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg Pro Val Arg Met Val
    215                 220                 225

cgc gac gcc gtc cta gaa ctc cgc cgc gcc aaa ggc atg gtc gtg gaa   835
Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys Gly Met Val Val Glu
230                 235                 240                 245

cac acc gac cac gac acc tgg tcc gcc gga tcc ttc ttc acc aac cca   883
His Thr Asp His Asp Thr Trp Ser Ala Gly Ser Phe Phe Thr Asn Pro
                250                 255                 260

atc gtc gac cca gcc ctt gcc gac gca gtc ttt gaa aaa gtc ggc gaa   931
Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe Glu Lys Val Gly Glu
            265                 270                 275

ccc acc atg ccc cgc ttc cca gcc ggc gat ggc aaa gaa aaa ctc tcc   979
Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly Lys Glu Lys Leu Ser
        280                 285                 290

gca gcc tgg ctc atc gaa cgc gcc ggc ttc aaa aag gga cac ccc ggc   1027
Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys Lys Gly His Pro Gly
    295                 300                 305

gca ggc gca aaa gcc tcc ctg agc acc aaa cac acc ctc gca ctc acc   1075
Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His Thr Leu Ala Leu Thr
310                 315                 320                 325

aac cgt ggc gac gcc cgc gcc tcc gac ctc gtc gca tta gcc aaa gaa   1123
Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val Ala Leu Ala Lys Glu
                330                 335                 340

atc cgc gac gga gtc ctc gaa acc ttc ggc gtc acc ctc gtc cca gaa   1171
Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val Thr Leu Val Pro Glu
            345                 350                 355

ccc gtc tgg att gga atc agc atc gat gac tgaattttcc gacgtccctg     1221
Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
        360                 365

gca                                                               1224


<210> 268
<211> 367
<212> PRT
<213> Corynebacterium glutamicum

<400> 268
Leu Asp Ser Ser Leu Ala Gln Glu Ile Ala Ala Ile Asp Gly Val Glu
  1               5                  10                  15

Leu Asp Ser Glu Val Thr Phe Ala Asp Leu Thr Thr Leu Arg Ile Gly
             20                  25                  30

Gly Lys Pro Arg Ser Ala Val Arg Cys Gln Thr Thr Glu Ala Leu Val
         35                  40                  45

Ser Ala Ile Lys Leu Leu Asp Asp Ala Ser Leu Pro Leu Leu Ile Val
```

```
     50                  55                  60

Gly Gly Gly Ser Asn Leu Val Val Ala Asp Gly Asp Leu Asp Val Ile
 65                  70                  75                  80

Ala Val Ile Ile Glu Thr Asp Asp Val Ser Ile Asn Leu Thr Asp Gly
                 85                  90                  95

Leu Leu Thr Ala Asp Ala Gly Ala Val Trp Asp Asp Val Val His Leu
            100                 105                 110

Ser Val Asp Ala Gly Leu Gly Gly Ile Glu Cys Leu Ser Gly Ile Pro
        115                 120                 125

Gly Ser Ala Gly Ala Thr Pro Val Gln Asn Val Gly Ala Tyr Gly Thr
    130                 135                 140

Glu Val Ser Asp Val Leu Thr Arg Val Gln Leu Leu Asp Arg Thr Thr
145                 150                 155                 160

His Gln Val Ser Trp Val Asp Ala Ser Glu Leu Asp Leu Ser Tyr Arg
                165                 170                 175

Tyr Ser Asn Leu Lys Phe Thr Asn Arg Ala Val Val Leu Ala Ile Glu
            180                 185                 190

Leu Gln Leu Leu Thr Asp Gly Leu Ser Ala Pro Leu Arg Phe Gly Glu
        195                 200                 205

Leu Gly Arg Arg Leu Ala Ile Ser Glu Ala Glu Pro His Pro Arg Arg
    210                 215                 220

Pro Val Arg Met Val Arg Asp Ala Val Leu Glu Leu Arg Arg Ala Lys
225                 230                 235                 240

Gly Met Val Val Glu His Thr Asp His Asp Thr Trp Ser Ala Gly Ser
                245                 250                 255

Phe Phe Thr Asn Pro Ile Val Asp Pro Ala Leu Ala Asp Ala Val Phe
            260                 265                 270

Glu Lys Val Gly Glu Pro Thr Met Pro Arg Phe Pro Ala Gly Asp Gly
        275                 280                 285

Lys Glu Lys Leu Ser Ala Ala Trp Leu Ile Glu Arg Ala Gly Phe Lys
    290                 295                 300

Lys Gly His Pro Gly Ala Gly Ala Lys Ala Ser Leu Ser Thr Lys His
305                 310                 315                 320

Thr Leu Ala Leu Thr Asn Arg Gly Asp Ala Arg Ala Ser Asp Leu Val
                325                 330                 335

Ala Leu Ala Lys Glu Ile Arg Asp Gly Val Leu Glu Thr Phe Gly Val
            340                 345                 350

Thr Leu Val Pro Glu Pro Val Trp Ile Gly Ile Ser Ile Asp Asp
        355                 360                 365
```

<210> 269

<211> 1641
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1618)
<223> RXS02539

<400> 269
ggctgctaag cgtgcgaatg tgcgcgttgt cacaatcgtt gaccaagtgt cacctgacgc 60

acaggtagtg ctcaggtgga ggtggcccaa aggagaccca atg act gtc tac gca 115
Met Thr Val Tyr Ala
1 5

aat cca gga acc gaa ggc tcg atc gtt aac tat gaa aag cgc tac gag 163
Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr Glu Lys Arg Tyr Glu
10 15 20

aac tac att ggt ggc aag tgg gtt cca ccg gta gag ggc cag tac ctt 211
Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val Glu Gly Gln Tyr Leu
25 30 35

gag aac att tca cct gtc act ggt gaa gtt ttc tgt gag gtc gca cgt 259
Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe Cys Glu Val Ala Arg
40 45 50

ggc acc gca gcg gac gtg gag ctt gca ctg gat gct gca cat gca gcc 307
Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp Ala Ala His Ala Ala
55 60 65

gct gat gcg tgg ggc aag act tct gtc gct gaa cgt gct ctg atc ctg 355
Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu Arg Ala Leu Ile Leu
70 75 80 85

cac cgc att gcg gac cgc atg gaa gag cac ctg gaa gaa atc gca gtt 403
His Arg Ile Ala Asp Arg Met Glu Glu His Leu Glu Glu Ile Ala Val
90 95 100

gca gaa acc tgg gag aac ggc aag gca gtc cgt gag act ctt gct gca 451
Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg Glu Thr Leu Ala Ala
105 110 115

gat atc cca ctg gca atc gac cac ttc cgc tac ttt gct ggc gcg atc 499
Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr Phe Ala Gly Ala Ile
120 125 130

cgt gct cag gaa gat cgt tcc tca cag atc gac cac aac act gtt gct 547
Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp His Asn Thr Val Ala
135 140 145

tac cac ttc aac gag cca atc ggt gtt gtt ggt cag atc att cct tgg 595
Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly Gln Ile Ile Pro Trp
150 155 160 165

aac ttc cca atc ctc atg gct acc tgg aag ctc gca ccg gca ctt gct 643
Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu Ala Pro Ala Leu Ala
170 175 180

gca ggt aac gcg atc gtc atg aag cca gct gag cag acc cca gca tcc 691

```
Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu Gln Thr Pro Ala Ser
            185                 190                 195

att ttg tat ctg att aac atc atc ggc gat ctc atc cca gag ggc gtc   739
Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu Ile Pro Glu Gly Val
        200                 205                 210

ctc aac atc gtc aac gga ctc ggc ggt gaa gca ggc gct gca ctg tcc   787
Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala Gly Ala Ala Leu Ser
    215                 220                 225

ggc tct aat cgg att ggc aag att gct ttc acc ggt tcc acc gag gtc   835
Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr Gly Ser Thr Glu Val
230                 235                 240                 245

ggc aag ctg atc aac cgc gct gca tcc gac aag atc att cct gtc acc   883
Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys Ile Ile Pro Val Thr
                250                 255                 260

ctg gag ctc ggc ggt aag tcc cca tcc atc ttc ttc tcc gat gtt ctg   931
Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe Phe Ser Asp Val Leu
            265                 270                 275

tca cag gat gac gcc ttc gca gag aag gca gtt gaa ggc ttc gcg atg   979
Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val Glu Gly Phe Ala Met
        280                 285                 290

ttc gcc ctc aat cag ggt gaa gtt tgt acc tgt cct tcc cgt gca ctt   1027
Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys Pro Ser Arg Ala Leu
    295                 300                 305

gtt cat gag tcc atc gct gat gaa ttc ctc gag ctt ggc gtg aag cga   1075
Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu Leu Gly Val Lys Arg
310                 315                 320                 325

gtt cag aac atc aag ctg ggt aac cca ctt gat act gaa acc atg atg   1123
Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp Thr Glu Thr Met Met
                330                 335                 340

ggt gct cag gcg tcc cag gag cag atg gac aag atc tcc tcc tac ctg   1171
Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys Ile Ser Ser Tyr Leu
            345                 350                 355

aag atc ggc cca gaa gaa ggc gct caa acc ctc act ggt ggc aag gtc   1219
Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu Thr Gly Gly Lys Val
        360                 365                 370

aac aag gtt gat ggc atg gag aac ggt tac tac att gag cca acc gtt   1267
Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr Ile Glu Pro Thr Val
    375                 380                 385

ttc cgc ggc acc aac gac atg agg atc ttc cgc gag gaa atc ttc gga   1315
Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg Glu Glu Ile Phe Gly
390                 395                 400                 405

cca gtc ctt tct gtt gct acc ttc agc gac ttc gat gag gcc atc cgt   1363
Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe Asp Glu Ala Ile Arg
                410                 415                 420

att gca aac gac acc aac tac ggc ctc ggc gct ggt gtc tgg agc cgt   1411
Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala Gly Val Trp Ser Arg
```

Sequence Listing

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            425                 430                 435

gac caa aac acc att tat cgt gca ggt cgc gca atc cag gct ggt cga   1459
Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala Ile Gln Ala Gly Arg
        440                 445                 450

gtt tgg gtc aac cag tac cac aac tac cca gcg cac tcc gct ttc ggt   1507
Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala His Ser Ala Phe Gly
    455                 460                 465

gga tac aag gag tcc ggc atc ggc cgt gag aac cac ctc atg atg ctg   1555
Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn His Leu Met Met Leu
470                 475                 480                 485

aac cac tac cag cag acc aag aac ctg ttg gtc tcc tac gat cca aac   1603
Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val Ser Tyr Asp Pro Asn
                490                 495                 500

cca acc gga ctg ttc tgatctaagc gttaagtcct aga                    1641
Pro Thr Gly Leu Phe
            505
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SEQUENCE LISTING

<210> 270
<211> 506
<212> PRT
<213> Corynebacterium glutamicum

<400> 270

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Met Thr Val Tyr Ala Asn Pro Gly Thr Glu Gly Ser Ile Val Asn Tyr
  1               5                  10                  15

Glu Lys Arg Tyr Glu Asn Tyr Ile Gly Gly Lys Trp Val Pro Pro Val
             20                  25                  30

Glu Gly Gln Tyr Leu Glu Asn Ile Ser Pro Val Thr Gly Glu Val Phe
         35                  40                  45

Cys Glu Val Ala Arg Gly Thr Ala Ala Asp Val Glu Leu Ala Leu Asp
     50                  55                  60

Ala Ala His Ala Ala Ala Asp Ala Trp Gly Lys Thr Ser Val Ala Glu
 65                  70                  75                  80

Arg Ala Leu Ile Leu His Arg Ile Ala Asp Arg Met Glu Glu His Leu
                 85                  90                  95

Glu Glu Ile Ala Val Ala Glu Thr Trp Glu Asn Gly Lys Ala Val Arg
            100                 105                 110

Glu Thr Leu Ala Ala Asp Ile Pro Leu Ala Ile Asp His Phe Arg Tyr
        115                 120                 125

Phe Ala Gly Ala Ile Arg Ala Gln Glu Asp Arg Ser Ser Gln Ile Asp
    130                 135                 140

His Asn Thr Val Ala Tyr His Phe Asn Glu Pro Ile Gly Val Val Gly
145                 150                 155                 160

Gln Ile Ile Pro Trp Asn Phe Pro Ile Leu Met Ala Thr Trp Lys Leu
                165                 170                 175
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Ala Pro Ala Leu Ala Ala Gly Asn Ala Ile Val Met Lys Pro Ala Glu
            180                 185                 190

Gln Thr Pro Ala Ser Ile Leu Tyr Leu Ile Asn Ile Ile Gly Asp Leu
        195                 200                 205

Ile Pro Glu Gly Val Leu Asn Ile Val Asn Gly Leu Gly Gly Glu Ala
    210                 215                 220

Gly Ala Ala Leu Ser Gly Ser Asn Arg Ile Gly Lys Ile Ala Phe Thr
225                 230                 235                 240

Gly Ser Thr Glu Val Gly Lys Leu Ile Asn Arg Ala Ala Ser Asp Lys
                245                 250                 255

Ile Ile Pro Val Thr Leu Glu Leu Gly Gly Lys Ser Pro Ser Ile Phe
            260                 265                 270

Phe Ser Asp Val Leu Ser Gln Asp Asp Ala Phe Ala Glu Lys Ala Val
        275                 280                 285

Glu Gly Phe Ala Met Phe Ala Leu Asn Gln Gly Glu Val Cys Thr Cys
    290                 295                 300

Pro Ser Arg Ala Leu Val His Glu Ser Ile Ala Asp Glu Phe Leu Glu
305                 310                 315                 320

Leu Gly Val Lys Arg Val Gln Asn Ile Lys Leu Gly Asn Pro Leu Asp
                325                 330                 335

Thr Glu Thr Met Met Gly Ala Gln Ala Ser Gln Glu Gln Met Asp Lys
            340                 345                 350

Ile Ser Ser Tyr Leu Lys Ile Gly Pro Glu Glu Gly Ala Gln Thr Leu
        355                 360                 365

Thr Gly Gly Lys Val Asn Lys Val Asp Gly Met Glu Asn Gly Tyr Tyr
    370                 375                 380

Ile Glu Pro Thr Val Phe Arg Gly Thr Asn Asp Met Arg Ile Phe Arg
385                 390                 395                 400

Glu Glu Ile Phe Gly Pro Val Leu Ser Val Ala Thr Phe Ser Asp Phe
                405                 410                 415

Asp Glu Ala Ile Arg Ile Ala Asn Asp Thr Asn Tyr Gly Leu Gly Ala
            420                 425                 430

Gly Val Trp Ser Arg Asp Gln Asn Thr Ile Tyr Arg Ala Gly Arg Ala
        435                 440                 445

Ile Gln Ala Gly Arg Val Trp Val Asn Gln Tyr His Asn Tyr Pro Ala
    450                 455                 460

His Ser Ala Phe Gly Gly Tyr Lys Glu Ser Gly Ile Gly Arg Glu Asn
465                 470                 475                 480

His Leu Met Met Leu Asn His Tyr Gln Gln Thr Lys Asn Leu Leu Val
                485                 490                 495
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Sheet 1 of 1

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Ser Tyr Asp Pro Asn Pro Thr Gly Leu Phe
            500                 505


<210> 271
<211> 1227
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1204)
<223> RXS02578

<400> 271
ggcaaaaatg aggaacagca cgcccgcaat aatgaggacc gttgcagatc gcttcataaa 60

aacagcccac acctttccgc taaactcgca tgttgaaata atg tct acc caa tca   115
                                          Met Ser Thr Gln Ser
                                            1               5

tat gca ccc atc cgc cat cgc gga ttc atc agc tca ctc gag gga cta   163
Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser Ser Leu Glu Gly Leu
                10                  15                  20

cgc gca atc gcc tcc ctg gga gtc ttg gcg acc cac gtt gca ttc caa   211
Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr His Val Ala Phe Gln
            25                  30                  35

acc tcc gtc gac ccc gcc agc aac atc ggt gca gta ctc gcg cgt ttc   259
Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala Val Leu Ala Arg Phe
        40                  45                  50

gac ttt ttc gtc gcc gtc ttc ttc gcc ctc tcc gcc ttc gtt ctt tgg   307
Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser Ala Phe Val Leu Trp
    55                  60                  65

cga cgc cgc gcc ggg caa cca gtg gga ctg tac tac ctc aaa cgc cta   355
Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr Tyr Leu Lys Arg Leu
70                  75                  80                  85

gcc cgc atc atg ccc gca tac tgg gca acg gtc att gca gtc ctg ctg   403
Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val Ile Ala Val Leu Leu
                90                  95                  100

ttt att ccc acc ggc ccc tgg tta gcc aac ctg acg atg acc caa atc   451
Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu Thr Met Thr Gln Ile
            105                 110                 115

tac tgg cca gac ggg ctc atg aca ggc ctc acc cac ctt tgg tcc ctg   499
Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr His Leu Trp Ser Leu
        120                 125                 130

tgc gtg gaa gtg gcg ttt tac ctg gtg atg ccg ctt ctc gcg tgg gtg   547
Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro Leu Leu Ala Trp Val
    135                 140                 145

ttg gat agg ttt ggt cgg ccg gtg cgc atc ctg ttg att gtt ggt ggg   595
Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu Leu Ile Val Gly Gly
150                 155                 160                 165
```

```
gca gtg ttg agt ctg gcg tgg ccg tgg att ccc ctt gtg gag cat gcg   643
Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro Leu Val Glu His Ala
                170                 175                 180

ttg gac gag ggg tgg gcg aac atg cag atc tgg cca ccc gct tac gct   691
Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp Pro Pro Ala Tyr Ala
            185                 190                 195

tgc tgg ttt gca gtc ggc atg atc gcc gca gaa att gaa gga gtt cga   739
Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu Ile Glu Gly Val Arg
        200                 205                 210

ttc cca cgg gtt ccg agc ttt gtg tgg gtg ggt tta gct tta gtg gtc   787
Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly Leu Ala Leu Val Val
    215                 220                 225

gct tgg atc gcg ggc caa gaa tgg ttc gga cca cta ggt tta gtg cac   835
Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro Leu Gly Leu Val His
230                 235                 240                 245

ccc agc ccc tgg gaa ttc aac tta aga gtc ctc gcg ggc aca ctt ttc   883
Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu Ala Gly Thr Leu Phe
                250                 255                 260

gct gta ttt ctg gtg gtt ccc tac gcg ctg ggt acg ccc tct cgg ctt   931
Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly Thr Pro Ser Arg Leu
            265                 270                 275

ctt gat tcc agt tgg atg aaa acg ctc ggc acc tgg tcg tat tcc atc   979
Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr Trp Ser Tyr Ser Ile
        280                 285                 290

ttc ctc tgg cac ctt ccc gtg ctg acg att gtg ttc cca ctg ctc ggg   1027
Phe Leu Trp His Leu Pro Val Leu Thr Ile Val Phe Pro Leu Leu Gly
    295                 300                 305

ttg cct tta ttt agt gga aat ttc ctg ttg gtg ttc atc gtg acg gtc   1075
Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val Phe Ile Val Thr Val
310                 315                 320                 325

ttg ttg acg atc cca gtt gcc gcc atc agc tac acc ttc atc gaa gag   1123
Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr Thr Phe Ile Glu Glu
                330                 335                 340

ccc atc agc ggt gga ccc ggc gcg cca ttc agg ctg ggg gtc gtt agg   1171
Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg Leu Gly Val Val Arg
            345                 350                 355

att cac cat ttt tct ggg ggt agg tct gga aaa tgatgaattg gcaccacgtc 1224
Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
        360                 365

aag                                                               1227
```

<210> 272
<211> 368
<212> PRT
<213> Corynebacterium glutamicum

<400> 272

```
Met Ser Thr Gln Ser Tyr Ala Pro Ile Arg His Arg Gly Phe Ile Ser
 1               5                  10                  15

Ser Leu Glu Gly Leu Arg Ala Ile Ala Ser Leu Gly Val Leu Ala Thr
            20                  25                  30

His Val Ala Phe Gln Thr Ser Val Asp Pro Ala Ser Asn Ile Gly Ala
        35                  40                  45

Val Leu Ala Arg Phe Asp Phe Phe Val Ala Val Phe Phe Ala Leu Ser
    50                  55                  60

Ala Phe Val Leu Trp Arg Arg Arg Ala Gly Gln Pro Val Gly Leu Tyr
65                  70                  75                  80

Tyr Leu Lys Arg Leu Ala Arg Ile Met Pro Ala Tyr Trp Ala Thr Val
                85                  90                  95

Ile Ala Val Leu Leu Phe Ile Pro Thr Gly Pro Trp Leu Ala Asn Leu
            100                 105                 110

Thr Met Thr Gln Ile Tyr Trp Pro Asp Gly Leu Met Thr Gly Leu Thr
        115                 120                 125

His Leu Trp Ser Leu Cys Val Glu Val Ala Phe Tyr Leu Val Met Pro
    130                 135                 140

Leu Leu Ala Trp Val Leu Asp Arg Phe Gly Arg Pro Val Arg Ile Leu
145                 150                 155                 160

Leu Ile Val Gly Gly Ala Val Leu Ser Leu Ala Trp Pro Trp Ile Pro
                165                 170                 175

Leu Val Glu His Ala Leu Asp Glu Gly Trp Ala Asn Met Gln Ile Trp
            180                 185                 190

Pro Pro Ala Tyr Ala Cys Trp Phe Ala Val Gly Met Ile Ala Ala Glu
        195                 200                 205

Ile Glu Gly Val Arg Phe Pro Arg Val Pro Ser Phe Val Trp Val Gly
    210                 215                 220

Leu Ala Leu Val Val Ala Trp Ile Ala Gly Gln Glu Trp Phe Gly Pro
225                 230                 235                 240

Leu Gly Leu Val His Pro Ser Pro Trp Glu Phe Asn Leu Arg Val Leu
                245                 250                 255

Ala Gly Thr Leu Phe Ala Val Phe Leu Val Val Pro Tyr Ala Leu Gly
            260                 265                 270

Thr Pro Ser Arg Leu Leu Asp Ser Ser Trp Met Lys Thr Leu Gly Thr
        275                 280                 285

Trp Ser Tyr Ser Ile Phe Leu Trp His Leu Pro Val Leu Thr Ile Val
    290                 295                 300

Phe Pro Leu Leu Gly Leu Pro Leu Phe Ser Gly Asn Phe Leu Leu Val
305                 310                 315                 320

Phe Ile Val Thr Val Leu Leu Thr Ile Pro Val Ala Ala Ile Ser Tyr
```

```
                325                 330                 335

Thr Phe Ile Glu Glu Pro Ile Ser Gly Gly Pro Gly Ala Pro Phe Arg
            340                 345                 350

Leu Gly Val Val Arg Ile His His Phe Ser Gly Gly Arg Ser Gly Lys
        355                 360                 365
```

<210> 273
<211> 1089
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1066)
<223> RXS02741

<400> 273

```
actggtcacc tggtttggtc tgcactctga ctcccctcaa aagggcacaa tttggtcaat 60

ttcccaacct tgtctttcag tcatggttag tgtgggaacc atg aag gca atc tta   115
                                           Met Lys Ala Ile Leu
                                             1               5

gtt tcc cgc acc ggc gga cca gag gtg ttg gag ttc acc gac act gac   163
Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu Phe Thr Asp Thr Asp
                10                  15                  20

gcc cca aag ccc act gat gat cag gtt tta gtt gaa gtt gat atg gct   211
Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val Glu Val Asp Met Ala
            25                  30                  35

ggc gtc aac ttt att gat act tac tat cgc cag ggt gaa tat cac gct   259
Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln Gly Glu Tyr His Ala
        40                  45                  50

cgc ctg ccg ttt atc cca ggt ttt gaa ggc act ggt cgg gtg ttg gag   307
Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr Gly Arg Val Leu Glu
    55                  60                  65

gat ccg cag ggg ttg att gcg gcg ggt acc aag gtg gcg tgg tgt gat   355
Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys Val Ala Trp Cys Asp
70                  75                  80                  85

gcc atg ggt tcg tat gct cag cag gtg tgt gtg ccg cgg gat cgc ttg   403
Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val Pro Arg Asp Arg Leu
                90                  95                  100

gtg gcg gtt ccc gag ggc gtg agt tcg gaa gtg gct gcg tcg atg ttg   451
Val Ala Val Pro Glu Gly Val Ser Ser Glu Val Ala Ala Ser Met Leu
            105                 110                 115

atg cag gga atc act gcg cat tat cta acc aat ggt gtg tat gag ctt   499
Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn Gly Val Tyr Glu Leu
        120                 125                 130
```

```
gaa gag ggc gat tct tgc ctc atc act gct ggc gcg ggt ggt gtt gga   547
Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly Ala Gly Gly Val Gly
    135                 140                 145

ttg ttg gct acg cag atg gcg gcg gcc aag gga gtg cgc gtg tac agc   595
Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly Val Arg Val Tyr Ser
150                 155                 160                 165

gtg gtg tcc acg gat gaa aaa gct gag ctt gct ttg gat gcc ggt gct   643
Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala Leu Asp Ala Gly Ala
                170                 175                 180

tat gag gtg ttt cgt tat tcc gat aat ttg gcg gag cag gtt cgt cgg   691
Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala Glu Gln Val Arg Arg
            185                 190                 195

cac aac ggg ggt cgc gga gtt gat gtg gtg tat gac ggt gtc ggc cag   739
His Asn Gly Gly Arg Gly Val Asp Val Val Tyr Asp Gly Val Gly Gln
        200                 205                 210

tcc acg ttc aat gag tcc tta gag gct gtt cgt ccg cgc ggc act gtg   787
Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg Pro Arg Gly Thr Val
    215                 220                 225

tgt ttg ttt ggt gcg gcg tcg ggt cct gtg gag cct ttt gat ccg cag   835
Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu Pro Phe Asp Pro Gln
230                 235                 240                 245

ctg ttg aac act cac ggt tcg atc ttc ttg acc cgc cca agc att ggc   883
Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr Arg Pro Ser Ile Gly
                250                 255                 260

gcg tgg acg tct gag gag ggc gaa ttt gcc aag cgt gca cag gcg gtc   931
Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys Arg Ala Gln Ala Val
            265                 270                 275

acg cag gcc atc gtc gaa ggc acc ttg cgg gtt cgc gtt act ggc aca   979
Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val Arg Val Thr Gly Thr
        280                 285                 290

tat tcg ctt gcc gac gcc tac atc gcc cac cgc gac ctt cag gcg cgt   1027
Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg Asp Leu Gln Ala Arg
    295                 300                 305

agc acg agc ggt tct ttg gtc ttg gaa atc ccg aag gac taaacacgca    1076
Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro Lys Asp
310                 315                 320

taaaaagatc ctg                                                   1089
```

<210> 274
<211> 322
<212> PRT
<213> Corynebacterium glutamicum

<400> 274

```
Met Lys Ala Ile Leu Val Ser Arg Thr Gly Gly Pro Glu Val Leu Glu
  1               5                  10                  15

Phe Thr Asp Thr Asp Ala Pro Lys Pro Thr Asp Asp Gln Val Leu Val
```

```
           20                  25                  30

Glu Val Asp Met Ala Gly Val Asn Phe Ile Asp Thr Tyr Tyr Arg Gln
         35                  40                  45

Gly Glu Tyr His Ala Arg Leu Pro Phe Ile Pro Gly Phe Glu Gly Thr
     50                  55                  60

Gly Arg Val Leu Glu Asp Pro Gln Gly Leu Ile Ala Ala Gly Thr Lys
 65                  70                  75                  80

Val Ala Trp Cys Asp Ala Met Gly Ser Tyr Ala Gln Gln Val Cys Val
                 85                  90                  95

Pro Arg Asp Arg Leu Val Ala Val Pro Glu Gly Val Ser Ser Glu Val
            100                 105                 110

Ala Ala Ser Met Leu Met Gln Gly Ile Thr Ala His Tyr Leu Thr Asn
        115                 120                 125

Gly Val Tyr Glu Leu Glu Glu Gly Asp Ser Cys Leu Ile Thr Ala Gly
    130                 135                 140

Ala Gly Gly Val Gly Leu Leu Ala Thr Gln Met Ala Ala Ala Lys Gly
145                 150                 155                 160

Val Arg Val Tyr Ser Val Val Ser Thr Asp Glu Lys Ala Glu Leu Ala
                165                 170                 175

Leu Asp Ala Gly Ala Tyr Glu Val Phe Arg Tyr Ser Asp Asn Leu Ala
            180                 185                 190

Glu Gln Val Arg Arg His Asn Gly Gly Arg Gly Val Asp Val Val Tyr
        195                 200                 205

Asp Gly Val Gly Gln Ser Thr Phe Asn Glu Ser Leu Glu Ala Val Arg
    210                 215                 220

Pro Arg Gly Thr Val Cys Leu Phe Gly Ala Ala Ser Gly Pro Val Glu
225                 230                 235                 240

Pro Phe Asp Pro Gln Leu Leu Asn Thr His Gly Ser Ile Phe Leu Thr
                245                 250                 255

Arg Pro Ser Ile Gly Ala Trp Thr Ser Glu Glu Gly Glu Phe Ala Lys
            260                 265                 270

Arg Ala Gln Ala Val Thr Gln Ala Ile Val Glu Gly Thr Leu Arg Val
        275                 280                 285

Arg Val Thr Gly Thr Tyr Ser Leu Ala Asp Ala Tyr Ile Ala His Arg
    290                 295                 300

Asp Leu Gln Ala Arg Ser Thr Ser Gly Ser Leu Val Leu Glu Ile Pro
305                 310                 315                 320

Lys Asp
```

<210> 275

<211> 430
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(430)
<223> RXS03061

<400> 275
ctgccaccac tggtcattgc agaggacact ctccgtgatg gtcttcaggt gttagtcgca 60

gccctagagc gcgaaaccgc gcaccagaag gtgggctaaa gtg tct ttg acc ttc 115
Val Ser Leu Thr Phe
1 5

cca gta atc aac ccc agc gat ggc tcc acc atc acc gag cta gaa aac 163
Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile Thr Glu Leu Glu Asn
10 15 20

cac gat tcc acc cag tgg atg tcc gcg ctc tct gat gca gtt gca gct 211
His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser Asp Ala Val Ala Ala
25 30 35

ggt cct tca tgg gct gcg aaa act ccc cgc gaa aga tcc gtg gta ctc 259
Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu Arg Ser Val Val Leu
40 45 50

acc gca atc ttc gaa gca ctg acc gaa cgc gcc caa gaa ctt gca gag 307
Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala Gln Glu Leu Ala Glu
55 60 65

atc atc cac ctg gaa gct gga aaa tcc gat gca gaa gct ctt ggt gaa 355
Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala Glu Ala Leu Gly Glu
70 75 80 85

gtc gct tat ggt gca gaa tac ttc cgt tgg ttt gcg gaa gaa gca gtg 403
Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe Ala Glu Glu Ala Val
90 95 100

cgc ctg ccc ggc cgc tac gga cag tca 430
Arg Leu Pro Gly Arg Tyr Gly Gln Ser
105 110

<210> 276
<211> 110
<212> PRT
<213> Corynebacterium glutamicum

<400> 276
Val Ser Leu Thr Phe Pro Val Ile Asn Pro Ser Asp Gly Ser Thr Ile
1 5 10 15

Thr Glu Leu Glu Asn His Asp Ser Thr Gln Trp Met Ser Ala Leu Ser
20 25 30

Asp Ala Val Ala Ala Gly Pro Ser Trp Ala Ala Lys Thr Pro Arg Glu
35 40 45

Arg Ser Val Val Leu Thr Ala Ile Phe Glu Ala Leu Thr Glu Arg Ala

```
     50                  55                  60

Gln Glu Leu Ala Glu Ile Ile His Leu Glu Ala Gly Lys Ser Asp Ala
 65                  70                  75                  80

Glu Ala Leu Gly Glu Val Ala Tyr Gly Ala Glu Tyr Phe Arg Trp Phe
                 85                  90                  95

Ala Glu Glu Ala Val Arg Leu Pro Gly Arg Tyr Gly Gln Ser
            100                 105                 110


<210> 277
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXS03150

<400> 277
tttaacagag tgcgtttcaa tgcctgtagt gttccggcaa ttttgaatgt cgttacggtt 60

acccaaggct gaattcctga gctcaccttg tacaagatca gtg gaa gcc cag ttc   115
                                            Val Glu Ala Gln Phe
                                              1               5

acc tct ccc ctg ctc aac aat ggg caa acc tgt ttc ctt ggt acc cga   163
Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys Phe Leu Gly Thr Arg
                10                  15                  20

atc ctt gct cca aaa tca cgt tac gcg gaa gta gtc gat gca ttc acc   211
Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val Val Asp Ala Phe Thr
            25                  30                  35

gct ttc gct ggc agc ctg cag gtt gga gtc acg tcc tcc cct gac act   259
Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr Ser Ser Pro Asp Thr
        40                  45                  50

cag atc gga ccg atg gcg act gcc cgg cag cgt gag cgc gtg gaa tcc   307
Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg Glu Arg Val Glu Ser
    55                  60                  65

tac att tcc caa ggc aaa aat gct gga gcc cgc atc act gtc ggt ggc   355
Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg Ile Thr Val Gly Gly
70                  75                  80                  85

agc cgt cca cga gat ctt gac gcc gga ttc ttc gtt gag cca aca gtg   403
Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe Val Glu Pro Thr Val
                90                  95                  100

ttc gcc gat gta gac aat cgc gca gcc att gcc caa gat gaa atc ttc   451
Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala Gln Asp Glu Ile Phe
            105                 110                 115

gga ccg gtg ccc tct gtt gtt tcc tac caa gac gat gaa cac gcc atc   499
Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp Asp Glu His Ala Ile
        120                 125                 130
```

```
caa cta gcc aac gat tcc gaa ttc ggt ctc ggc gga act gtc tgg acg   547
Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly Gly Thr Val Trp Thr
    135                 140                 145

agc gat ccc gag cgc ggc gct gca ttg gcc cgc cga gtt cac aca gga   595
Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg Arg Val His Thr Gly
150                 155                 160                 165

acc att ggc atc aac cgc tat atc cct gat ccc gcc gca cca ttt gga   643
Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro Ala Ala Pro Phe Gly
                170                 175                 180

ggt gtg aaa aac agt ggc ctt ggc aga gaa ctc ggc ccc gaa ggt ctt   691
Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu Gly Pro Glu Gly Leu
            185                 190                 195

gct tcc tac caa gaa acc caa acc att tat ctc taatccaaac tgcacctata 744
Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
        200                 205

tat                                                               747
```

Sequence Listing

<210> 278
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 278

```
Val Glu Ala Gln Phe Thr Ser Pro Leu Leu Asn Asn Gly Gln Thr Cys
  1               5                  10                  15

Phe Leu Gly Thr Arg Ile Leu Ala Pro Lys Ser Arg Tyr Ala Glu Val
             20                  25                  30

Val Asp Ala Phe Thr Ala Phe Ala Gly Ser Leu Gln Val Gly Val Thr
         35                  40                  45

Ser Ser Pro Asp Thr Gln Ile Gly Pro Met Ala Thr Ala Arg Gln Arg
     50                  55                  60

Glu Arg Val Glu Ser Tyr Ile Ser Gln Gly Lys Asn Ala Gly Ala Arg
 65                  70                  75                  80

Ile Thr Val Gly Gly Ser Arg Pro Arg Asp Leu Asp Ala Gly Phe Phe
                 85                  90                  95

Val Glu Pro Thr Val Phe Ala Asp Val Asp Asn Arg Ala Ala Ile Ala
            100                 105                 110

Gln Asp Glu Ile Phe Gly Pro Val Pro Ser Val Val Ser Tyr Gln Asp
        115                 120                 125

Asp Glu His Ala Ile Gln Leu Ala Asn Asp Ser Glu Phe Gly Leu Gly
    130                 135                 140

Gly Thr Val Trp Thr Ser Asp Pro Glu Arg Gly Ala Ala Leu Ala Arg
145                 150                 155                 160

Arg Val His Thr Gly Thr Ile Gly Ile Asn Arg Tyr Ile Pro Asp Pro
                165                 170                 175
```

```
Ala Ala Pro Phe Gly Gly Val Lys Asn Ser Gly Leu Gly Arg Glu Leu
            180                 185                 190

Gly Pro Glu Gly Leu Ala Ser Tyr Gln Glu Thr Gln Thr Ile Tyr Leu
        195                 200                 205
```

<210> 279
<211> 747
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(724)
<223> RXS02554

<400> 279

```
gcttttgaag tgtgtcgcgt gtgcggactg aaatagtttc cgcttcaact tggttgctaa 60

ggataggctc cataaaaata accaaaggcg gaaaatttca atg tca cac act aag   115
                                              Met Ser His Thr Lys
                                                1               5

cca tcc att gcc atc ctc ggt gct ggc cga gtg ggt tct tca ctt gcc   163
Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val Gly Ser Ser Leu Ala
                10                  15                  20

agg tca gcg gtc gcc gca ggc tat gag gta aag gtt gct ggt tca ggt   211
Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys Val Ala Gly Ser Gly
            25                  30                  35

gct gtg gac aaa atc gct ctt acc gct gag atc ctt atg ccc ggc gcg   259
Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile Leu Met Pro Gly Ala
        40                  45                  50

gtt cca agc act gct gac cag gct gta aag gat gca gat att gtg ttc   307
Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp Ala Asp Ile Val Phe
    55                  60                  65

ttg gct gtt ccc ctg cat aaa ttc cgc agt gtc aat cca gcc act tta   355
Leu Ala Val Pro Leu His Lys Phe Arg Ser Val Asn Pro Ala Thr Leu
70                  75                  80                  85

gag ggc aag atc gtt att gac acg atg aac cac tgg gtt ccg gtc aat   403
Glu Gly Lys Ile Val Ile Asp Thr Met Asn His Trp Val Pro Val Asn
                90                  95                  100

ggt gag ttg gag gaa att gat cag gat ccg cgc agc act tcg gag att   451
Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg Ser Thr Ser Glu Ile
            105                 110                 115

att gcg gag ttt ttc gcg gga tca acc atg gtg aag tct ttt aac cac   499
Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val Lys Ser Phe Asn His
        120                 125                 130

att ggt tat cac gag att gag cag gat gcg ggt acc ggg cgt gcg att   547
```

```
Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly Thr Gly Arg Ala Ile
    135                 140                 145

gcg tat gcc acg gat gat gtg gat gca ggt gcc cag gtt gca cag cta   595
Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala Gln Val Ala Gln Leu
150                 155                 160                 165

att aag agt ttt ggg ttt gtt cct tta aat att ggc gca ttg gaa aac   643
Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile Gly Ala Leu Glu Asn
                170                 175                 180

ggc cgt att ctg gaa cct ggc caa gaa gct ttc ggc gcg cac ctt aat   691
Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe Gly Ala His Leu Asn
            185                 190                 195

aaa gat tcg cgc cta gaa ctt gtt aat cag cgg tagtacctcg atcttcagcc 744
Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        200                 205

aac                                                               747
```

<210> 280
<211> 208
<212> PRT
<213> Corynebacterium glutamicum

<400> 280

```
Met Ser His Thr Lys Pro Ser Ile Ala Ile Leu Gly Ala Gly Arg Val
  1               5                  10                  15

Gly Ser Ser Leu Ala Arg Ser Ala Val Ala Ala Gly Tyr Glu Val Lys
             20                  25                  30

Val Ala Gly Ser Gly Ala Val Asp Lys Ile Ala Leu Thr Ala Glu Ile
         35                  40                  45

Leu Met Pro Gly Ala Val Pro Ser Thr Ala Asp Gln Ala Val Lys Asp
     50                  55                  60

Ala Asp Ile Val Phe Leu Ala Val Pro Leu His Lys Phe Arg Ser Val
 65                  70                  75                  80

Asn Pro Ala Thr Leu Glu Gly Lys Ile Val Ile Asp Thr Met Asn His
                 85                  90                  95

Trp Val Pro Val Asn Gly Glu Leu Glu Glu Ile Asp Gln Asp Pro Arg
            100                 105                 110

Ser Thr Ser Glu Ile Ile Ala Glu Phe Phe Ala Gly Ser Thr Met Val
        115                 120                 125

Lys Ser Phe Asn His Ile Gly Tyr His Glu Ile Glu Gln Asp Ala Gly
    130                 135                 140

Thr Gly Arg Ala Ile Ala Tyr Ala Thr Asp Asp Val Asp Ala Gly Ala
145                 150                 155                 160

Gln Val Ala Gln Leu Ile Lys Ser Phe Gly Phe Val Pro Leu Asn Ile
                165                 170                 175
```

```
Gly Ala Leu Glu Asn Gly Arg Ile Leu Glu Pro Gly Gln Glu Ala Phe
            180                 185                 190

Gly Ala His Leu Asn Lys Asp Ser Arg Leu Glu Leu Val Asn Gln Arg
        195                 200                 205
```

<210> 281
<211> 606
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(583)
<223> RXS03058

<400> 281

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acgagcttcc gctctgcaca agccgctaga agccccgcat agccctaatg tagagctcat 60

gcccatttgg aatcacaaca ccgcatatcg gccatggctg gtg tca aag ctc aaa   115
                                          Val Ser Lys Leu Lys
                                            1               5

ggc tca aga tcg ctt ctc gac gtc ggc tcc ggc gat cac tcc ttc gcc   163
Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly Asp His Ser Phe Ala
                10                  15                  20

gac ctg gcc ggc cgc cag gtc gcg cat gtc gat gtc gtg gat cct ctt   211
Asp Leu Ala Gly Arg Gln Val Ala His Val Asp Val Val Asp Pro Leu
            25                  30                  35

att aat aca acc ttt gaa gaa ttc cag ccg acc caa agc tac gat gcc   259
Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr Gln Ser Tyr Asp Ala
        40                  45                  50

atc acg ttc atc gcg tcc ctc cat cac atg aac gcg gaa gaa gga ctt   307
Ile Thr Phe Ile Ala Ser Leu His His Met Asn Ala Glu Glu Gly Leu
    55                  60                  65

aac aaa gca gtc cga atc ctc aat cct ggc ggc aag ctc ctc atc gta   355
Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly Lys Leu Leu Ile Val
70                  75                  80                  85

ggc ctc gcc aaa aac aaa acc gcc tcc gac tgg atc atc tcc gga cta   403
Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp Ile Ile Ser Gly Leu
                90                  95                  100

caa gct ttt ctc tcc cga cca atc agc ctc atc aat agg gaa caa caa   451
Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile Asn Arg Glu Gln Gln
            105                 110                 115

atc tac ccc ttc cct acc aaa gaa ccc tca gag agt ctc cac gaa ata   499
Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu Ser Leu His Glu Ile
        120                 125                 130

cga caa ctc acc aag cag ctc ctc cct cac cgc cgt att cgc cgt gga   547
Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg Arg Ile Arg Arg Gly
```

```
    135                 140                 145

atc cac ttc cga tac ctc ctc gag tgg aca aag cct taaacagccc        593
Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys Pro
150                 155                 160

tataaaccaa aaa                                                    606
```

<210> 282
<211> 161
<212> PRT
<213> Corynebacterium glutamicum

<400> 282

```
Val Ser Lys Leu Lys Gly Ser Arg Ser Leu Leu Asp Val Gly Ser Gly
  1               5                  10                  15

Asp His Ser Phe Ala Asp Leu Ala Gly Arg Gln Val Ala His Val Asp
             20                  25                  30

Val Val Asp Pro Leu Ile Asn Thr Thr Phe Glu Glu Phe Gln Pro Thr
         35                  40                  45

Gln Ser Tyr Asp Ala Ile Thr Phe Ile Ala Ser Leu His His Met Asn
     50                  55                  60

Ala Glu Glu Gly Leu Asn Lys Ala Val Arg Ile Leu Asn Pro Gly Gly
 65                  70                  75                  80

Lys Leu Leu Ile Val Gly Leu Ala Lys Asn Lys Thr Ala Ser Asp Trp
                 85                  90                  95

Ile Ile Ser Gly Leu Gln Ala Phe Leu Ser Arg Pro Ile Ser Leu Ile
            100                 105                 110

Asn Arg Glu Gln Gln Ile Tyr Pro Phe Pro Thr Lys Glu Pro Ser Glu
        115                 120                 125

Ser Leu His Glu Ile Arg Gln Leu Thr Lys Gln Leu Leu Pro His Arg
    130                 135                 140

Arg Ile Arg Arg Gly Ile His Phe Arg Tyr Leu Leu Glu Trp Thr Lys
145                 150                 155                 160

Pro
```

<210> 283
<211> 544
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> RXS03218

<400> 283

```
ttggtacggg ggttaacaac ctagctttgt atctgaaggc ttcggagatt tcctgtatac 60
```

```
atcaacaatt gccctttaac caggagtatt cttagcttct atg act cct gat ctt   115
                                            Met Thr Pro Asp Leu
                                              1               5

gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca   163
Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly Gln Glu Phe Asp Ala
                 10                  15                  20

gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc   211
Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn Leu Glu Ser Glu Ser
             25                  30                  35

gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt   259
Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile Ser Pro Lys Ser Val
         40                  45                  50

ctc gag cta ggc aca tcc aat ggt tac tcg act att tgg atg gca gat   307
Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr Ile Trp Met Ala Asp
     55                  60                  65

gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat   355
Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp
 70                  75                  80                  85

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga   403
Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg
                 90                  95                 100

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa   451
Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln
             105                 110                 115

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg   499
Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp
         120                 125                 130

tgg cct gac ctg caa tgagttctag caaatggcgg cttgttagtg             544
Trp Pro Asp Leu Gln
    135
```

<210> 284
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 284

```
Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
  1               5                  10                  15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
             20                  25                  30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile
         35                  40                  45

Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr
     50                  55                  60

Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro
```

```
 65                  70                  75                  80

Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu
                 85                  90                  95

Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp
            100                 105                 110

Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser
        115                 120                 125

Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln
    130                 135
```

<210> 285
<211> 537
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> FRXA01918

<400> 285

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ttggtacggg ggttaacaac ctagctttgt atctgaaggc ttcggagatt tcctgtatac 60

atcaacaatt gcccttaac caggagtatt cttagcttct atg act cct gat ctt   115
                                          Met Thr Pro Asp Leu
                                            1               5

gca gct ttt ctg gac aaa ctt tat gcc gag ggg cag gaa ttt gat gca   163
Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly Gln Glu Phe Asp Ala
                10                  15                  20

gag caa ccg gat cgg ctt gat cgc agg aga aac ctt gaa tct gaa agc   211
Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn Leu Glu Ser Glu Ser
            25                  30                  35

gct gcg cta ctt cgc tcg ctc atc tac gga att agt cca aag tca gtt   259
Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile Ser Pro Lys Ser Val
        40                  45                  50

ctc gag cta ggc aca tcc aat ggt tac tcg act att tgg atg gca gat   307
Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr Ile Trp Met Ala Asp
    55                  60                  65

gtc gtg aat tta aca aca gta gac aat gat cct gag cgg tct ttg gat   355
Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro Glu Arg Ser Leu Asp
70                  75                  80                  85

gct gca gca aac ctt cgc gcc gct gga gtt gaa gaa aaa gtt caa cga   403
Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu Glu Lys Val Gln Arg
                90                  95                  100

atc gtc gcc gat gga gca acc gta ctt gcc gat tcc gcc gat gaa caa   451
Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp Ser Ala Asp Glu Gln
            105                 110                 115

tgg gat ttc att ttc ctt gat gcc gaa caa tca ctc tat gta aat tgg   499
```

```
Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser Leu Tyr Val Asn Trp
        120                 125                 130

tgg cct gac ctg caa tgagttctag caaatggcgg ctt                    537
Trp Pro Asp Leu Gln
    135


<210> 286
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 286
Met Thr Pro Asp Leu Ala Ala Phe Leu Asp Lys Leu Tyr Ala Glu Gly
  1               5                  10                  15

Gln Glu Phe Asp Ala Glu Gln Pro Asp Arg Leu Asp Arg Arg Arg Asn
             20                  25                  30

Leu Glu Ser Glu Ser Ala Ala Leu Leu Arg Ser Leu Ile Tyr Gly Ile
         35                  40                  45

Ser Pro Lys Ser Val Leu Glu Leu Gly Thr Ser Asn Gly Tyr Ser Thr
     50                  55                  60

Ile Trp Met Ala Asp Val Val Asn Leu Thr Thr Val Asp Asn Asp Pro
 65                  70                  75                  80

Glu Arg Ser Leu Asp Ala Ala Ala Asn Leu Arg Ala Ala Gly Val Glu
                 85                  90                  95

Glu Lys Val Gln Arg Ile Val Ala Asp Gly Ala Thr Val Leu Ala Asp
            100                 105                 110

Ser Ala Asp Glu Gln Trp Asp Phe Ile Phe Leu Asp Ala Glu Gln Ser
        115                 120                 125

Leu Tyr Val Asn Trp Trp Pro Asp Leu Gln
    130                 135


<210> 287
<211> 672
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(649)
<223> RXC00110

<400> 287
atatcgaatg tccagtcacg ctaaacttca cccaagatga gatttcgtgg cacgattggg 60

aataacgaac gctaatttta aacactggag gagcttccac gtg agc aac aaa gac   115
                                              Val Ser Asn Lys Asp
                                                1               5

ggc ctt ttt act gac ggt aac agc acg ttt gca cct aag gtg gat tca   163
Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala Pro Lys Val Asp Ser
```

```
                  10                  15                  20

att ccc ctc agc gat gtg gat acc agc gtt agc ggt gaa gcc tcc atc   211
Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser Gly Glu Ala Ser Ile
            25                  30                  35

ggc acg ctg atc tcc aac gca acc tcc caa atg tcc agc ctt ttc cgc   259
Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met Ser Ser Leu Phe Arg
        40                  45                  50

gca gaa gtt gag ctg gcg aag act gaa ctc gca ggc gaa gcc aag aaa   307
Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala Gly Glu Ala Lys Lys
    55                  60                  65

gct gcc atc ggc ggc ggc gca ttc agc gtt gct ggc gta atc gca ctg   355
Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala Gly Val Ile Ala Leu
70                  75                  80                  85

tac agc tcc ttc ttc ttt ttc ttc ttc gtc gca gca ctg ctg agc gag   403
Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala Ala Leu Leu Ser Glu
                90                  95                  100

tgg att aag cct tgg gca gca ttc ctc atc gtg ttc ctc ttc atg ctg   451
Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val Phe Leu Phe Met Leu
            105                 110                 115

gtc atc gcc gca gct ctc gca ctg ttc ggc tgg cgc aag gtg aag aag   499
Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp Arg Lys Val Lys Lys
        120                 125                 130

atg ggc gct ccg aag aac acc atc caa tcg gtc aac caa ctg aag aac   547
Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val Asn Gln Leu Lys Asn
    135                 140                 145

ctg gtc cca ggt cag gca tcc gag aag ctg gag aag gcc aac aag cgt   595
Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu Lys Ala Asn Lys Arg
150                 155                 160                 165

ggc ctc tac acc tcc gcg tcc ttc cac agc ccc ggc gcc atc act ggc   643
Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro Gly Ala Ile Thr Gly
                170                 175                 180

gac cac taaaaaagga gacttcgatg gcc                                672
Asp His
```

<210> 288
<211> 183
<212> PRT
<213> Corynebacterium glutamicum

<400> 288

```
Val Ser Asn Lys Asp Gly Leu Phe Thr Asp Gly Asn Ser Thr Phe Ala
  1               5                  10                  15

Pro Lys Val Asp Ser Ile Pro Leu Ser Asp Val Asp Thr Ser Val Ser
            20                  25                  30

Gly Glu Ala Ser Ile Gly Thr Leu Ile Ser Asn Ala Thr Ser Gln Met
        35                  40                  45
```

```
Ser Ser Leu Phe Arg Ala Glu Val Glu Leu Ala Lys Thr Glu Leu Ala
 50                  55                  60

Gly Glu Ala Lys Lys Ala Ala Ile Gly Gly Gly Ala Phe Ser Val Ala
 65                  70                  75                  80

Gly Val Ile Ala Leu Tyr Ser Ser Phe Phe Phe Phe Phe Phe Val Ala
                 85                  90                  95

Ala Leu Leu Ser Glu Trp Ile Lys Pro Trp Ala Ala Phe Leu Ile Val
            100                 105                 110

Phe Leu Phe Met Leu Val Ile Ala Ala Ala Leu Ala Leu Phe Gly Trp
        115                 120                 125

Arg Lys Val Lys Lys Met Gly Ala Pro Lys Asn Thr Ile Gln Ser Val
    130                 135                 140

Asn Gln Leu Lys Asn Leu Val Pro Gly Gln Ala Ser Glu Lys Leu Glu
145                 150                 155                 160

Lys Ala Asn Lys Arg Gly Leu Tyr Thr Ser Ala Ser Phe His Ser Pro
                165                 170                 175

Gly Ala Ile Thr Gly Asp His
            180
```

Sequence Listing

<210> 289
<211> 954
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(931)
<223> RXC01971

<400> 289

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aggtcttgtt tatttcggct actgattcag tagctgcgct ccgataggat tcttagtttt 60

cagttcagta tctttgagcc acggctagaa tgtgaatcct atg tct aag aag aag   115
                                          Met Ser Lys Lys Lys
                                            1               5

cct cgc ccc att ccg gtt cct gcc caa ttt atc cct ggt ctc att gat   163
Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile Pro Gly Leu Ile Asp
                  10                  15                  20

gcg cat aca cat ttg gca tcg tgt gga gga gat ctt gca ggg ttg gtg   211
Ala His Thr His Leu Ala Ser Cys Gly Gly Asp Leu Ala Gly Leu Val
              25                  30                  35

gaa agg gcc aag gag gcg ggc gtc gaa aag ctt tgt acc gtc ggt gat   259
Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu Cys Thr Val Gly Asp
          40                  45                  50

ggt ttg gct gag gcc gag ctt gcg ctg gag gcc gcg caa cag ttt ggc   307
Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala Ala Gln Gln Phe Gly
      55                  60                  65
```

```
aat gtg ttt gct gcg tgt gcg att cat ccg acg aag gct gat cag ttg   355
Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr Lys Ala Asp Gln Leu
 70                  75                  80                  85

gat ggg gct gcg cgt gcg cgg ctg acg cag atg gcg gcg gat ccg aat   403
Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met Ala Ala Asp Pro Asn
                 90                  95                 100

tgt gtg gcc att ggt gag act ggt ttg gat tcg tat tgg atc aag cac   451
Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser Tyr Trp Ile Lys His
            105                 110                 115

gat cca gag gac acg gcg gcg ttg gat gtg caa gag gag gcg ctg cgc   499
Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln Glu Glu Ala Leu Arg
        120                 125                 130

tgg cat att gat ttg gca att agt gcg gat aag ccg ttg atg att cac   547
Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys Pro Leu Met Ile His
    135                 140                 145

aat cgt gag gcg gat gct gat ttg atg cga gtg ttg gcg gat gct cca   595
Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val Leu Ala Asp Ala Pro
150                 155                 160                 165

cct cca aaa gat acg att ctg cat tgt ttt tct tcg ccg ttg gac gtg   643
Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser Ser Pro Leu Asp Val
                170                 175                 180

gcg aag gaa gcg ttg gat cgt gga tat gtg ttg agt ttt gcg ggc aat   691
Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu Ser Phe Ala Gly Asn
            185                 190                 195

gtg acg ttt aag cgt aat gag gag ttg cgg gag gct gct cgt att gcg   739
Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu Ala Ala Arg Ile Ala
        200                 205                 210

ccg att tcc cag att ttg att gaa acc gat gcg ccg tat atg acg ccg   787
Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala Pro Tyr Met Thr Pro
    215                 220                 225

gag ccg ttt cgg ggg agt agg aat gag ccg tcg ttg att ggt cat acg   835
Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser Leu Ile Gly His Thr
230                 235                 240                 245

gcg cta tgc att gcg gag gtt cgg ggg atg gct gtg gag gat gtt gcg   883
Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala Val Glu Asp Val Ala
                250                 255                 260

gcg gct ttg aat gag aat ttt gat cgc gtt tat ggg gtc aca aat cta   931
Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr Gly Val Thr Asn Leu
            265                 270                 275

taacgtgagg tagctcacag tca                                        954
```

<210> 290
<211> 277
<212> PRT
<213> Corynebacterium glutamicum

<400> 290

```
Met Ser Lys Lys Lys Pro Arg Pro Ile Pro Val Pro Ala Gln Phe Ile
  1               5                  10                  15

Pro Gly Leu Ile Asp Ala His Thr His Leu Ala Ser Cys Gly Gly Asp
             20                  25                  30

Leu Ala Gly Leu Val Glu Arg Ala Lys Glu Ala Gly Val Glu Lys Leu
         35                  40                  45

Cys Thr Val Gly Asp Gly Leu Ala Glu Ala Glu Leu Ala Leu Glu Ala
     50                  55                  60

Ala Gln Gln Phe Gly Asn Val Phe Ala Ala Cys Ala Ile His Pro Thr
 65                  70                  75                  80

Lys Ala Asp Gln Leu Asp Gly Ala Ala Arg Ala Arg Leu Thr Gln Met
                 85                  90                  95

Ala Ala Asp Pro Asn Cys Val Ala Ile Gly Glu Thr Gly Leu Asp Ser
            100                 105                 110

Tyr Trp Ile Lys His Asp Pro Glu Asp Thr Ala Ala Leu Asp Val Gln
        115                 120                 125

Glu Glu Ala Leu Arg Trp His Ile Asp Leu Ala Ile Ser Ala Asp Lys
    130                 135                 140

Pro Leu Met Ile His Asn Arg Glu Ala Asp Ala Asp Leu Met Arg Val
145                 150                 155                 160

Leu Ala Asp Ala Pro Pro Pro Lys Asp Thr Ile Leu His Cys Phe Ser
                165                 170                 175

Ser Pro Leu Asp Val Ala Lys Glu Ala Leu Asp Arg Gly Tyr Val Leu
            180                 185                 190

Ser Phe Ala Gly Asn Val Thr Phe Lys Arg Asn Glu Glu Leu Arg Glu
        195                 200                 205

Ala Ala Arg Ile Ala Pro Ile Ser Gln Ile Leu Ile Glu Thr Asp Ala
    210                 215                 220

Pro Tyr Met Thr Pro Glu Pro Phe Arg Gly Ser Arg Asn Glu Pro Ser
225                 230                 235                 240

Leu Ile Gly His Thr Ala Leu Cys Ile Ala Glu Val Arg Gly Met Ala
                245                 250                 255

Val Glu Asp Val Ala Ala Ala Leu Asn Glu Asn Phe Asp Arg Val Tyr
            260                 265                 270

Gly Val Thr Asn Leu
        275
```

<210> 291
<211> 465
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(442)
<223> RXA02118

<400> 291
gggctggtgc gggttgcttt aatggaggtc atgctcgcag gctaacagaa ttggtggttt 60

tagtgctgtt accagggaca tcggctagaa tctgctgaat atg tct gat caa tta 115
Met Ser Asp Gln Leu
1 5

gct ccc tgc cct gag tgc agc agt gaa tat acc tac gaa aac ggc ggc 163
Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr Tyr Glu Asn Gly Gly
10 15 20

gtt ctg gtc tgc cca atg tgt gcc cac gaa tgg gtc gaa ggt gaa gta 211
Val Leu Val Cys Pro Met Cys Ala His Glu Trp Val Glu Gly Glu Val
25 30 35

gcg gaa gaa acc gcg act gtc atc aaa gac tct gtg gga aat atc ctc 259
Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser Val Gly Asn Ile Leu
40 45 50

aat gat ggc gat tcc gta tcg att gtg aag agc ctc aaa gtc aag ggt 307
Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser Leu Lys Val Lys Gly
55 60 65

ggc ggt gcc atc aag att ggc acc aaa gtc agc gga att cgt ctt ctt 355
Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser Gly Ile Arg Leu Leu
70 75 80 85

gaa gag cca gtt gac ggc cac gac atc gac gct aag gtc cct gga ttt 403
Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala Lys Val Pro Gly Phe
90 95 100

ggt caa atg cga ctc aag tcc agt gtt gta aag aag gcc taaacccttt 452
Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys Lys Ala
105 110

taaggagctt tag 465

<210> 292
<211> 114
<212> PRT
<213> Corynebacterium glutamicum

<400> 292
Met Ser Asp Gln Leu Ala Pro Cys Pro Glu Cys Ser Ser Glu Tyr Thr
1 5 10 15

Tyr Glu Asn Gly Gly Val Leu Val Cys Pro Met Cys Ala His Glu Trp
20 25 30

Val Glu Gly Glu Val Ala Glu Glu Thr Ala Thr Val Ile Lys Asp Ser
35 40 45

Val Gly Asn Ile Leu Asn Asp Gly Asp Ser Val Ser Ile Val Lys Ser
50 55 60

```
Leu Lys Val Lys Gly Gly Gly Ala Ile Lys Ile Gly Thr Lys Val Ser
 65                  70                  75                  80

Gly Ile Arg Leu Leu Glu Glu Pro Val Asp Gly His Asp Ile Asp Ala
                 85                  90                  95

Lys Val Pro Gly Phe Gly Gln Met Arg Leu Lys Ser Ser Val Val Lys
            100                 105                 110

Lys Ala
```

<210> 293
<211> 537
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(514)
<223> RXA00078

<400> 293

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cggtgctgag gagggtgaca tgtctggaag cagattgacg catgctttct agcgtaatgt 60

gggtcacaga aaatgctctc gcttggaagg caggaatccg atg aaa gcc gat ctc   115
                                            Met Lys Ala Asp Leu
                                              1               5

acc ccg tac cgt cag ttc aat gga aat gcc aaa gaa gca atg gag ttc   163
Thr Pro Tyr Arg Gln Phe Asn Gly Asn Ala Lys Glu Ala Met Glu Phe
                 10                  15                  20

tac caa aca gtt ttt ggt ggc gag ctt cag atg atg ccg ttt tcc gcc   211
Tyr Gln Thr Val Phe Gly Gly Glu Leu Gln Met Met Pro Phe Ser Ala
             25                  30                  35

atg cat tct gag gag gaa gtt ggt ggt gac ggc gag aaa atc atg cac   259
Met His Ser Glu Glu Glu Val Gly Gly Asp Gly Glu Lys Ile Met His
         40                  45                  50

gct gag ctg gtc gtt gat ggt cag aag ttg ctt ttt gcc agt gat att   307
Ala Glu Leu Val Val Asp Gly Gln Lys Leu Leu Phe Ala Ser Asp Ile
     55                  60                  65

ccg cgc gtg atg caa cga atg aag ggc gag gac act ccg ttg tcg ctg   355
Pro Arg Val Met Gln Arg Met Lys Gly Glu Asp Thr Pro Leu Ser Leu
 70                  75                  80                  85

act ggt ggc gct gag ctg gaa gag gaa att cgt ggc tac tgg gag aag   403
Thr Gly Gly Ala Glu Leu Glu Glu Glu Ile Arg Gly Tyr Trp Glu Lys
                 90                  95                 100

ttg tct gag ggc ggc acc gtg acc atg cct ttg gaa gct gtt cct tgg   451
Leu Ser Glu Gly Gly Thr Val Thr Met Pro Leu Glu Ala Val Pro Trp
            105                 110                 115

ggt gcg gtt tat ggt gcg ctg gag gat cgc ttt gga act cac tgg atg   499
Gly Ala Val Tyr Gly Ala Leu Glu Asp Arg Phe Gly Thr His Trp Met
        120                 125                 130
```

```
ttc aac atc ggt ggc taaaactttt ggaaacttat tga                          537
Phe Asn Ile Gly Gly
    135
```

<210> 294
<211> 138
<212> PRT
<213> Corynebacterium glutamicum

<400> 294

```
Met Lys Ala Asp Leu Thr Pro Tyr Arg Gln Phe Asn Gly Asn Ala Lys
  1               5                  10                  15

Glu Ala Met Glu Phe Tyr Gln Thr Val Phe Gly Gly Glu Leu Gln Met
             20                  25                  30

Met Pro Phe Ser Ala Met His Ser Glu Glu Glu Val Gly Gly Asp Gly
         35                  40                  45

Glu Lys Ile Met His Ala Glu Leu Val Val Asp Gly Gln Lys Leu Leu
     50                  55                  60

Phe Ala Ser Asp Ile Pro Arg Val Met Gln Arg Met Lys Gly Glu Asp
 65                  70                  75                  80

Thr Pro Leu Ser Leu Thr Gly Gly Ala Glu Leu Glu Glu Glu Ile Arg
                 85                  90                  95

Gly Tyr Trp Glu Lys Leu Ser Glu Gly Gly Thr Val Thr Met Pro Leu
            100                 105                 110

Glu Ala Val Pro Trp Gly Ala Val Tyr Gly Ala Leu Glu Asp Arg Phe
        115                 120                 125

Gly Thr His Trp Met Phe Asn Ile Gly Gly
    130                 135
```

<210> 295
<211> 391
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA02105

<400> 295

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gcgggcgtcg aaaagcggcg acctgcggat ctgtgacccg cgccataaat gggtacgatg 60

gcggttggaa aattccgtaa cttctttgag ggagaaaccc atg gtc ggc acg att   115
                                              Met Val Gly Thr Ile
                                                1               5

tcc acc tac atc gca ttc aat gga aac acc acg gaa gct ctg aaa cat   163
Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr Glu Ala Leu Lys His
                10                  15                  20
```

```
tgg caa gag gtt ttt ggt ggt gaa ctt aat ctt tta acc tac ggt cag   211
Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu Leu Thr Tyr Gly Gln
            25                  30                  35

ctc acc ttg gaa ggt atg ccg ttt gat cct cca gcg gat gcg ttg gcg   259
Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro Ala Asp Ala Leu Ala
        40                  45                  50

cac ggc gtc ctc acg ttg gac aat ggt ggt ttg att tct ggc agt gat   307
His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu Ile Ser Gly Ser Asp
    55                  60                  65

tct ttt gag gga gaa atg ctc gtc aaa gac acc gcg tac tcc atg ttg   355
Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr Ala Tyr Ser Met Leu
70                  75                  80                  85

tat aac gcg gag tca gtg gaa gat ggt cgc gcg cgg                   391
Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala Arg
                90                  95
```

<210> 296
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 296

```
Met Val Gly Thr Ile Ser Thr Tyr Ile Ala Phe Asn Gly Asn Thr Thr
  1               5                  10                  15

Glu Ala Leu Lys His Trp Gln Glu Val Phe Gly Gly Glu Leu Asn Leu
            20                  25                  30

Leu Thr Tyr Gly Gln Leu Thr Leu Glu Gly Met Pro Phe Asp Pro Pro
        35                  40                  45

Ala Asp Ala Leu Ala His Gly Val Leu Thr Leu Asp Asn Gly Gly Leu
    50                  55                  60

Ile Ser Gly Ser Asp Ser Phe Glu Gly Glu Met Leu Val Lys Asp Thr
65                  70                  75                  80

Ala Tyr Ser Met Leu Tyr Asn Ala Glu Ser Val Glu Asp Gly Arg Ala
                85                  90                  95

Arg
```

<210> 297
<211> 1497
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1474)
<223> RXN00663

<400> 297

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ctgaacgatt ggtgaccggc tcatgaaaac ttgacgagtc cccggtattc gccagcggtg 60
```

```
actactaccg tgggcgacaa gcccacttag aggaggactt gtg aca acc acc tat   115
                                            Val Thr Thr Thr Tyr
                                              1               5

cca gat ttc ctt gga aat tct tcg ctc caa aca gat acg gag cac tgg   163
Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr Asp Thr Glu His Trp
                 10                  15                  20

gaa atg gaa gga ggt gcg cag gaa gtc tct gtt act tat gtt ttg gac   211
Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val Thr Tyr Val Leu Asp
             25                  30                  35

acg tca gtg ttg ctg tct gat ccg ttg tcg ttg aca cgg ttc gcg gag   259
Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu Thr Arg Phe Ala Glu
         40                  45                  50

cac gat gta gtt ctg cca att gtt gta att acg gaa tta gaa gcc aag   307
His Asp Val Val Leu Pro Ile Val Val Ile Thr Glu Leu Glu Ala Lys
     55                  60                  65

cgt cat cac ccg gac ctt ggc ttt ttt gct cgc caa gcg ctt cgg atg   355
Arg His His Pro Asp Leu Gly Phe Phe Ala Arg Gln Ala Leu Arg Met
 70                  75                  80                  85

ctg gat gag ctg cgt gag atc cat ggg gat ttg tcc aag cca ctg cca   403
Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu Ser Lys Pro Leu Pro
                 90                  95                 100

att ggc gat gaa ggc gga cac atc cat gtt gag ctg aat cac caa aac   451
Ile Gly Asp Glu Gly Gly His Ile His Val Glu Leu Asn His Gln Asn
             105                 110                 115

acg ggg tcc ttg ccc gtg gga ttc cgc ctt ggt gac aat gac acc cgc   499
Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly Asp Asn Asp Thr Arg
         120                 125                 130

atc ctt gca gtg gcc aag aat ctg cag gaa gag ggc cac aat gtg gtt   547
Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu Gly His Asn Val Val
     135                 140                 145

ctg gtg tcg aag gac ctg ccg atg cgg att aag gcg tcg gca agc gga   595
Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys Ala Ser Ala Ser Gly
150                 155                 160                 165

atc gcc gca cag gaa tac cgc gct gcc ctg gcg cgc gac cgt ggt tac   643
Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala Arg Asp Arg Gly Tyr
                170                 175                 180

acc ggc atg acc cac gcc aat atc acc gat gac cag ctc agc gag ctc   691
Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp Gln Leu Ser Glu Leu
            185                 190                 195

tac gac acc ggc gag gtg cgc att gag gag ctc gaa aag ctg ccc gtc   739
Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu Glu Lys Leu Pro Val
        200                 205                 210

aac cac ggc ttc acc ctc aaa tcc aac agc ggt tcg gcg ctt ggt cgt   787
Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly Ser Ala Leu Gly Arg
    215                 220                 225
```

```
atg aat tcc gac aag atc atc gag ctt gtc ccc ggc gac cag cag gta   835
Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro Gly Asp Gln Gln Val
230                 235                 240                 245

ttc ggt atc agc ggg cgt agc gct gag cag cgg gtt gcc att gat ttg   883
Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg Val Ala Ile Asp Leu
                250                 255                 260

ctt aac gac gac gcc gtc ggc atc gta tcc atc ggc ggc ccc gcg ggt   931
Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile Gly Gly Pro Ala Gly
            265                 270                 275

aca ggt aaa agc gca ctc gca ctg tgt gcc ggc ctg gaa gct gtg atg   979
Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly Leu Glu Ala Val Met
        280                 285                 290

gag cgt cgc att cag cgc aag att atc gtg ttc cgc cca ctc ttt gcc   1027
Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe Arg Pro Leu Phe Ala
    295                 300                 305

gtt ggc gga cag gaa ctt ggc tac ctg cct ggc gac caa gaa gaa aaa   1075
Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly Asp Gln Glu Glu Lys
310                 315                 320                 325

atg ggg cct tgg gcg caa gcg gtt ttt gac acc cta agc tcc atg gtc   1123
Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr Leu Ser Ser Met Val
                330                 335                 340

agc caa aac atc atc gat gaa gcc ctc tcc cgc ggc ctc atc gaa gtt   1171
Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg Gly Leu Ile Glu Val
            345                 350                 355

ctc cca ctt act cac atc cgc gga cgc tca ctc cac gat gct ttc gtc   1219
Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu His Asp Ala Phe Val
        360                 365                 370

atc gtc gac gag gcc caa tcc cta gaa cgc aac gtg ttg ctc acc atg   1267
Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn Val Leu Leu Thr Met
    375                 380                 385

ctg tct cgc atc ggc cag aat tcc cga gta gtt ctc acc cat gac gta   1315
Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val Leu Thr His Asp Val
390                 395                 400                 405

gcg cag cgc gac aac ctg cgc gtt ggt cgc tac gac ggc atc gtc tct   1363
Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr Asp Gly Ile Val Ser
                410                 415                 420

gtg gtg gaa gca ctc aag gat cac gaa ctg ttt ggc cac atc acg ttg   1411
Val Val Glu Ala Leu Lys Asp His Glu Leu Phe Gly His Ile Thr Leu
            425                 430                 435

cag cgt tcc gaa cgc tcc cga atc gct gag ttg gtc acc caa gtt ttg   1459
Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu Val Thr Gln Val Leu
        440                 445                 450

gat gcg ccg tct ctg tagtcgcgca gtctgtggcg att                    1497
Asp Ala Pro Ser Leu
    455
```

<210> 298
<211> 458
<212> PRT
<213> Corynebacterium glutamicum

<400> 298

```
Val Thr Thr Thr Tyr Pro Asp Phe Leu Gly Asn Ser Ser Leu Gln Thr
  1               5                  10                  15

Asp Thr Glu His Trp Glu Met Glu Gly Gly Ala Gln Glu Val Ser Val
             20                  25                  30

Thr Tyr Val Leu Asp Thr Ser Val Leu Leu Ser Asp Pro Leu Ser Leu
         35                  40                  45

Thr Arg Phe Ala Glu His Asp Val Val Leu Pro Ile Val Val Ile Thr
     50                  55                  60

Glu Leu Glu Ala Lys Arg His His Pro Asp Leu Gly Phe Phe Ala Arg
 65                  70                  75                  80

Gln Ala Leu Arg Met Leu Asp Glu Leu Arg Glu Ile His Gly Asp Leu
                 85                  90                  95

Ser Lys Pro Leu Pro Ile Gly Asp Glu Gly Gly His Ile His Val Glu
            100                 105                 110

Leu Asn His Gln Asn Thr Gly Ser Leu Pro Val Gly Phe Arg Leu Gly
        115                 120                 125

Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln Glu Glu
    130                 135                 140

Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg Ile Lys
145                 150                 155                 160

Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala Leu Ala
                165                 170                 175

Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr Asp Asp
            180                 185                 190

Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu Glu Leu
        195                 200                 205

Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn Ser Gly
    210                 215                 220

Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu Val Pro
225                 230                 235                 240

Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu Gln Arg
                245                 250                 255

Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val Ser Ile
            260                 265                 270

Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys Ala Gly
        275                 280                 285

Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile Val Phe
```

```
    290                 295                 300

Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu Pro Gly
305                 310                 315                 320

Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe Asp Thr
                325                 330                 335

Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu Ser Arg
            340                 345                 350

Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg Ser Leu
        355                 360                 365

His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu Arg Asn
    370                 375                 380

Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg Val Val
385                 390                 395                 400

Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly Arg Tyr
                405                 410                 415

Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu Leu Phe
            420                 425                 430

Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala Glu Leu
        435                 440                 445

Val Thr Gln Val Leu Asp Ala Pro Ser Leu
    450                 455


<210> 299
<211> 1019
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(996)
<223> FRXA00663

<400> 299
ctt ggt gac aat gac acc cgc atc ctt gca gtg gcc aag aat ctg cag   48
Leu Gly Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln
  1               5                  10                  15

gaa gag ggc cac aat gtg gtt ctg gtg tcg aag gac ctg ccg atg cgg   96
Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg
             20                  25                  30

att aag gcg tcg gca agc gga atc gcc gca cag gaa tac cgc gct gcc   144
Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala
         35                  40                  45

ctg gcg cgc gac cgt ggt tac acc ggc atg acc cac gcc aat atc acc   192
Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr
     50                  55                  60

gat gac cag ctc agc gag ctc tac gac acc ggc gag gtg cgc att gag   240
```

```
Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu
 65                  70                  75                  80

gag ctc gaa aag ctg ccc gtc aac cac ggc ttc acc ctc aaa tcc aac   288
Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn
                 85                  90                  95

agc ggt tcg gcg ctt ggt cgt atg aat tcc gac aag atc atc gag ctt   336
Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu
            100                 105                 110

gtc ccc ggc gac cag cag gta ttc ggt atc agc ggg cgt agc gct gag   384
Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu
        115                 120                 125

cag cgg gtt gcc att gat ttg ctt aac gac gac gcc gtc ggc atc gta   432
Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val
    130                 135                 140

tcc atc ggc ggc ccc gcg ggt aca ggt aaa agc gca ctc gca ctg tgt   480
Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys
145                 150                 155                 160

gcc ggc ctg gaa gct gtg atg gag cgt cgc att cag cgc aag att atc   528
Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile
                165                 170                 175

gtg ttc cgc cca ctc ttt gcc gtt ggc gga cag gaa ctt ggc tac ctg   576
Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu
            180                 185                 190

cct ggc gac caa gaa gaa aaa atg ggg cct tgg gcg caa gcg gtt ttt   624
Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe
        195                 200                 205

gac acc cta agc tcc atg gtc agc caa aac atc atc gat gaa gcc ctc   672
Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu
    210                 215                 220

tcc cgc ggc ctc atc gaa gtt ctc cca ctt act cac atc cgc gga cgc   720
Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg
225                 230                 235                 240

tca ctc cac gat gct ttc gtc atc gtc gac gag gcc caa tcc cta gaa   768
Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu
                245                 250                 255

cgc aac gtg ttg ctc acc atg ctg tct cgc atc ggc cag aat tcc cga   816
Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg
            260                 265                 270

gta gtt ctc acc cat gac gta gcg cag cgc gac aac ctg cgc gtt ggt   864
Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly
        275                 280                 285

cgc tac gac ggc atc gtc tct gtg gtg gaa gca ctc aag gat cac gaa   912
Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu
    290                 295                 300

ctg ttt ggc cac atc acg ttg cag cgt tcc gaa cgc tcc cga atc gct   960
Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala
```

```
305                 310                 315                 320

gag ttg gtc acc caa gtt ttg gat gcg ccg tct ctg tagtcgcgca        1006
Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu
                325                 330

gtctgtggcg att                                                    1019
```

<210> 300
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 300

```
Leu Gly Asp Asn Asp Thr Arg Ile Leu Ala Val Ala Lys Asn Leu Gln
  1               5                  10                  15

Glu Glu Gly His Asn Val Val Leu Val Ser Lys Asp Leu Pro Met Arg
             20                  25                  30

Ile Lys Ala Ser Ala Ser Gly Ile Ala Ala Gln Glu Tyr Arg Ala Ala
         35                  40                  45

Leu Ala Arg Asp Arg Gly Tyr Thr Gly Met Thr His Ala Asn Ile Thr
     50                  55                  60

Asp Asp Gln Leu Ser Glu Leu Tyr Asp Thr Gly Glu Val Arg Ile Glu
 65                  70                  75                  80

Glu Leu Glu Lys Leu Pro Val Asn His Gly Phe Thr Leu Lys Ser Asn
                 85                  90                  95

Ser Gly Ser Ala Leu Gly Arg Met Asn Ser Asp Lys Ile Ile Glu Leu
            100                 105                 110

Val Pro Gly Asp Gln Gln Val Phe Gly Ile Ser Gly Arg Ser Ala Glu
        115                 120                 125

Gln Arg Val Ala Ile Asp Leu Leu Asn Asp Asp Ala Val Gly Ile Val
    130                 135                 140

Ser Ile Gly Gly Pro Ala Gly Thr Gly Lys Ser Ala Leu Ala Leu Cys
145                 150                 155                 160

Ala Gly Leu Glu Ala Val Met Glu Arg Arg Ile Gln Arg Lys Ile Ile
                165                 170                 175

Val Phe Arg Pro Leu Phe Ala Val Gly Gly Gln Glu Leu Gly Tyr Leu
            180                 185                 190

Pro Gly Asp Gln Glu Glu Lys Met Gly Pro Trp Ala Gln Ala Val Phe
        195                 200                 205

Asp Thr Leu Ser Ser Met Val Ser Gln Asn Ile Ile Asp Glu Ala Leu
    210                 215                 220

Ser Arg Gly Leu Ile Glu Val Leu Pro Leu Thr His Ile Arg Gly Arg
225                 230                 235                 240

Ser Leu His Asp Ala Phe Val Ile Val Asp Glu Ala Gln Ser Leu Glu
```

```
                245                 250                 255

Arg Asn Val Leu Leu Thr Met Leu Ser Arg Ile Gly Gln Asn Ser Arg
            260                 265                 270

Val Val Leu Thr His Asp Val Ala Gln Arg Asp Asn Leu Arg Val Gly
        275                 280                 285

Arg Tyr Asp Gly Ile Val Ser Val Val Glu Ala Leu Lys Asp His Glu
    290                 295                 300

Leu Phe Gly His Ile Thr Leu Gln Arg Ser Glu Arg Ser Arg Ile Ala
305                 310                 315                 320

Glu Leu Val Thr Gln Val Leu Asp Ala Pro Ser Leu
                325                 330
```

<210> 301
<211> 1140
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1117)
<223> RXA00888

<400> 301

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atggtggcgc tcgcagctat cggcgtgctg tctgaccgct ggtaacattt ctctgacata 60

acctttcttg aacattccga aagcaggccg aactagcact gtg act gcc ccg cga   115
                                              Val Thr Ala Pro Arg
                                                1               5

aaa acc cgc aca gaa gta atc acc act gtc ctc aat cta gaa cgc acg   163
Lys Thr Arg Thr Glu Val Ile Thr Thr Val Leu Asn Leu Glu Arg Thr
                  10                  15                  20

ctc gcg caa acc gtt tta gga atc aac gac gaa aac ctg cgt gtg ttg   211
Leu Ala Gln Thr Val Leu Gly Ile Asn Asp Glu Asn Leu Arg Val Leu
              25                  30                  35

gac aat caa att gat tgc gat att cac gtg cgt ggc acc cac gtg gaa   259
Asp Asn Gln Ile Asp Cys Asp Ile His Val Arg Gly Thr His Val Glu
          40                  45                  50

ctc acc ggg cca gcc cac gaa gtc tcc cgc gcc tcg aaa ata ttt gag   307
Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala Ser Lys Ile Phe Glu
      55                  60                  65

gaa ctg cag gcg att gcc cgt cga gga cat gtg att agc cct gag aca   355
Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val Ile Ser Pro Glu Thr
  70                  75                  80                  85

gta aaa aat gtc atc agc atg att aac gtg gag acg ccg caa acc gtc   403
Val Lys Asn Val Ile Ser Met Ile Asn Val Glu Thr Pro Gln Thr Val
                  90                  95                 100

tct gaa atc ttg acc ggc gat atc ctt gct cgc cgt ggc aaa gtg atc   451
Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg Arg Gly Lys Val Ile
```

```
            105                 110                 115

cgc cct aag acg ctt ggc caa aag cac tac gtg gac gcg att gat acc   499
Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val Asp Ala Ile Asp Thr
        120                 125                 130

aac acg att gtg ttc ggt ctg ggc cca gcc ggt tcc ggt aaa acc tat   547
Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly Ser Gly Lys Thr Tyr
    135                 140                 145

ctg gcc atg gca aaa gcc gtc caa gcg ctg caa tca aag cag gtc agc   595
Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln Ser Lys Gln Val Ser
150                 155                 160                 165

cgc atc atc ttg acc cgc ccc gca gtg gaa gcc ggc gag aaa ctc ggc   643
Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala Gly Glu Lys Leu Gly
                170                 175                 180

ttc ttg ccc ggc acc ctg aac gaa aag atc gac ccc tac ctg cgc ccg   691
Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp Pro Tyr Leu Arg Pro
            185                 190                 195

ctt cac gac gcg ctg cgc gac atg gtc gaa cca gaa gtc att cca aaa   739
Leu His Asp Ala Leu Arg Asp Met Val Glu Pro Glu Val Ile Pro Lys
        200                 205                 210

ctc atg gaa gcc ggc atc gta gaa gtc gcc cca ctt gcc tac atg cgc   787
Leu Met Glu Ala Gly Ile Val Glu Val Ala Pro Leu Ala Tyr Met Arg
    215                 220                 225

gga cgc acc ctc aac gat gca ttc gtg atc ctg gat gaa gcc cag aac   835
Gly Arg Thr Leu Asn Asp Ala Phe Val Ile Leu Asp Glu Ala Gln Asn
230                 235                 240                 245

acc acc cca gca cag atg aag atg ttc ctc acc cgc ctg gga ttc ggt   883
Thr Thr Pro Ala Gln Met Lys Met Phe Leu Thr Arg Leu Gly Phe Gly
                250                 255                 260

tcc aaa atg gta gtc aca ggt gac atc acc cag gtg gac ctc cca gga   931
Ser Lys Met Val Val Thr Gly Asp Ile Thr Gln Val Asp Leu Pro Gly
            265                 270                 275

ggc caa aag tcc ggc ctg cgc ctg gtt cgc cac atc ctg cgc gga gta   979
Gly Gln Lys Ser Gly Leu Arg Leu Val Arg His Ile Leu Arg Gly Val
        280                 285                 290

gac gat gtg cac ttc tcc gag ctc acc tca tcc gac gtg gtc cgc cac   1027
Asp Asp Val His Phe Ser Glu Leu Thr Ser Ser Asp Val Val Arg His
    295                 300                 305

caa ctg gtt gga cac att gtg gat gca tac gaa gac tat gaa gaa cgc   1075
Gln Leu Val Gly His Ile Val Asp Ala Tyr Glu Asp Tyr Glu Glu Arg
310                 315                 320                 325

gag gcc cgc gaa ttg aaa cgc aaa cgc cag gag aca cgg cca           1117
Glu Ala Arg Glu Leu Lys Arg Lys Arg Gln Glu Thr Arg Pro
                330                 335

tgagcattga ggtattcaac gaa                                        1140
```

<210> 302
<211> 339
<212> PRT
<213> Corynebacterium glutamicum

<400> 302
Val Thr Ala Pro Arg Lys Thr Arg Thr Glu Val Ile Thr Thr Val Leu
1 5 10 15

Asn Leu Glu Arg Thr Leu Ala Gln Thr Val Leu Gly Ile Asn Asp Glu
20 25 30

Asn Leu Arg Val Leu Asp Asn Gln Ile Asp Cys Asp Ile His Val Arg
35 40 45

Gly Thr His Val Glu Leu Thr Gly Pro Ala His Glu Val Ser Arg Ala
50 55 60

Ser Lys Ile Phe Glu Glu Leu Gln Ala Ile Ala Arg Arg Gly His Val
65 70 75 80

Ile Ser Pro Glu Thr Val Lys Asn Val Ile Ser Met Ile Asn Val Glu
85 90 95

Thr Pro Gln Thr Val Ser Glu Ile Leu Thr Gly Asp Ile Leu Ala Arg
100 105 110

Arg Gly Lys Val Ile Arg Pro Lys Thr Leu Gly Gln Lys His Tyr Val
115 120 125

Asp Ala Ile Asp Thr Asn Thr Ile Val Phe Gly Leu Gly Pro Ala Gly
130 135 140

Ser Gly Lys Thr Tyr Leu Ala Met Ala Lys Ala Val Gln Ala Leu Gln
145 150 155 160

Ser Lys Gln Val Ser Arg Ile Ile Leu Thr Arg Pro Ala Val Glu Ala
165 170 175

Gly Glu Lys Leu Gly Phe Leu Pro Gly Thr Leu Asn Glu Lys Ile Asp
180 185 190

Pro Tyr Leu Arg Pro Leu His Asp Ala Leu Arg Asp Met Val Glu Pro
195 200 205

Glu Val Ile Pro Lys Leu Met Glu Ala Gly Ile Val Glu Val Ala Pro
210 215 220

Leu Ala Tyr Met Arg Gly Arg Thr Leu Asn Asp Ala Phe Val Ile Leu
225 230 235 240

Asp Glu Ala Gln Asn Thr Thr Pro Ala Gln Met Lys Met Phe Leu Thr
245 250 255

Arg Leu Gly Phe Gly Ser Lys Met Val Val Thr Gly Asp Ile Thr Gln
260 265 270

Val Asp Leu Pro Gly Gly Gln Lys Ser Gly Leu Arg Leu Val Arg His
275 280 285

Ile Leu Arg Gly Val Asp Asp Val His Phe Ser Glu Leu Thr Ser Ser

```
    290                 295                 300

Asp Val Val Arg His Gln Leu Val Gly His Ile Val Asp Ala Tyr Glu
305                 310                 315                 320

Asp Tyr Glu Glu Arg Glu Ala Arg Glu Leu Lys Arg Lys Arg Gln Glu
                325                 330                 335

Thr Arg Pro
```

<210> 303
<211> 1506
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1483)
<223> RXA01437

<400> 303

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actatgtaag aaatcacaac ctcccctcat tagtgccagg aggcacaagc ctgaagtgtc 60

atcaatgaga aggttcaggc tgaaattaga aaggcgatgt atg tct gac aca ccg   115
                                              Met Ser Asp Thr Pro
                                                1               5

acc tca gct ctg atc acc acg gtc aac cgc agc ttc gat gga ttc gat   163
Thr Ser Ala Leu Ile Thr Thr Val Asn Arg Ser Phe Asp Gly Phe Asp
                  10                  15                  20

ttg gaa gaa gta gca gca gac ctt gga gtt cgg ctc acc tac ctg ccc   211
Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg Leu Thr Tyr Leu Pro
              25                  30                  35

gac gaa gaa cta gaa gta tcc aaa gtt ctc gcg gcg gac ctc ctc gct   259
Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala Ala Asp Leu Leu Ala
          40                  45                  50

gag ggg cca gct ctc atc atc ggt gta gga aac acg ttt ttc gac gcc   307
Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn Thr Phe Phe Asp Ala
      55                  60                  65

cag gtc gcc gct gcc ctc ggc gtc cca gtg cta ctg ctg gta gac aag   355
Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu Leu Leu Val Asp Lys
  70                  75                  80                  85

caa ggc aag cac gtt gct ctt gct cgc acc cag gta aac aat gcc ggc   403
Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln Val Asn Asn Ala Gly
                  90                  95                 100

gca gtt gtt gca gca gca ttt acc gct gaa caa gag cca atg ccg gat   451
Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln Glu Pro Met Pro Asp
              105                 110                 115

aag ctg cgc aag gct gtg cgc aac cac agc aac ctc gaa cca gtc atg   499
Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn Leu Glu Pro Val Met
          120                 125                 130
```

```
agc gcc gaa ctc ttt gaa aac tgg ctg ctc aag cgc gca cgc gca gag   547
Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys Arg Ala Arg Ala Glu
    135                 140                 145

cac tcc cac att gtg ctg cca gaa ggt gac gac gac cgc atc ttg atg   595
His Ser His Ile Val Leu Pro Glu Gly Asp Asp Asp Arg Ile Leu Met
150                 155                 160                 165

gct gcc cac cag ctg ctt gat caa gac atc tgt gac atc acg atc ctg   643
Ala Ala His Gln Leu Leu Asp Gln Asp Ile Cys Asp Ile Thr Ile Leu
                170                 175                 180

ggc gat cca gta aag atc aag gag cgc gct acc gaa ctt ggc ctg cac   691
Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr Glu Leu Gly Leu His
            185                 190                 195

ctt aac act gca tac ctg gtc aat ccg ctg aca gat cct cgc ctg gag   739
Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr Asp Pro Arg Leu Glu
        200                 205                 210

gaa ttc gcc gaa caa ttc gcg gag ctg cgc aag tca aag agc gtc act   787
Glu Phe Ala Glu Gln Phe Ala Glu Leu Arg Lys Ser Lys Ser Val Thr
    215                 220                 225

atc gat gaa gcc cgc gaa atc atg aag gat att tcc tac ttc ggc acc   835
Ile Asp Glu Ala Arg Glu Ile Met Lys Asp Ile Ser Tyr Phe Gly Thr
230                 235                 240                 245

atg atg gtc cac aac ggc gac gcc gac gga atg gta tcc ggt gca gca   883
Met Met Val His Asn Gly Asp Ala Asp Gly Met Val Ser Gly Ala Ala
                250                 255                 260

aac acc acc gca cac acc att aag cca agc ttc cag atc atc aaa act   931
Asn Thr Thr Ala His Thr Ile Lys Pro Ser Phe Gln Ile Ile Lys Thr
            265                 270                 275

gtt cca gaa gca tcc gtc gtt tct tcc atc ttc ctc atg gtg ctg cgc   979
Val Pro Glu Ala Ser Val Val Ser Ser Ile Phe Leu Met Val Leu Arg
        280                 285                 290

ggg cga ctg tgg gca ttc ggc gac tgt gct gtt aac ccg aac cca act   1027
Gly Arg Leu Trp Ala Phe Gly Asp Cys Ala Val Asn Pro Asn Pro Thr
    295                 300                 305

gct gaa cag ctt ggt gaa atc gcc gtt gtg tca gca aaa act gca gca   1075
Ala Glu Gln Leu Gly Glu Ile Ala Val Val Ser Ala Lys Thr Ala Ala
310                 315                 320                 325

caa ttt ggc att gat cct cgc gta gcc atc ttg tcc tac tcc act ggc   1123
Gln Phe Gly Ile Asp Pro Arg Val Ala Ile Leu Ser Tyr Ser Thr Gly
                330                 335                 340

aac tcc ggc gga ggc tca gat gtg gat cgc gcc atc gac gct ctt gca   1171
Asn Ser Gly Gly Gly Ser Asp Val Asp Arg Ala Ile Asp Ala Leu Ala
            345                 350                 355

gaa gca cgc cga ctt aac cca gaa cta tgc gtc gat gga cca ctt cag   1219
Glu Ala Arg Arg Leu Asn Pro Glu Leu Cys Val Asp Gly Pro Leu Gln
        360                 365                 370

ttc gac gcc gcc gtc gac ccg ggt gtg gcg cgc aag aag atg cca gac   1267
```

```
Phe Asp Ala Ala Val Asp Pro Gly Val Ala Arg Lys Lys Met Pro Asp
    375                 380                 385

tct gac gtc gct ggc cag gca aat gtg ttt atc ttc cct gac ctg gaa   1315
Ser Asp Val Ala Gly Gln Ala Asn Val Phe Ile Phe Pro Asp Leu Glu
390                 395                 400                 405

gcc gga aac atc ggc tac aaa act gca caa cgc acc ggt cac gcc ctg   1363
Ala Gly Asn Ile Gly Tyr Lys Thr Ala Gln Arg Thr Gly His Ala Leu
                410                 415                 420

gca gtt ggt ccg att ctg cag ggc cta aac aaa cca gtc aac gac ctt   1411
Ala Val Gly Pro Ile Leu Gln Gly Leu Asn Lys Pro Val Asn Asp Leu
            425                 430                 435

tcc cgt ggc gca aca gtc cct gac atc gtc aac aca gta gcc atc aca   1459
Ser Arg Gly Ala Thr Val Pro Asp Ile Val Asn Thr Val Ala Ile Thr
        440                 445                 450

gca att cag gca gga gga cgc agc taatggcatt ggcacttgtt ttg         1506
Ala Ile Gln Ala Gly Gly Arg Ser
    455                 460
```

<210> 304
<211> 461
<212> PRT
<213> Corynebacterium glutamicum

<400> 304

```
Met Ser Asp Thr Pro Thr Ser Ala Leu Ile Thr Thr Val Asn Arg Ser
  1               5                  10                  15

Phe Asp Gly Phe Asp Leu Glu Glu Val Ala Ala Asp Leu Gly Val Arg
             20                  25                  30

Leu Thr Tyr Leu Pro Asp Glu Glu Leu Glu Val Ser Lys Val Leu Ala
         35                  40                  45

Ala Asp Leu Leu Ala Glu Gly Pro Ala Leu Ile Ile Gly Val Gly Asn
     50                  55                  60

Thr Phe Phe Asp Ala Gln Val Ala Ala Ala Leu Gly Val Pro Val Leu
 65                  70                  75                  80

Leu Leu Val Asp Lys Gln Gly Lys His Val Ala Leu Ala Arg Thr Gln
                 85                  90                  95

Val Asn Asn Ala Gly Ala Val Val Ala Ala Ala Phe Thr Ala Glu Gln
            100                 105                 110

Glu Pro Met Pro Asp Lys Leu Arg Lys Ala Val Arg Asn His Ser Asn
        115                 120                 125

Leu Glu Pro Val Met Ser Ala Glu Leu Phe Glu Asn Trp Leu Leu Lys
    130                 135                 140

Arg Ala Arg Ala Glu His Ser His Ile Val Leu Pro Glu Gly Asp Asp
145                 150                 155                 160

Asp Arg Ile Leu Met Ala Ala His Gln Leu Leu Asp Gln Asp Ile Cys
```

```
                165                 170                 175

Asp Ile Thr Ile Leu Gly Asp Pro Val Lys Ile Lys Glu Arg Ala Thr
            180                 185                 190

Glu Leu Gly Leu His Leu Asn Thr Ala Tyr Leu Val Asn Pro Leu Thr
        195                 200                 205

Asp Pro Arg Leu Glu Glu Phe Ala Glu Gln Phe Ala Glu Leu Arg Lys
    210                 215                 220

Ser Lys Ser Val Thr Ile Asp Glu Ala Arg Glu Ile Met Lys Asp Ile
225                 230                 235                 240

Ser Tyr Phe Gly Thr Met Met Val His Asn Gly Asp Ala Asp Gly Met
                245                 250                 255

Val Ser Gly Ala Ala Asn Thr Thr Ala His Thr Ile Lys Pro Ser Phe
            260                 265                 270

Gln Ile Ile Lys Thr Val Pro Glu Ala Ser Val Val Ser Ser Ile Phe
        275                 280                 285

Leu Met Val Leu Arg Gly Arg Leu Trp Ala Phe Gly Asp Cys Ala Val
    290                 295                 300

Asn Pro Asn Pro Thr Ala Glu Gln Leu Gly Glu Ile Ala Val Val Ser
305                 310                 315                 320

Ala Lys Thr Ala Ala Gln Phe Gly Ile Asp Pro Arg Val Ala Ile Leu
                325                 330                 335

Ser Tyr Ser Thr Gly Asn Ser Gly Gly Gly Ser Asp Val Asp Arg Ala
            340                 345                 350

Ile Asp Ala Leu Ala Glu Ala Arg Arg Leu Asn Pro Glu Leu Cys Val
        355                 360                 365

Asp Gly Pro Leu Gln Phe Asp Ala Ala Val Asp Pro Gly Val Ala Arg
    370                 375                 380

Lys Lys Met Pro Asp Ser Asp Val Ala Gly Gln Ala Asn Val Phe Ile
385                 390                 395                 400

Phe Pro Asp Leu Glu Ala Gly Asn Ile Gly Tyr Lys Thr Ala Gln Arg
                405                 410                 415

Thr Gly His Ala Leu Ala Val Gly Pro Ile Leu Gln Gly Leu Asn Lys
            420                 425                 430

Pro Val Asn Asp Leu Ser Arg Gly Ala Thr Val Pro Asp Ile Val Asn
        435                 440                 445

Thr Val Ala Ile Thr Ala Ile Gln Ala Gly Gly Arg Ser
    450                 455                 460
```

<210> 305
<211> 1248
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1225)
<223> RXN00778

<400> 305
aggtcttagg tttttaagtc gtgagcaatc cggagggaaa ctagcccgcc tacaggatct 60

gctcagacga tgtcttcact taaaccggaa aggcttcccc gtg aac ctc act ctt 115
Val Asn Leu Thr Leu
1 5

aag cgc tcc atc gcc ctt gtg ggc gca gtt act gca ggc tcc ttc gct 163
Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr Ala Gly Ser Phe Ala
10 15 20

ctt gta gct tgc tcc gac tcc aat gag tct gat tcc acc tcc tca tct 211
Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp Ser Thr Ser Ser Ser
25 30 35

gca gct tcc acc ggt tct tcc gat gct gca tcc att gag ggc ctt tcc 259
Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser Ile Glu Gly Leu Ser
40 45 50

ggt gtt acc ggt cag ctc gtt gct gaa ggt gca tct tcc cag cag tcc 307
Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala Ser Ser Gln Gln Ser
55 60 65

gca atg gac tac ttt ggt atc cgt tac tcc gag gct gtc agc ggt gca 355
Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu Ala Val Ser Gly Ala
70 75 80 85

tct ctg gct tac acc cct tca ggt tcc ggt tcc ggc cgc acc aac ttc 403
Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser Gly Arg Thr Asn Phe
90 95 100

gct gca ggc cag gtt gct ttc ggt ggc tcc gac tcc gca atg aag gac 451
Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp Ser Ala Met Lys Asp
105 110 115

gac cag gct gca gaa gca gaa gca cgt tgc aac ggc aac gaa gca tgg 499
Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly Asn Glu Ala Trp
120 125 130

cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct tac aac ctg cct 547
His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala Tyr Asn Leu Pro
135 140 145

ggc gtt gac acc ctg aac ctg gac acc aac atc atc gct cag atc ttc 595
Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile Ala Gln Ile Phe
150 155 160 165

aag ggc gag atc acc aag tgg aac gac gaa gca atc gct tcc cag aac 643
Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile Ala Ser Gln Asn
170 175 180

gag ggc acc gac ctc cca gac cag gac atc tcc gtt ctg tac cgt tcc 691
Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val Leu Tyr Arg Ser
185 190 195

```
gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc ctc gga gct tcc   739
Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe Leu Gly Ala Ser
        200                 205                 210

acc gac atc tgg gag acc gaa ggc cag cag ttc cca acc gag gtt ggc   787
Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro Thr Glu Val Gly
    215                 220                 225

tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag gct tcc aac atc   835
Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu Ala Ser Asn Ile
230                 235                 240                 245

gag ggt gca atc acc tac gtt gaa gct ggt ttc gct aac cag tcc ggc   883
Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala Asn Gln Ser Gly
                250                 255                 260

ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca gtt gaa ctc aac   931
Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro Val Glu Leu Asn
            265                 270                 275

gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac ttc ctg act gag   979
Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp Phe Leu Thr Glu
        280                 285                 290

ggc cac aac atg gtt gtt gac acc gac gct atg ttc gca atg aac gaa   1027
Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe Ala Met Asn Glu
    295                 300                 305

gcc ggt gct tac cca ctg atc ctc acc acc tac gaa atc gtc tgc tcc   1075
Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu Ile Val Cys Ser
310                 315                 320                 325

gca ggc tac gac gag acc acc cgc gac cag gtc aag gac ttc ctg acc   1123
Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys Asp Phe Leu Thr
                330                 335                 340

gtt gca ctg gac tcc cag gat gac cag ctc gag gct ctc ggc tac atc   1171
Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala Leu Gly Tyr Ile
            345                 350                 355

cca gtt acc ggc gag cac tac gat cgc ctc gtt gca gca gtt gaa gca   1219
Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala Ala Val Glu Ala
        360                 365                 370

att cag taataaaccg ctgccgtagc ttc                                1248
Ile Gln
    375
```

Replacement Sheet

<210> 306
<211> 375
<212> PRT
<213> Corynebacterium glutamicum

<400> 306

```
Val Asn Leu Thr Leu Lys Arg Ser Ile Ala Leu Val Gly Ala Val Thr
  1               5                  10                  15

Ala Gly Ser Phe Ala Leu Val Ala Cys Ser Asp Ser Asn Glu Ser Asp
             20                  25                  30
```

```
Ser Thr Ser Ser Ser Ala Ala Ser Thr Gly Ser Ser Asp Ala Ala Ser
          35                  40                  45

Ile Glu Gly Leu Ser Gly Val Thr Gly Gln Leu Val Ala Glu Gly Ala
     50                  55                  60

Ser Ser Gln Gln Ser Ala Met Asp Tyr Phe Gly Ile Arg Tyr Ser Glu
 65                  70                  75                  80

Ala Val Ser Gly Ala Ser Leu Ala Tyr Thr Pro Ser Gly Ser Gly Ser
                 85                  90                  95

Gly Arg Thr Asn Phe Ala Ala Gly Gln Val Ala Phe Gly Gly Ser Asp
            100                 105                 110

Ser Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn
        115                 120                 125

Gly Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val
    130                 135                 140

Ala Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile
145                 150                 155                 160

Ile Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala
                165                 170                 175

Ile Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser
            180                 185                 190

Val Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys
        195                 200                 205

Phe Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe
    210                 215                 220

Pro Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser
225                 230                 235                 240

Glu Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe
                245                 250                 255

Ala Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly
            260                 265                 270

Pro Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu
        275                 280                 285

Asp Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met
    290                 295                 300

Phe Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr
305                 310                 315                 320

Glu Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val
                325                 330                 335

Lys Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu
            340                 345                 350

Ala Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val
```

```
        355                 360                 365

Ala Ala Val Glu Ala Ile Gln
    370                 375


<210> 307
<211> 857
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(834)
<223> FRXA00778

<400> 307
cgc aac aac ttc gct gca gcc cag gtt gct ttc ggt ggc tcc gac tcc   48
Arg Asn Asn Phe Ala Ala Ala Gln Val Ala Phe Gly Gly Ser Asp Ser
  1               5                  10                  15

gca atg aag gac gac cag gct gca gaa gca gaa gca cgt tgc aac ggc   96
Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly
             20                  25                  30

aac gaa gca tgg cac ctg cca ttc gtt atc ggc cca gtt gca gtt gct   144
Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala
         35                  40                  45

tac aac ctg cct ggc gtt gac acc ctg aac ctg gac acc aac atc atc   192
Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile
     50                  55                  60

gct cag atc ttc aag ggc gag atc acc aag tgg aac gac gaa gca atc   240
Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile
 65                  70                  75                  80

gct tcc cag aac gag ggc acc gac ctc cca gac cag gac atc tcc gtt   288
Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val
                 85                  90                  95

ctg tac cgt tcc gaa gag tcc ggt acc tcc gac aac ttc cag aag ttc   336
Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe
            100                 105                 110

ctc gga gct tcc acc gac atc tgg gag acc gaa ggc cag cag ttc cca   384
Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro
        115                 120                 125

acc gag gtt ggc tcc ggt gcg cag ggc tcc aac ggt gta gct tct gag   432
Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu
    130                 135                 140

gct tcc aac atc gag ggt gca atc acc tac gtt gaa gct ggt ttc gct   480
Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala
145                 150                 155                 160

aac cag tcc ggc ctg ggc gtt gca aac atc gac ttc ggt tcc ggc cca   528
Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro
                165                 170                 175
```

```
gtt gaa ctc aac gct gag tcc gtt ggc gtt gca ctt ggt gca ctc gac   576
Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp
            180                 185                 190

ttc ctg act gag ggc cac aac atg gtt gtt gac acc gac gct atg ttc   624
Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe
        195                 200                 205

gca atg aac gaa gcc ggt gct tac cca ctg atc ctc acc acc tac gaa   672
Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu
    210                 215                 220

atc gtc tgc tcc gca ggc tac gac gag acc acc cgc gac cag gtc aag   720
Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys
225                 230                 235                 240

gac ttc ctg acc gtt gca ctg gac tcc cag gat gac cag ctc gag gct   768
Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala
                245                 250                 255

ctc ggc tac atc cca gtt acc ggc gag cac tac gat cgc ctc gtt gca   816
Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala
            260                 265                 270

gca gtt gaa gca att cag taataaaccg ctgccgtagc ttc                 857
Ala Val Glu Ala Ile Gln
        275
```

<210> 308
<211> 278
<212> PRT
<213> Corynebacterium glutamicum

<400> 308

```
Arg Asn Asn Phe Ala Ala Ala Gln Val Ala Phe Gly Gly Ser Asp Ser
  1               5                  10                  15

Ala Met Lys Asp Asp Gln Ala Ala Glu Ala Glu Ala Arg Cys Asn Gly
            20                  25                  30

Asn Glu Ala Trp His Leu Pro Phe Val Ile Gly Pro Val Ala Val Ala
        35                  40                  45

Tyr Asn Leu Pro Gly Val Asp Thr Leu Asn Leu Asp Thr Asn Ile Ile
    50                  55                  60

Ala Gln Ile Phe Lys Gly Glu Ile Thr Lys Trp Asn Asp Glu Ala Ile
65                  70                  75                  80

Ala Ser Gln Asn Glu Gly Thr Asp Leu Pro Asp Gln Asp Ile Ser Val
                85                  90                  95

Leu Tyr Arg Ser Glu Glu Ser Gly Thr Ser Asp Asn Phe Gln Lys Phe
            100                 105                 110

Leu Gly Ala Ser Thr Asp Ile Trp Glu Thr Glu Gly Gln Gln Phe Pro
        115                 120                 125

Thr Glu Val Gly Ser Gly Ala Gln Gly Ser Asn Gly Val Ala Ser Glu
    130                 135                 140
```

```
Ala Ser Asn Ile Glu Gly Ala Ile Thr Tyr Val Glu Ala Gly Phe Ala
145                 150                 155                 160

Asn Gln Ser Gly Leu Gly Val Ala Asn Ile Asp Phe Gly Ser Gly Pro
                165                 170                 175

Val Glu Leu Asn Ala Glu Ser Val Gly Val Ala Leu Gly Ala Leu Asp
            180                 185                 190

Phe Leu Thr Glu Gly His Asn Met Val Val Asp Thr Asp Ala Met Phe
        195                 200                 205

Ala Met Asn Glu Ala Gly Ala Tyr Pro Leu Ile Leu Thr Thr Tyr Glu
    210                 215                 220

Ile Val Cys Ser Ala Gly Tyr Asp Glu Thr Thr Arg Asp Gln Val Lys
225                 230                 235                 240

Asp Phe Leu Thr Val Ala Leu Asp Ser Gln Asp Asp Gln Leu Glu Ala
                245                 250                 255

Leu Gly Tyr Ile Pro Val Thr Gly Glu His Tyr Asp Arg Leu Val Ala
            260                 265                 270

Ala Val Glu Ala Ile Gln
        275
```

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<210> 309
<211> 1050
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1027)
<223> RXA02497

<400> 309
tcgatgccgc cgctggcgaa gactcgggga aacctaaaaa taccgaagaa gaatttgacc 60

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gattcacact ttgccaccct agaccgtcta acctttaggt gtg aga tta ggt gta   115
                                            Val Arg Leu Gly Val
                                              1               5

tta gat gtg ggc agc aat act gtc cac cta gtt gca gta gac gcg cgt   163
Leu Asp Val Gly Ser Asn Thr Val His Leu Val Ala Val Asp Ala Arg
                  10                  15                  20

ccc ggt gga cac ccc acc ccg atg agc aat tgg cgt acc cca ctg cgc   211
Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp Arg Thr Pro Leu Arg
              25                  30                  35

ctt gtt gag ctt ctt gat gac tcc ggg gcg atc tcc gaa aag ggc atc   259
Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile Ser Glu Lys Gly Ile
          40                  45                  50

aac aaa ctc acc tca gca gtc ggg gaa gca gca gac cta gcg aaa acg   307
Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala Asp Leu Ala Lys Thr
      55                  60                  65
```

```
ctc ggc tgc gct gaa ctg atg cca ttt gct aca tcg gca gtc cgc tcc   355
Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr Ser Ala Val Arg Ser
 70                  75                  80                  85

gcc acc aac agc gag gca gtg ctc gac cac gtg gag aag gaa acc ggc   403
Ala Thr Asn Ser Glu Ala Val Leu Asp His Val Glu Lys Glu Thr Gly
                 90                  95                 100

gtc cgc ctg tcc atc ctt tcc ggt gaa gac gaa gca cgc caa act ttc   451
Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu Ala Arg Gln Thr Phe
            105                 110                 115

ctc gca gtt cga cgt tgg tat gga tgg tcc gca ggg cgc ata act aac   499
Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala Gly Arg Ile Thr Asn
        120                 125                 130

ctc gac atc ggt ggc ggc tcc ctg gaa cta tcc tcc gga acc gac gaa   547
Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser Ser Gly Thr Asp Glu
    135                 140                 145

tcc cca gac ctc gcg ttc tca ctg gat ctg ggt gcg ggc cgc ttg acc   595
Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly Ala Gly Arg Leu Thr
150                 155                 160                 165

cac aac tgg ttc gac acc gat cca ccg gca cgt aag aaa atc aac ctc   643
His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg Lys Lys Ile Asn Leu
                170                 175                 180

ctg cgc gat tat atc gat gcg gaa ctt gca gaa ccc gcc cgc cag atg   691
Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu Pro Ala Arg Gln Met
            185                 190                 195

cgc acc cta ggg ccc gcg cgc ctg gca gtg gga aca tcc aaa act ttc   739
Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly Thr Ser Lys Thr Phe
        200                 205                 210

cgc acc ctg gca cga ctg act ggt gct gcg ccc tca tcc gca gga cca   787
Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro Ser Ser Ala Gly Pro
    215                 220                 225

cac gtc acc cga acc ctc acc gcg ccg ggt ctg cgc cag ctg atc gca   835
His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu Arg Gln Leu Ile Ala
230                 235                 240                 245

ttt atc tca cga atg act gcg gcg gac cgc gct gag ctg gaa ggt atc   883
Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala Glu Leu Glu Gly Ile
                250                 255                 260

agc tcg gat cgg tca cat cag atc gtg gca ggt gcg cta gtt gcg gaa   931
Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly Ala Leu Val Ala Glu
            265                 270                 275

gct gcg atg cgt gcg ttg gat att gac aag gta gaa att tgt ccg tgg   979
Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val Glu Ile Cys Pro Trp
        280                 285                 290

gca ctt cgt gaa ggt gtg atc ctc acc agg atc gac aaa gga ctc gag  1027
Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile Asp Lys Gly Leu Glu
    295                 300                 305
```

taacatttac ccggaaagga gtt 1050

<210> 310
<211> 309
<212> PRT
<213> Corynebacterium glutamicum

<400> 310

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Val Arg Leu Gly Val Leu Asp Val Gly Ser Asn Thr Val His Leu Val
  1               5                  10                  15

Ala Val Asp Ala Arg Pro Gly Gly His Pro Thr Pro Met Ser Asn Trp
             20                  25                  30

Arg Thr Pro Leu Arg Leu Val Glu Leu Leu Asp Asp Ser Gly Ala Ile
         35                  40                  45

Ser Glu Lys Gly Ile Asn Lys Leu Thr Ser Ala Val Gly Glu Ala Ala
     50                  55                  60

Asp Leu Ala Lys Thr Leu Gly Cys Ala Glu Leu Met Pro Phe Ala Thr
 65                  70                  75                  80

Ser Ala Val Arg Ser Ala Thr Asn Ser Glu Ala Val Leu Asp His Val
                 85                  90                  95

Glu Lys Glu Thr Gly Val Arg Leu Ser Ile Leu Ser Gly Glu Asp Glu
            100                 105                 110

Ala Arg Gln Thr Phe Leu Ala Val Arg Arg Trp Tyr Gly Trp Ser Ala
        115                 120                 125

Gly Arg Ile Thr Asn Leu Asp Ile Gly Gly Gly Ser Leu Glu Leu Ser
    130                 135                 140

Ser Gly Thr Asp Glu Ser Pro Asp Leu Ala Phe Ser Leu Asp Leu Gly
145                 150                 155                 160

Ala Gly Arg Leu Thr His Asn Trp Phe Asp Thr Asp Pro Pro Ala Arg
                165                 170                 175

Lys Lys Ile Asn Leu Leu Arg Asp Tyr Ile Asp Ala Glu Leu Ala Glu
            180                 185                 190

Pro Ala Arg Gln Met Arg Thr Leu Gly Pro Ala Arg Leu Ala Val Gly
        195                 200                 205

Thr Ser Lys Thr Phe Arg Thr Leu Ala Arg Leu Thr Gly Ala Ala Pro
    210                 215                 220

Ser Ser Ala Gly Pro His Val Thr Arg Thr Leu Thr Ala Pro Gly Leu
225                 230                 235                 240

Arg Gln Leu Ile Ala Phe Ile Ser Arg Met Thr Ala Ala Asp Arg Ala
                245                 250                 255

Glu Leu Glu Gly Ile Ser Ser Asp Arg Ser His Gln Ile Val Ala Gly
            260                 265                 270

Ala Leu Val Ala Glu Ala Ala Met Arg Ala Leu Asp Ile Asp Lys Val
```

```
        275                 280                 285

Glu Ile Cys Pro Trp Ala Leu Arg Glu Gly Val Ile Leu Thr Arg Ile
    290                 295                 300

Asp Lys Gly Leu Glu
305
```

<210> 311
<211> 1671
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1648)
<223> RXA01477

<400> 311

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taatttgaat taagccctct tcaattttcc gctttcgctg cgaggtgtgc caatgtggcg 60

cattatttaa tgcatactcg gcgctatttt gaggagcctc atg cca cag tta agc   115
                                            Met Pro Gln Leu Ser
                                              1               5

aga cgc cag ttc ttg cag aca acc gcc gtt act gca ggt cta gcc act   163
Arg Arg Gln Phe Leu Gln Thr Thr Ala Val Thr Ala Gly Leu Ala Thr
                10                  15                  20

ttt gcg ggc aca cct gca cgc gct gaa gaa cgc caa ttc cag cat ggc   211
Phe Ala Gly Thr Pro Ala Arg Ala Glu Glu Arg Gln Phe Gln His Gly
            25                  30                  35

gtg gct tcc ggg gac ccc acc gca acc tct gcc att ttg tgg act cgg   259
Val Ala Ser Gly Asp Pro Thr Ala Thr Ser Ala Ile Leu Trp Thr Arg
        40                  45                  50

ctg acc cca att ccc gac gcc aca cct gga agt ggc ctt ggc ccc gac   307
Leu Thr Pro Ile Pro Asp Ala Thr Pro Gly Ser Gly Leu Gly Pro Asp
    55                  60                  65

tct cct gtc acc tgg gaa gtc tcc ccc act cct gat ttc gcc agc atc   355
Ser Pro Val Thr Trp Glu Val Ser Pro Thr Pro Asp Phe Ala Ser Ile
70                  75                  80                  85

acg cgc tcg gga acc gta atc acc tcc gca gca agc gat cac acc gtc   403
Thr Arg Ser Gly Thr Val Ile Thr Ser Ala Ala Ser Asp His Thr Val
                90                  95                  100

cac gcg cac gcc acg ggt ttg agc cca tcc acc cgc tat ttc tac cgc   451
His Ala His Ala Thr Gly Leu Ser Pro Ser Thr Arg Tyr Phe Tyr Arg
            105                 110                 115

ttc atc tcc tcc acc ggc gag gtc tcc cct gtg ggg cgc acg caa aca   499
Phe Ile Ser Ser Thr Gly Glu Val Ser Pro Val Gly Arg Thr Gln Thr
        120                 125                 130

aca tcg ctt gtc gac gct ccc ctc ccg cac ctt cgc ttt gcc ctt gcg   547
Thr Ser Leu Val Asp Ala Pro Leu Pro His Leu Arg Phe Ala Leu Ala
    135                 140                 145
```

```
tcg tgt gcc aat tgg gag gca gga ttt ttt gcc gcc tac ggc gac atc   595
Ser Cys Ala Asn Trp Glu Ala Gly Phe Phe Ala Ala Tyr Gly Asp Ile
150                 155                 160                 165

gcc cgg cgc gct gac gcc ggc gaa ttg gag atg ttg att ttt ttg ggt   643
Ala Arg Arg Ala Asp Ala Gly Glu Leu Glu Met Leu Ile Phe Leu Gly
                170                 175                 180

gat tac atc tac gag tac gcc acc ggt atg ttc gcc gga aag gac ggt   691
Asp Tyr Ile Tyr Glu Tyr Ala Thr Gly Met Phe Ala Gly Lys Asp Gly
            185                 190                 195

gtg gtg cgc ccg cat cag cct ctt cat gaa acc atc acg ttg gag cac   739
Val Val Arg Pro His Gln Pro Leu His Glu Thr Ile Thr Leu Glu His
        200                 205                 210

tac cgc act cgt tat ggc cat tac cgc agt gac aat cac ttg cag gca   787
Tyr Arg Thr Arg Tyr Gly His Tyr Arg Ser Asp Asn His Leu Gln Ala
    215                 220                 225

gcg cat gcg gcg ttg ccg tgg att gtc atg tgg gat gac cat gag tcg   835
Ala His Ala Ala Leu Pro Trp Ile Val Met Trp Asp Asp His Glu Ser
230                 235                 240                 245

gcc aac aac tct aat cgt gag ggc gcg cag aat cat tcc gct gat gag   883
Ala Asn Asn Ser Asn Arg Glu Gly Ala Gln Asn His Ser Ala Asp Glu
                250                 255                 260

ggt tcg tgg gtg gat cgt caa aat gct gct cgg cag gtc ttt ttg gag   931
Gly Ser Trp Val Asp Arg Gln Asn Ala Ala Arg Gln Val Phe Leu Glu
            265                 270                 275

tgg atg ccg atc cgc cag gag gac acg ctc tat cgt tcc ttc act ttt   979
Trp Met Pro Ile Arg Gln Glu Asp Thr Leu Tyr Arg Ser Phe Thr Phe
        280                 285                 290

ggt gac ctc gcc acg ctg tca ctt ctt gat ctt cga agt ttc aga gat   1027
Gly Asp Leu Ala Thr Leu Ser Leu Leu Asp Leu Arg Ser Phe Arg Asp
    295                 300                 305

cca gca ccc tcc cag caa cag tgg ctg gag ggt caa cgt gcg gac acc   1075
Pro Ala Pro Ser Gln Gln Gln Trp Leu Glu Gly Gln Arg Ala Asp Thr
310                 315                 320                 325

atg atg ggg tcg cag cag ttt gag tgg ctg aaa tcc aac gtg gaa cac   1123
Met Met Gly Ser Gln Gln Phe Glu Trp Leu Lys Ser Asn Val Glu His
                330                 335                 340

acc acc acg acg tgg aat atc atc ggc agc tca gtg atg ttt gcc ccc   1171
Thr Thr Thr Thr Trp Asn Ile Ile Gly Ser Ser Val Met Phe Ala Pro
            345                 350                 355

atg gca att acc ggg cag cct ctt ttc cag atc cct gaa cct att ccc   1219
Met Ala Ile Thr Gly Gln Pro Leu Phe Gln Ile Pro Glu Pro Ile Pro
        360                 365                 370

gcc aat ttg gat cag tgg gac ggc tac tcc cgt gag cgc gac cga ctc   1267
Ala Asn Leu Asp Gln Trp Asp Gly Tyr Ser Arg Glu Arg Asp Arg Leu
    375                 380                 385
```

```
cta gct gta ctt gcc gat ttc gcc act cca acg ctt ttt cta tct ggc   1315
Leu Ala Val Leu Ala Asp Phe Ala Thr Pro Thr Leu Phe Leu Ser Gly
390                 395                 400                 405

gat atc cac tcc gaa tgg gca aac gcc atc cgg ttt aat ggt cga gaa   1363
Asp Ile His Ser Glu Trp Ala Asn Ala Ile Arg Phe Asn Gly Arg Glu
                410                 415                 420

atc ggt gtc gag gca gta tgc agc tcc atc acc tca gct aat gtc aac   1411
Ile Gly Val Glu Ala Val Cys Ser Ser Ile Thr Ser Ala Asn Val Asn
            425                 430                 435

gac ttc gcc aaa ctc cct gag gac aat ccg gtc tcc ctg caa gcg gaa   1459
Asp Phe Ala Lys Leu Pro Glu Asp Asn Pro Val Ser Leu Gln Ala Glu
        440                 445                 450

caa gta atc cga gcc aac agt tcg cat gtg cgc cac gtt gat ctt gac   1507
Gln Val Ile Arg Ala Asn Ser Ser His Val Arg His Val Asp Leu Asp
    455                 460                 465

gcc cac ggc tac gcc acg gtg aat ctc acc caa gat ggc gcg cac atg   1555
Ala His Gly Tyr Ala Thr Val Asn Leu Thr Gln Asp Gly Ala His Met
470                 475                 480                 485

gtc tgg cac cgc gtc gcc gat ctc tcc ctt ccg gac tca gaa gtt gct   1603
Val Trp His Arg Val Ala Asp Leu Ser Leu Pro Asp Ser Glu Val Ala
                490                 495                 500

ccg gca att gca ctt gag tgg aaa cca ggc gtc gga ttc act act       1648
Pro Ala Ile Ala Leu Glu Trp Lys Pro Gly Val Gly Phe Thr Thr
            505                 510                 515

tgagctgctg atttgtaggt ttt                                        1671
```

<210> 312
<211> 516
<212> PRT
<213> Corynebacterium glutamicum

<400> 312

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Met Pro Gln Leu Ser Arg Arg Gln Phe Leu Gln Thr Thr Ala Val Thr
  1               5                  10                  15

Ala Gly Leu Ala Thr Phe Ala Gly Thr Pro Ala Arg Ala Glu Glu Arg
             20                  25                  30

Gln Phe Gln His Gly Val Ala Ser Gly Asp Pro Thr Ala Thr Ser Ala
         35                  40                  45

Ile Leu Trp Thr Arg Leu Thr Pro Ile Pro Asp Ala Thr Pro Gly Ser
     50                  55                  60

Gly Leu Gly Pro Asp Ser Pro Val Thr Trp Glu Val Ser Pro Thr Pro
 65                  70                  75                  80

Asp Phe Ala Ser Ile Thr Arg Ser Gly Thr Val Ile Thr Ser Ala Ala
                 85                  90                  95

Ser Asp His Thr Val His Ala His Ala Thr Gly Leu Ser Pro Ser Thr
            100                 105                 110
```

Arg Tyr Phe Tyr Arg Phe Ile Ser Ser Thr Gly Glu Val Ser Pro Val
115 120 125

Gly Arg Thr Gln Thr Thr Ser Leu Val Asp Ala Pro Leu Pro His Leu
130 135 140

Arg Phe Ala Leu Ala Ser Cys Ala Asn Trp Glu Ala Gly Phe Phe Ala
145 150 155 160

Ala Tyr Gly Asp Ile Ala Arg Arg Ala Asp Ala Gly Glu Leu Glu Met
165 170 175

Leu Ile Phe Leu Gly Asp Tyr Ile Tyr Glu Tyr Ala Thr Gly Met Phe
180 185 190

Ala Gly Lys Asp Gly Val Val Arg Pro His Gln Pro Leu His Glu Thr
195 200 205

Ile Thr Leu Glu His Tyr Arg Thr Arg Tyr Gly His Tyr Arg Ser Asp
210 215 220

Asn His Leu Gln Ala Ala His Ala Ala Leu Pro Trp Ile Val Met Trp
225 230 235 240

Asp Asp His Glu Ser Ala Asn Asn Ser Asn Arg Glu Gly Ala Gln Asn
245 250 255

His Ser Ala Asp Glu Gly Ser Trp Val Asp Arg Gln Asn Ala Ala Arg
260 265 270

Gln Val Phe Leu Glu Trp Met Pro Ile Arg Gln Glu Asp Thr Leu Tyr
275 280 285

Arg Ser Phe Thr Phe Gly Asp Leu Ala Thr Leu Ser Leu Leu Asp Leu
290 295 300

Arg Ser Phe Arg Asp Pro Ala Pro Ser Gln Gln Gln Trp Leu Glu Gly
305 310 315 320

Gln Arg Ala Asp Thr Met Met Gly Ser Gln Gln Phe Glu Trp Leu Lys
325 330 335

Ser Asn Val Glu His Thr Thr Thr Thr Trp Asn Ile Ile Gly Ser Ser
340 345 350

Val Met Phe Ala Pro Met Ala Ile Thr Gly Gln Pro Leu Phe Gln Ile
355 360 365

Pro Glu Pro Ile Pro Ala Asn Leu Asp Gln Trp Asp Gly Tyr Ser Arg
370 375 380

Glu Arg Asp Arg Leu Leu Ala Val Leu Ala Asp Phe Ala Thr Pro Thr
385 390 395 400

Leu Phe Leu Ser Gly Asp Ile His Ser Glu Trp Ala Asn Ala Ile Arg
405 410 415

Phe Asn Gly Arg Glu Ile Gly Val Glu Ala Val Cys Ser Ser Ile Thr
420 425 430

```
Ser Ala Asn Val Asn Asp Phe Ala Lys Leu Pro Glu Asp Asn Pro Val
        435                 440                 445

Ser Leu Gln Ala Glu Gln Val Ile Arg Ala Asn Ser Ser His Val Arg
    450                 455                 460

His Val Asp Leu Asp Ala His Gly Tyr Ala Thr Val Asn Leu Thr Gln
465                 470                 475                 480

Asp Gly Ala His Met Val Trp His Arg Val Ala Asp Leu Ser Leu Pro
                485                 490                 495

Asp Ser Glu Val Ala Pro Ala Ile Ala Leu Glu Trp Lys Pro Gly Val
            500                 505                 510

Gly Phe Thr Thr
        515
```

<210> 313
<211> 597
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(574)
<223> RXA01509

<400> 313

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ttccaaaatt ttcgaggatt tccttgcccc gggtctcgtt tatttttgaa cacgctagaa 60

ttcaagggca gtaactaatt tcaacccggg agaaatacct atg agc atc gaa gta   115
                                            Met Ser Ile Glu Val
                                              1               5

acc gtc gaa atc cct aag gga tca cgc aac aag tac gaa atc gac cac   163
Thr Val Glu Ile Pro Lys Gly Ser Arg Asn Lys Tyr Glu Ile Asp His
                  10                  15                  20

gag acc gga aag gtc tac ctc gac cgc tac ctg ttc act cca atg gca   211
Glu Thr Gly Lys Val Tyr Leu Asp Arg Tyr Leu Phe Thr Pro Met Ala
              25                  30                  35

tac cca ctg gac tac ggc tac atc gac cac acc ctc ggc gaa gac ggc   259
Tyr Pro Leu Asp Tyr Gly Tyr Ile Asp His Thr Leu Gly Glu Asp Gly
          40                  45                  50

gac cca ttg gat gca ctg gtc atc ctc ccc gag tcc gtt ttt cca gca   307
Asp Pro Leu Asp Ala Leu Val Ile Leu Pro Glu Ser Val Phe Pro Ala
      55                  60                  65

gtt gtg gtt aag tcc cga atc atc ggt gtt ttc aag atg acc gac gaa   355
Val Val Val Lys Ser Arg Ile Ile Gly Val Phe Lys Met Thr Asp Glu
  70                  75                  80                  85

gcc ggc ggc gac gac aag ctg ctc tcc gtt ctc gac gac cca cgc tac   403
Ala Gly Gly Asp Asp Lys Leu Leu Ser Val Leu Asp Asp Pro Arg Tyr
                  90                  95                 100

gac cac atc cag gac atc tcc gac gtg tcc gat ttc ctc aag gat gag   451
```

```
Asp His Ile Gln Asp Ile Ser Asp Val Ser Asp Phe Leu Lys Asp Glu
            105                 110                 115

atc gag cac ttc ttc gtc cac tac aag gac ctg gaa aag ggc aag cac   499
Ile Glu His Phe Phe Val His Tyr Lys Asp Leu Glu Lys Gly Lys His
        120                 125                 130

gtt gac ggt tcc ggc tgg ggc gac aag gct gag gct gaa aag atc cac   547
Val Asp Gly Ser Gly Trp Gly Asp Lys Ala Glu Ala Glu Lys Ile His
    135                 140                 145

gct gag gca atc gac cgc tac aag gca taagtctttt gtaaattaag         594
Ala Glu Ala Ile Asp Arg Tyr Lys Ala
150                 155

agc                                                               597
```

<210> 314
<211> 158
<212> PRT
<213> Corynebacterium glutamicum

<400> 314

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Met Ser Ile Glu Val Thr Val Glu Ile Pro Lys Gly Ser Arg Asn Lys
  1               5                  10                  15

Tyr Glu Ile Asp His Glu Thr Gly Lys Val Tyr Leu Asp Arg Tyr Leu
             20                  25                  30

Phe Thr Pro Met Ala Tyr Pro Leu Asp Tyr Gly Tyr Ile Asp His Thr
         35                  40                  45

Leu Gly Glu Asp Gly Asp Pro Leu Asp Ala Leu Val Ile Leu Pro Glu
     50                  55                  60

Ser Val Phe Pro Ala Val Val Val Lys Ser Arg Ile Ile Gly Val Phe
 65                  70                  75                  80

Lys Met Thr Asp Glu Ala Gly Gly Asp Asp Lys Leu Leu Ser Val Leu
                 85                  90                  95

Asp Asp Pro Arg Tyr Asp His Ile Gln Asp Ile Ser Asp Val Ser Asp
            100                 105                 110

Phe Leu Lys Asp Glu Ile Glu His Phe Phe Val His Tyr Lys Asp Leu
        115                 120                 125

Glu Lys Gly Lys His Val Asp Gly Ser Gly Trp Gly Asp Lys Ala Glu
    130                 135                 140

Ala Glu Lys Ile His Ala Glu Ala Ile Asp Arg Tyr Lys Ala
145                 150                 155
```

<210> 315
<211> 723
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(700)
<223> RXA00100

<400> 315
gttttgcggt gttgaattgg gtgtttaatg tgcagtgggc gtggggaatg ctcattgcgt 60

atccgcttgt ttcacatgcg gtgatcgcgc ggagtaaacg atg att ttg gat tgg 115
Met Ile Leu Asp Trp
1 5

gtt atc tcc atc atg gag gca ctc ggc gcc gtt ggc gtg ggt gtc gcg 163
Val Ile Ser Ile Met Glu Ala Leu Gly Ala Val Gly Val Gly Val Ala
10 15 20

gtg ttt ttg gag aac gtt ttc ccg ccg att cca agt gag gtg gtg ctt 211
Val Phe Leu Glu Asn Val Phe Pro Pro Ile Pro Ser Glu Val Val Leu
25 30 35

ccg ctc gcg ggt ttc acc acc acg caa ggc gat ctc aat gtg tgg gcg 259
Pro Leu Ala Gly Phe Thr Thr Thr Gln Gly Asp Leu Asn Val Trp Ala
40 45 50

gcg ctt atg tgg tcg gtg atc ggg tcg gtt tcc gga gcg ttt ttg ctt 307
Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser Gly Ala Phe Leu Leu
55 60 65

tac ggg ttg ggg cgc tca atc ggg gcg gca cgg ttg cgg cag gtc gcc 355
Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg Leu Arg Gln Val Ala
70 75 80 85

gac tgg atg tgg ctt gtc gac gcg acc gac gtg gat aaa tcc cta tcg 403
Asp Trp Met Trp Leu Val Asp Ala Thr Asp Val Asp Lys Ser Leu Ser
90 95 100

tgg ttc gaa aag tac ggg aag tat tcg gtg ttt ttc ggt cgg ttg gtg 451
Trp Phe Glu Lys Tyr Gly Lys Tyr Ser Val Phe Phe Gly Arg Leu Val
105 110 115

ccg ggt gtc cga agt ttg att tcg att ccg gcg ggc gtc gac aag atg 499
Pro Gly Val Arg Ser Leu Ile Ser Ile Pro Ala Gly Val Asp Lys Met
120 125 130

aat ccg gtt ctc ttc ggt gtg ctc act gcg gtg ggc agc acc att tgg 547
Asn Pro Val Leu Phe Gly Val Leu Thr Ala Val Gly Ser Thr Ile Trp
135 140 145

aat gcg gtt ctg att tgg act ggt gtg tgg ttg ggg gcg gaa tgg gag 595
Asn Ala Val Leu Ile Trp Thr Gly Val Trp Leu Gly Ala Glu Trp Glu
150 155 160 165

acg gtg tcg atg tgg ttt gag agc tat tca acg atc att tac gta ggt 643
Thr Val Ser Met Trp Phe Glu Ser Tyr Ser Thr Ile Ile Tyr Val Gly
170 175 180

atc gcg ctc att gtn gct tac gtg ttg ttt ggt tta gtc cgt cgc cga 691
Ile Ala Leu Ile Val Ala Tyr Val Leu Phe Gly Leu Val Arg Arg Arg
185 190 195

att aaa act taaccatcgg ttcgtagccg aag 723
Ile Lys Thr

200

<210> 316
<211> 200
<212> PRT
<213> Corynebacterium glutamicum

<400> 316
Met Ile Leu Asp Trp Val Ile Ser Ile Met Glu Ala Leu Gly Ala Val
1 5 10 15

Gly Val Gly Val Ala Val Phe Leu Glu Asn Val Phe Pro Pro Ile Pro
20 25 30

Ser Glu Val Val Leu Pro Leu Ala Gly Phe Thr Thr Thr Gln Gly Asp
35 40 45

Leu Asn Val Trp Ala Ala Leu Met Trp Ser Val Ile Gly Ser Val Ser
50 55 60

Gly Ala Phe Leu Leu Tyr Gly Leu Gly Arg Ser Ile Gly Ala Ala Arg
65 70 75 80

Leu Arg Gln Val Ala Asp Trp Met Trp Leu Val Asp Ala Thr Asp Val
85 90 95

Asp Lys Ser Leu Ser Trp Phe Glu Lys Tyr Gly Lys Tyr Ser Val Phe
100 105 110

Phe Gly Arg Leu Val Pro Gly Val Arg Ser Leu Ile Ser Ile Pro Ala
115 120 125

Gly Val Asp Lys Met Asn Pro Val Leu Phe Gly Val Leu Thr Ala Val
130 135 140

Gly Ser Thr Ile Trp Asn Ala Val Leu Ile Trp Thr Gly Val Trp Leu
145 150 155 160

Gly Ala Glu Trp Glu Thr Val Ser Met Trp Phe Glu Ser Tyr Ser Thr
165 170 175

Ile Ile Tyr Val Gly Ile Ala Leu Ile Val Ala Tyr Val Leu Phe Gly
180 185 190

Leu Val Arg Arg Arg Ile Lys Thr
195 200

<210> 317
<211> 705
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(682)
<223> RXA00615

<400> 317
aaattgccag gattgatcat taatatcggc tcattaaggc tcttttaat gagagggatt 60

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cccattgaat gatcagttgg tgagttgggt ggaaacactc atg aca gca tcg gtg   115
                                            Met Thr Ala Ser Val
                                              1               5

ttt tat ccg gtg ctg tca gtt gtg gtg ctc atc gac tgc att ttg ccg   163
Phe Tyr Pro Val Leu Ser Val Val Val Leu Ile Asp Cys Ile Leu Pro
                10                  15                  20

ctt atc ccc agt gag act gtt ctt gct ttg gca ggg gcg tgg tca gga   211
Leu Ile Pro Ser Glu Thr Val Leu Ala Leu Ala Gly Ala Trp Ser Gly
            25                  30                  35

gct cgg gga act cca aac ttg tgg ttg gtt att tca gta gca acg ttg   259
Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile Ser Val Ala Thr Leu
        40                  45                  50

gcc gcg atc att ggt gac aac ctg tgt tat ttc ttt ggc acg cgg ttg   307
Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe Phe Gly Thr Arg Leu
    55                  60                  65

atc aat atg gtg aac agg att ccg gga gaa tcg agg cgc gga aaa gcg   355
Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser Arg Arg Gly Lys Ala
70                  75                  80                  85

ctg gag tgg gcg cgg aag aac ctt aat gaa cgg gat gtt tcg aca atc   403
Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg Asp Val Ser Thr Ile
                90                  95                  100

att atc gcc cgc ttt att ccg tgg gct agg tgg ttt gtc acc atc att   451
Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp Phe Val Thr Ile Ile
            105                 110                 115

ttg gga tct gtg gga tat tcc tgg tcg agg ttt atc gtg tgg gat tcc   499
Leu Gly Ser Val Gly Tyr Ser Trp Ser Arg Phe Ile Val Trp Asp Ser
        120                 125                 130

att gga gcg cta att tgg gca acc cag gca act ttg ttg ggt tat gtg   547
Ile Gly Ala Leu Ile Trp Ala Thr Gln Ala Thr Leu Leu Gly Tyr Val
    135                 140                 145

ggc gga tgg ctt ttc caa gaa caa ccg ttg atc ggc ctg gtt gca ggc   595
Gly Gly Trp Leu Phe Gln Glu Gln Pro Leu Ile Gly Leu Val Ala Gly
150                 155                 160                 165

gca gct ttg gga atc ttc ttc ggg ttc ttt ttg cag tgg ctc aac aaa   643
Ala Ala Leu Gly Ile Phe Phe Gly Phe Phe Leu Gln Trp Leu Asn Lys
                170                 175                 180

atg tgg gag agg cgt cgt ctg gcg aaa gtg gct gca gaa tgaaaatcag    692
Met Trp Glu Arg Arg Arg Leu Ala Lys Val Ala Ala Glu
            185                 190

gccagacagt ggg                                                   705


<210> 318
<211> 194
<212> PRT
<213> Corynebacterium glutamicum
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<400> 318
Met Thr Ala Ser Val Phe Tyr Pro Val Leu Ser Val Val Val Leu Ile
1 5 10 15

Asp Cys Ile Leu Pro Leu Ile Pro Ser Glu Thr Val Leu Ala Leu Ala
20 25 30

Gly Ala Trp Ser Gly Ala Arg Gly Thr Pro Asn Leu Trp Leu Val Ile
35 40 45

Ser Val Ala Thr Leu Ala Ala Ile Ile Gly Asp Asn Leu Cys Tyr Phe
50 55 60

Phe Gly Thr Arg Leu Ile Asn Met Val Asn Arg Ile Pro Gly Glu Ser
65 70 75 80

Arg Arg Gly Lys Ala Leu Glu Trp Ala Arg Lys Asn Leu Asn Glu Arg
85 90 95

Asp Val Ser Thr Ile Ile Ile Ala Arg Phe Ile Pro Trp Ala Arg Trp
100 105 110

Phe Val Thr Ile Ile Leu Gly Ser Val Gly Tyr Ser Trp Ser Arg Phe
115 120 125

Ile Val Trp Asp Ser Ile Gly Ala Leu Ile Trp Ala Thr Gln Ala Thr
130 135 140

Leu Leu Gly Tyr Val Gly Gly Trp Leu Phe Gln Glu Gln Pro Leu Ile
145 150 155 160

Gly Leu Val Ala Gly Ala Ala Leu Gly Ile Phe Phe Gly Phe Phe Leu
165 170 175

Gln Trp Leu Asn Lys Met Trp Glu Arg Arg Arg Leu Ala Lys Val Ala
180 185 190

Ala Glu

<210> 319
<211> 870
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(847)
<223> RXN00250

<400> 319
acaacaccag accaccccaa ccctgaataa acccctattt ttctaaaaag tcacactttg 60

ccgtatagaa attcagtcaa ccaagagtac tctgtccacc atg gtt ttt act ctt 115
Met Val Phe Thr Leu
1 5

gcg gac tcc gtc tcc cag gtt gcg cta ggt ccg tcc tgg ctg gac cct 163
Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro Ser Trp Leu Asp Pro
10 15 20

```
atg gaa ctt ctt tcc ggc tcc ggc ccg ttc ggt agc ttc att ctt ccg   211
Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro
             25                  30                  35

gcg atg ctt gcc att gtc ttt atc gaa tca ggc cta ctt ttc cca ctt   259
Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu
         40                  45                  50

cta cca ggt gat tct ctc ctt ttc acc ggt ggt ctc cta gct aac cag   307
Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln
     55                  60                  65

gct gac cct ttt gca ccg ctg tgg ctg gtg ctg atc ctc tgc cct atc   355
Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu Ile Leu Cys Pro Ile
 70                  75                  80                  85

gcc gca att ctt ggc gat cag gtg ggt tac tgg att ggc cac aag ttc   403
Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp Ile Gly His Lys Phe
                 90                  95                 100

cac cct cgc ctg gtc aat cgt ccg gat ggc agg att ttc aag cag gaa   451
His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu
             105                 110                 115

tac ctc aag cag act gag gat ttc ttt gag aag cat ggc ccc gtg acg   499
Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys His Gly Pro Val Thr
         120                 125                 130

atc att ttg tgc cgt ttc gtg ccc atc gtc cgt act tac gca cct ctg   547
Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
     135                 140                 145

gtc gca ggt atg gct ggc atg cgt tac cgc acg ttc att att tac aac   595
Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr Phe Ile Ile Tyr Asn
150                 155                 160                 165

atg atc ggt ggc att ttg tgg ggt tcc ggc gtg gtg gct ttg ggt gct   643
Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val Val Ala Leu Gly Ala
                170                 175                 180

gcg ttg ggt cag ttc gat ttc gtc cgc aac aat att gat ctg att ttc   691
Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn Ile Asp Leu Ile Phe
             185                 190                 195

ttg ctg atc gtg ttc att tcg gtg gtt cct ggt ttg gtc ggc atg gcc   739
Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly Leu Val Gly Met Ala
         200                 205                 210

cgc aag ctg gct gac ggc cac aag caa gcc aac acc gag cca caa gaa   787
Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn Thr Glu Pro Gln Glu
     215                 220                 225

aac ccc gca gtc cag aca gcc cca gta aaa acc cag gaa gcc cag gaa   835
Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr Gln Glu Ala Gln Glu
230                 235                 240                 245

gcc ccc cag aac taatctttcc ggtccgccag ttc                        870
Ala Pro Gln Asn
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<210> 320
<211> 249
<212> PRT
<213> Corynebacterium glutamicum

<400> 320
Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
1 5 10 15

Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
20 25 30

Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
35 40 45

Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
50 55 60

Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
65 70 75 80

Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
85 90 95

Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
100 105 110

Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
115 120 125

His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
130 135 140

Thr Tyr Ala Pro Leu Val Ala Gly Met Ala Gly Met Arg Tyr Arg Thr
145 150 155 160

Phe Ile Ile Tyr Asn Met Ile Gly Gly Ile Leu Trp Gly Ser Gly Val
165 170 175

Val Ala Leu Gly Ala Ala Leu Gly Gln Phe Asp Phe Val Arg Asn Asn
180 185 190

Ile Asp Leu Ile Phe Leu Leu Ile Val Phe Ile Ser Val Val Pro Gly
195 200 205

Leu Val Gly Met Ala Arg Lys Leu Ala Asp Gly His Lys Gln Ala Asn
210 215 220

Thr Glu Pro Gln Glu Asn Pro Ala Val Gln Thr Ala Pro Val Lys Thr
225 230 235 240

Gln Glu Ala Gln Glu Ala Pro Gln Asn
245

<210> 321
<211> 525
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (79)..(525)
<223> FRXA02010

<400> 321
cctgaataaa cccctatttt tctaaaaagt acactttgcc gtatagaaat tcagtcaacc 60

aagagtactc tgtccaccatg gtt ttt act ctt gcg gac tcc gtc tcc cag 111
Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln
1 5 10

gtt gcg cta ggt ccg tcc tgg ctg gac cct atg gaa ctt ctt tcc ggc 159
Val Ala Leu Gly Pro Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly
15 20 25

tcc ggc ccg ttc ggt agc ttc att ctt ccg gcg atg ctt gcc att gtc 207
Ser Gly Pro Phe Gly Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val
30 35 40

ttt atc gaa tca ggc cta ctt ttc cca ctt cta cca ggt gat tct ctc 255
Phe Ile Glu Ser Gly Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu
45 50 55

ctt ttc acc ggt ggt ctc cta gct aac cag gct gac cct ttt gca ccg 303
Leu Phe Thr Gly Gly Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro
60 65 70 75

ctg tgg ctg gtg ctg atc ctc tgc cct atc gcc gca att ctt ggc gat 351
Leu Trp Leu Val Leu Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp
80 85 90

cag gtg ggt tac tgg att ggc cac aag ttc cac cct cgc ctg gtc aat 399
Gln Val Gly Tyr Trp Ile Gly His Lys Phe His Pro Arg Leu Val Asn
95 100 105

cgt ccg gat ggc agg att ttc aag cag gaa tac ctc aag cag act gag 447
Arg Pro Asp Gly Arg Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu
110 115 120

gat ttc ttt gag aag cat ggc ccc gtg acg atc att ttg tgc cgt ttc 495
Asp Phe Phe Glu Lys His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe
125 130 135

gtg ccc atc gtc cgt act tac gca cct ctg 525
Val Pro Ile Val Arg Thr Tyr Ala Pro Leu
140 145

<210> 322
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 322
Met Val Phe Thr Leu Ala Asp Ser Val Ser Gln Val Ala Leu Gly Pro
1 5 10 15

Ser Trp Leu Asp Pro Met Glu Leu Leu Ser Gly Ser Gly Pro Phe Gly
20 25 30

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Ser Phe Ile Leu Pro Ala Met Leu Ala Ile Val Phe Ile Glu Ser Gly
         35                  40                  45

Leu Leu Phe Pro Leu Leu Pro Gly Asp Ser Leu Leu Phe Thr Gly Gly
     50                  55                  60

Leu Leu Ala Asn Gln Ala Asp Pro Phe Ala Pro Leu Trp Leu Val Leu
 65                  70                  75                  80

Ile Leu Cys Pro Ile Ala Ala Ile Leu Gly Asp Gln Val Gly Tyr Trp
                 85                  90                  95

Ile Gly His Lys Phe His Pro Arg Leu Val Asn Arg Pro Asp Gly Arg
            100                 105                 110

Ile Phe Lys Gln Glu Tyr Leu Lys Gln Thr Glu Asp Phe Phe Glu Lys
        115                 120                 125

His Gly Pro Val Thr Ile Ile Leu Cys Arg Phe Val Pro Ile Val Arg
    130                 135                 140

Thr Tyr Ala Pro Leu
145
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<210> 323
<211> 885
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(862)
<223> RXA02120

<400> 323

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ttggccactt gtttgagtag gctggcgggc aggtgcttga aatactctga ttagttccaa 60

gcaaattagc acaacttcac actttattta ggagcatgtt atg tct gac ctg aag   115
                                        Met Ser Asp Leu Lys
                                          1               5

tca ctt gcc acg aaa ttt gct agc gat cat gaa tcc gga aag ctg ctg   163
Ser Leu Ala Thr Lys Phe Ala Ser Asp His Glu Ser Gly Lys Leu Leu
                 10                  15                  20

gtc ctg cct acc gtc tgg gat acc tgg agc gcg ggg ctc gta gaa gaa   211
Val Leu Pro Thr Val Trp Asp Thr Trp Ser Ala Gly Leu Val Glu Glu
             25                  30                  35

gca gga ttt agt ggc ctg acc att ggt agc cac cca gtc gcg gat gcg   259
Ala Gly Phe Ser Gly Leu Thr Ile Gly Ser His Pro Val Ala Asp Ala
         40                  45                  50

aca gga agc tcc gat ggt gaa aac atg aat ttt gca gat tat atg gcg   307
Thr Gly Ser Ser Asp Gly Glu Asn Met Asn Phe Ala Asp Tyr Met Ala
     55                  60                  65

gtg gtc aag aag atc acc tcg gcg gta tcc atc ccc gta agc gtt gat   355
Val Val Lys Lys Ile Thr Ser Ala Val Ser Ile Pro Val Ser Val Asp
 70                  75                  80                  85
```

```
gtg gaa tcc ggt tat ggt ctc tcg cct gcg gat ttg atc gca cag att   403
Val Glu Ser Gly Tyr Gly Leu Ser Pro Ala Asp Leu Ile Ala Gln Ile
                 90                  95                 100

ttg gaa gct ggc gca gtg ggc atc aat gtg gaa gat gtt gtg cac agc   451
Leu Glu Ala Gly Ala Val Gly Ile Asn Val Glu Asp Val Val His Ser
            105                 110                 115

gag ggt aag cgt gtt cgt gag gcg cag gag cac gct gat tac atc gct   499
Glu Gly Lys Arg Val Arg Glu Ala Gln Glu His Ala Asp Tyr Ile Ala
        120                 125                 130

gcg gca cgt caa gct gcc gat gtg gca ggt gta gat gtg gtg atc aac   547
Ala Ala Arg Gln Ala Ala Asp Val Ala Gly Val Asp Val Val Ile Asn
    135                 140                 145

ggt cgc acg gat gcc gtc aaa ctt ggt gca gac gtt ttt gaa gat ccg   595
Gly Arg Thr Asp Ala Val Lys Leu Gly Ala Asp Val Phe Glu Asp Pro
150                 155                 160                 165

atg gtg gag gcc atc aag cgc atc aag ctc atg gaa cag gca ggc gcg   643
Met Val Glu Ala Ile Lys Arg Ile Lys Leu Met Glu Gln Ala Gly Ala
                170                 175                 180

cgt tcg gtg tac ccc gtg ggt ctg agc acc gcc gag cag gtt gag cgc   691
Arg Ser Val Tyr Pro Val Gly Leu Ser Thr Ala Glu Gln Val Glu Arg
            185                 190                 195

ctg gtg gac gct gtg tca gtg ccg gtc aac atc acc gcg cac ccg gtt   739
Leu Val Asp Ala Val Ser Val Pro Val Asn Ile Thr Ala His Pro Val
        200                 205                 210

gat ggg cac ggc gca ggc gat ctg gcc acc ctc gca ggc ctt ggc gtg   787
Asp Gly His Gly Ala Gly Asp Leu Ala Thr Leu Ala Gly Leu Gly Val
    215                 220                 225

cgc cgc gtg acc ttc ggt ccg ctc tgg caa aaa tgg ctg gct gcc acc   835
Arg Arg Val Thr Phe Gly Pro Leu Trp Gln Lys Trp Leu Ala Ala Thr
230                 235                 240                 245

tcg gcg cag cag ctt aag ggc tgg gct taaattgctt gtcgacgcct         882
Ser Ala Gln Gln Leu Lys Gly Trp Ala
                250

agt                                                              885
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<210> 324
<211> 254
<212> PRT
<213> Corynebacterium glutamicum

<400> 324

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Met Ser Asp Leu Lys Ser Leu Ala Thr Lys Phe Ala Ser Asp His Glu
  1               5                  10                  15

Ser Gly Lys Leu Leu Val Leu Pro Thr Val Trp Asp Thr Trp Ser Ala
             20                  25                  30

Gly Leu Val Glu Glu Ala Gly Phe Ser Gly Leu Thr Ile Gly Ser His
```

```
         35                  40                  45

Pro Val Ala Asp Ala Thr Gly Ser Ser Asp Gly Glu Asn Met Asn Phe
     50                  55                  60

Ala Asp Tyr Met Ala Val Val Lys Lys Ile Thr Ser Ala Val Ser Ile
 65                  70                  75                  80

Pro Val Ser Val Asp Val Glu Ser Gly Tyr Gly Leu Ser Pro Ala Asp
                 85                  90                  95

Leu Ile Ala Gln Ile Leu Glu Ala Gly Ala Val Gly Ile Asn Val Glu
            100                 105                 110

Asp Val Val His Ser Glu Gly Lys Arg Val Arg Glu Ala Gln Glu His
        115                 120                 125

Ala Asp Tyr Ile Ala Ala Ala Arg Gln Ala Ala Asp Val Ala Gly Val
    130                 135                 140

Asp Val Val Ile Asn Gly Arg Thr Asp Ala Val Lys Leu Gly Ala Asp
145                 150                 155                 160

Val Phe Glu Asp Pro Met Val Glu Ala Ile Lys Arg Ile Lys Leu Met
                165                 170                 175

Glu Gln Ala Gly Ala Arg Ser Val Tyr Pro Val Gly Leu Ser Thr Ala
            180                 185                 190

Glu Gln Val Glu Arg Leu Val Asp Ala Val Ser Val Pro Val Asn Ile
        195                 200                 205

Thr Ala His Pro Val Asp Gly His Gly Ala Gly Asp Leu Ala Thr Leu
    210                 215                 220

Ala Gly Leu Gly Val Arg Arg Val Thr Phe Gly Pro Leu Trp Gln Lys
225                 230                 235                 240

Trp Leu Ala Ala Thr Ser Ala Gln Gln Leu Lys Gly Trp Ala
                245                 250
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<210> 325
<211> 969
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(946)
<223> RXS01000

<400> 325
ctttctatgc ctacgcggat gtttccgtga tcattctgga aatcctcatc gtggtgattg 60

tcattgaagt aatctccaac gcacttcgaa agaggctggt atg agc acc tta acc 115
                                                Met Ser Thr Leu Thr
                                                  1   5

tct cac cgc aca gta ccg gcc ccc agc tct ccc ccg gcg cgc ccc aac 163
Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro Pro Ala Arg Pro Asn

```
                    10                  15                  20

aaa ctg gcg cgc aat atc gtt gca att gtc gct gcg ctg att gtc ctt   211
Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala Ala Leu Ile Val Leu
                25                  30                  35

ata gct acc ggc acg ctc aag atc gag tgg aat gag ctt ccg cag atg   259
Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn Glu Leu Pro Gln Met
            40                  45                  50

ccc gcg cag gtg tgg cat tac tta gag ctg atg ttt agc gat ccc gat   307
Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met Phe Ser Asp Pro Asp
        55                  60                  65

tgg tcg aag ttt ggc cgc gcc gtc cag gaa atg tgg cgt tcc atc gcc   355
Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met Trp Arg Ser Ile Ala
    70                  75                  80                  85

atg gcg tgg ttg ggt gcc att tta tgc gtg gtg gtc tct gtc cct ctg   403
Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val Val Ser Val Pro Leu
                90                  95                  100

gga atg ttg gct gcc cgc ggg gtg gga cct tat tgg ctg cgt acc gtt   451
Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr Trp Leu Arg Thr Val
            105                 110                 115

tta cgg ttc gtg ttc gcg gtg att cgt gcg ttc ccc gaa gtg gtt atc   499
Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe Pro Glu Val Val Ile
        120                 125                 130

gca att att ttg cta act gtc acc ggc cta act cct ttt act ggt gcg   547
Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr Pro Phe Thr Gly Ala
    135                 140                 145

ctc gca ttg ggt atc tcc ggt att gga caa cag gca aag tgg acc tat   595
Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln Ala Lys Trp Thr Tyr
150                 155                 160                 165

gaa gcc att gag tcc act ccc acc ggc ccg tca gag gca gtg cgt gca   643
Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser Glu Ala Val Arg Ala
                170                 175                 180

gcg ggt gga act acg ccg gag gtt ctg cgg tgg gcg ttg tgg cca cag   691
Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp Ala Leu Trp Pro Gln
            185                 190                 195

gtt gcg cca tcc att gca tct ttt gcc ctg tac cgc ttt gag atc aac   739
Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr Arg Phe Glu Ile Asn
        200                 205                 210

atc cgt acc tct gcg gta ttg ggc atc gtt ggt gca ggt ggt atc ggt   787
Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly Ala Gly Gly Ile Gly
    215                 220                 225

agt atg ctt gcc aat tac acc aac tac agg cag tgg gac acc gtg ggc   835
Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln Trp Asp Thr Val Gly
230                 235                 240                 245

atg ctg ctc atc gtc gtg gtt gtc gca acg atg atc gtc gat ctc atc   883
Met Leu Leu Ile Val Val Val Val Ala Thr Met Ile Val Asp Leu Ile
                250                 255                 260
```

```
tcc ggc acc atc cgc cgc cgc atc atg aag ggg gct agt gac cgt gtc   931
Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly Ala Ser Asp Arg Val
            265                 270                 275

gtg gca cca agc aac tgacgctcca ccaagcatcc gca                    969
Val Ala Pro Ser Asn
        280
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<210> 326
<211> 282
<212> PRT
<213> Corynebacterium glutamicum

<400> 326

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Met Ser Thr Leu Thr Ser His Arg Thr Val Pro Ala Pro Ser Ser Pro
  1               5                  10                  15

Pro Ala Arg Pro Asn Lys Leu Ala Arg Asn Ile Val Ala Ile Val Ala
             20                  25                  30

Ala Leu Ile Val Leu Ile Ala Thr Gly Thr Leu Lys Ile Glu Trp Asn
         35                  40                  45

Glu Leu Pro Gln Met Pro Ala Gln Val Trp His Tyr Leu Glu Leu Met
     50                  55                  60

Phe Ser Asp Pro Asp Trp Ser Lys Phe Gly Arg Ala Val Gln Glu Met
 65                  70                  75                  80

Trp Arg Ser Ile Ala Met Ala Trp Leu Gly Ala Ile Leu Cys Val Val
                 85                  90                  95

Val Ser Val Pro Leu Gly Met Leu Ala Ala Arg Gly Val Gly Pro Tyr
            100                 105                 110

Trp Leu Arg Thr Val Leu Arg Phe Val Phe Ala Val Ile Arg Ala Phe
        115                 120                 125

Pro Glu Val Val Ile Ala Ile Ile Leu Leu Thr Val Thr Gly Leu Thr
    130                 135                 140

Pro Phe Thr Gly Ala Leu Ala Leu Gly Ile Ser Gly Ile Gly Gln Gln
145                 150                 155                 160

Ala Lys Trp Thr Tyr Glu Ala Ile Glu Ser Thr Pro Thr Gly Pro Ser
                165                 170                 175

Glu Ala Val Arg Ala Ala Gly Gly Thr Thr Pro Glu Val Leu Arg Trp
            180                 185                 190

Ala Leu Trp Pro Gln Val Ala Pro Ser Ile Ala Ser Phe Ala Leu Tyr
        195                 200                 205

Arg Phe Glu Ile Asn Ile Arg Thr Ser Ala Val Leu Gly Ile Val Gly
    210                 215                 220

Ala Gly Gly Ile Gly Ser Met Leu Ala Asn Tyr Thr Asn Tyr Arg Gln
225                 230                 235                 240
```

```
Trp Asp Thr Val Gly Met Leu Leu Ile Val Val Val Ala Thr Met
                245                 250                 255

Ile Val Asp Leu Ile Ser Gly Thr Ile Arg Arg Arg Ile Met Lys Gly
            260                 265                 270

Ala Ser Asp Arg Val Val Ala Pro Ser Asn
        275                 280


<210> 327
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXS01002

<400> 327
gactgctgat accgcacagg atgaaatcac tcgttacggc gagatcctga agaagttctc 60

caactaattt ccctgtttcc aatactcaag gtgtgcgcat atg aat tct gat gct   115
                                            Met Asn Ser Asp Ala
                                              1               5

tcg gct acc acc aac tcc tgg gct atc aac ttc gac cat gtg tcg gtg   163
Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe Asp His Val Ser Val
                  10                  15                  20

acg tat ccc aat ggg acg aaa gcc ctc gat gat gtt tcc ctc acc atc   211
Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp Val Ser Leu Thr Ile
              25                  30                  35

aat ccc ggt gag atg gtt gcc atc gtg ggt ctg tca gga tcg ggt aaa   259
Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu Ser Gly Ser Gly Lys
          40                  45                  50

tcc acg ctg att cgc acg atc aac ggt ctt gtc cgc gct acg gaa ggc   307
Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val Arg Ala Thr Glu Gly
      55                  60                  65

acc gtg acg gtg ggg ccg cat cag atc aac acc ttg aag ggg aaa gca   355
Thr Val Thr Val Gly Pro His Gln Ile Asn Thr Leu Lys Gly Lys Ala
  70                  75                  80                  85

ctg cgt gat gcc cgt ggg cag atc ggc atg att ttc cag ggg ttc aac   403
Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile Phe Gln Gly Phe Asn
                  90                  95                 100

ctg tcg gaa cgc agc agt gtg ttc cag aat gtt ttg gtg ggc cgc ttc   451
Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val Leu Val Gly Arg Phe
            105                 110                 115

gcg cac aca gcg tgg tgg cgt aac ctc ctc ggg ttt ccc acg gag cac   499
Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly Phe Pro Thr Glu His
        120                 125                 130

gac aag cag att gct ttt cac gcg ttg gag tcc gtg ggc att ttg cac   547
Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser Val Gly Ile Leu His
```

```
    135                 140                 145

aaa gtg tgg acc cga gct ggt gct ttg tcg ggt gga cag aaa cag cgc   595
Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly Gly Gln Lys Gln Arg
150                 155                 160                 165

gtt gct att gcg cgc gcc tta tcg caa gat ccg tct gtc atg ctg gca   643
Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro Ser Val Met Leu Ala
                170                 175                 180

gat gag cct gtg gca agc ctt gat ccg cca acc gcg cat tcc gtg atg   691
Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr Ala His Ser Val Met
            185                 190                 195

cgc gat cta gaa aac atc aac aac gtg gaa ggc ctc acc gtg ttg gtg   739
Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly Leu Thr Val Leu Val
        200                 205                 210

aac ttg cac ttg att gat ttg gct cgt caa tac acc aca agg ctt gtg   787
Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr Thr Thr Arg Leu Val
    215                 220                 225

ggt ttg cgt gcc ggc aag ctg gtc tat gac ggt cct atc tct gag gcc   835
Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly Pro Ile Ser Glu Ala
230                 235                 240                 245

acc gat aaa gac ttt gaa gct atc tat ggt cgc ccc atc cag gct aaa   883
Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg Pro Ile Gln Ala Lys
                250                 255                 260

gac ctg cta ggt gat cgc gca tgaccacgcc ttcttctaca ctt             927
Asp Leu Leu Gly Asp Arg Ala
            265
```

Sequence Listing

<210> 328
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 328

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Met Asn Ser Asp Ala Ser Ala Thr Thr Asn Ser Trp Ala Ile Asn Phe
  1               5                  10                  15

Asp His Val Ser Val Thr Tyr Pro Asn Gly Thr Lys Ala Leu Asp Asp
             20                  25                  30

Val Ser Leu Thr Ile Asn Pro Gly Glu Met Val Ala Ile Val Gly Leu
         35                  40                  45

Ser Gly Ser Gly Lys Ser Thr Leu Ile Arg Thr Ile Asn Gly Leu Val
     50                  55                  60

Arg Ala Thr Glu Gly Thr Val Thr Val Gly Pro His Gln Ile Asn Thr
 65                  70                  75                  80

Leu Lys Gly Lys Ala Leu Arg Asp Ala Arg Gly Gln Ile Gly Met Ile
                 85                  90                  95

Phe Gln Gly Phe Asn Leu Ser Glu Arg Ser Ser Val Phe Gln Asn Val
            100                 105                 110
```

```
Leu Val Gly Arg Phe Ala His Thr Ala Trp Trp Arg Asn Leu Leu Gly
        115                 120                 125

Phe Pro Thr Glu His Asp Lys Gln Ile Ala Phe His Ala Leu Glu Ser
    130                 135                 140

Val Gly Ile Leu His Lys Val Trp Thr Arg Ala Gly Ala Leu Ser Gly
145                 150                 155                 160

Gly Gln Lys Gln Arg Val Ala Ile Ala Arg Ala Leu Ser Gln Asp Pro
                165                 170                 175

Ser Val Met Leu Ala Asp Glu Pro Val Ala Ser Leu Asp Pro Pro Thr
            180                 185                 190

Ala His Ser Val Met Arg Asp Leu Glu Asn Ile Asn Asn Val Glu Gly
        195                 200                 205

Leu Thr Val Leu Val Asn Leu His Leu Ile Asp Leu Ala Arg Gln Tyr
    210                 215                 220

Thr Thr Arg Leu Val Gly Leu Arg Ala Gly Lys Leu Val Tyr Asp Gly
225                 230                 235                 240

Pro Ile Ser Glu Ala Thr Asp Lys Asp Phe Glu Ala Ile Tyr Gly Arg
                245                 250                 255

Pro Ile Gln Ala Lys Asp Leu Leu Gly Asp Arg Ala
            260                 265


<210> 329
<211> 927
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(904)
<223> RXS01003

<400> 329
agctggtcta tgacggtcct atctctgagg ccaccgataa agactttgaa gctatctatg 60

gtcgccccat ccaggctaaa gacctgctag gtgatcgcgc atg acc acg cct tct   115
                                        Met Thr Thr Pro Ser
                                          1               5

tct aca ctt atc cca caa aag cct cgg gct ggg gta aag acc tat ctc   163
Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly Val Lys Thr Tyr Leu
                10                  15                  20

atc atc ggc gcc atc gtt gtc ttc acc gtg gca aca gca acc cca gcg   211
Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala Thr Ala Thr Pro Ala
            25                  30                  35

cta ggt ggc att gag ctt gat ttc gct tcc att gct gcg aat tgg cgc   259
Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile Ala Ala Asn Trp Arg
        40                  45                  50
```

```
aat ggt gcc aac aaa ctc ctg caa atg ctg cag ccc aac ttt gcg ttc   307
Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln Pro Asn Phe Ala Phe
     55                  60                  65

ttg cct cgt acg tgg ctt ccc atg ttg gaa acc ctg cag atg gcg ctt   355
Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr Leu Gln Met Ala Leu
 70                  75                  80                  85

gtt gga gct gtc ttg tct gct gcc gta tcg gtg cct ttg acg ttg tgg   403
Val Gly Ala Val Leu Ser Ala Ala Val Ser Val Pro Leu Thr Leu Trp
                 90                  95                 100

gca gcg cag gca acc aac acc agt gcg att ggt cgt ggc att gtc cgc   451
Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly Arg Gly Ile Val Arg
            105                 110                 115

acc atc att aac gtg gtg cgc tct gtc ccc gac ttg gtg tat gcc acc   499
Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp Leu Val Tyr Ala Thr
        120                 125                 130

atc ttg gtc gcc atg gtt ggt gtc ggc gca tta cct ggc att ttg acg   547
Ile Leu Val Ala Met Val Gly Val Gly Ala Leu Pro Gly Ile Leu Thr
    135                 140                 145

ctg ttt ctg ttc aac ctg ggc atc gtg gtc aag ctt gtc tct gag gcc   595
Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys Leu Val Ser Glu Ala
150                 155                 160                 165

att gat tcc act gag cat ccc tat atg gaa gca gga cgc gca gca ggt   643
Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala Gly Arg Ala Ala Gly
                170                 175                 180

gga tca cag ttc caa atc aac cga gtc tcc gcg ctt cct gaa gtc atg   691
Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala Leu Pro Glu Val Met
            185                 190                 195

ccg ctc ttt gcc aac caa tgg ctc tac acc cta gag ctg aat gta cgc   739
Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu Glu Leu Asn Val Arg
        200                 205                 210

atc tcc gcc atc ctt ggc atc gtg ggc gca ggt ggc atc ggc agg ctg   787
Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly Gly Ile Gly Arg Leu
    215                 220                 225

ctt gat gaa cgc cga gct ttc tat gcc tac gcg gat gtt tcc gtg atc   835
Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala Asp Val Ser Val Ile
230                 235                 240                 245

att ctg gaa atc ctc atc gtg gtg att gtc att gaa gta atc tcc aac   883
Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile Glu Val Ile Ser Asn
                250                 255                 260

gca ctt cga aag agg ctg gta tgagcacctt aacctctcac cgc            927
Ala Leu Arg Lys Arg Leu Val
            265
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<210> 330
<211> 268
<212> PRT
<213> Corynebacterium glutamicum

<400> 330

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Met Thr Thr Pro Ser Ser Thr Leu Ile Pro Gln Lys Pro Arg Ala Gly
  1               5                  10                  15

Val Lys Thr Tyr Leu Ile Ile Gly Ala Ile Val Val Phe Thr Val Ala
             20                  25                  30

Thr Ala Thr Pro Ala Leu Gly Gly Ile Glu Leu Asp Phe Ala Ser Ile
         35                  40                  45

Ala Ala Asn Trp Arg Asn Gly Ala Asn Lys Leu Leu Gln Met Leu Gln
     50                  55                  60

Pro Asn Phe Ala Phe Leu Pro Arg Thr Trp Leu Pro Met Leu Glu Thr
 65                  70                  75                  80

Leu Gln Met Ala Leu Val Gly Ala Val Leu Ser Ala Ala Val Ser Val
                 85                  90                  95

Pro Leu Thr Leu Trp Ala Ala Gln Ala Thr Asn Thr Ser Ala Ile Gly
            100                 105                 110

Arg Gly Ile Val Arg Thr Ile Ile Asn Val Val Arg Ser Val Pro Asp
        115                 120                 125

Leu Val Tyr Ala Thr Ile Leu Val Ala Met Val Gly Val Gly Ala Leu
    130                 135                 140

Pro Gly Ile Leu Thr Leu Phe Leu Phe Asn Leu Gly Ile Val Val Lys
145                 150                 155                 160

Leu Val Ser Glu Ala Ile Asp Ser Thr Glu His Pro Tyr Met Glu Ala
                165                 170                 175

Gly Arg Ala Ala Gly Gly Ser Gln Phe Gln Ile Asn Arg Val Ser Ala
            180                 185                 190

Leu Pro Glu Val Met Pro Leu Phe Ala Asn Gln Trp Leu Tyr Thr Leu
        195                 200                 205

Glu Leu Asn Val Arg Ile Ser Ala Ile Leu Gly Ile Val Gly Ala Gly
    210                 215                 220

Gly Ile Gly Arg Leu Leu Asp Glu Arg Arg Ala Phe Tyr Ala Tyr Ala
225                 230                 235                 240

Asp Val Ser Val Ile Ile Leu Glu Ile Leu Ile Val Val Ile Val Ile
                245                 250                 255

Glu Val Ile Ser Asn Ala Leu Arg Lys Arg Leu Val
            260                 265
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<210> 331
<211> 1182
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1159)
<223> RXS01902

<400> 331
ggctggtccg aagtgcaaac cttcaacacc ggcacctacg gtgacaactg gaacttcctc 60

ttcttcggcg acacccagct gtacaacacc cactccaacc gtg cag aag aag tcc 115
Val Gln Lys Lys Ser
1 5

aga act ggg caa aca acc tgg aac ggc ggc cca cca atc gaa aac cca 163
Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro Pro Ile Glu Asn Pro
10 15 20

gga acc tcc ttc atc ctc tcc gcg ggt gat cag gca aac cac tcc agc 211
Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln Ala Asn His Ser Ser
25 30 35

tgg gac gag cac tcc gca tac atc tcc cca gaa acc ctg cgc aac tac 259
Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu Thr Leu Arg Asn Tyr
40 45 50

cgt ctg gcc gtg aac aat gga aac cac gac cag tac aac tac gac gcc 307
Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln Tyr Asn Tyr Asp Ala
55 60 65

tac aac gcg atg tac cca cgc cct aac cag gtc gat gag aac tac ttc 355
Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val Asp Glu Asn Tyr Phe
70 75 80 85

ttc gag tac aac aat gca ctc ttc ctg tcc ctg gac tcc aac gac tac 403
Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu Asp Ser Asn Asp Tyr
90 95 100

ttg gac atc gac gac gac atc gca ttc ctt cgc gac acc gtc gca gca 451
Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg Asp Thr Val Ala Ala
105 110 115

cac ggt gac gac aag gac tgg atc gtc ctg acc tac cac cat tcc act 499
His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr Tyr His His Ser Thr
120 125 130

ttc tcc cag gcc tac cac atg gat gac gct cgc att aag tac cag cgc 547
Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg Ile Lys Tyr Gln Arg
135 140 145

gaa cgc ctc acc cca gtg atc tct gaa ctg aac gtt gac ttg gtt ctc 595
Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn Val Asp Leu Val Leu
150 155 160 165

ggt gga cac gac cac atc tac acc cgc tcc cac ctg atg aac ggc ttc 643
Gly Gly His Asp His Ile Tyr Thr Arg Ser His Leu Met Asn Gly Phe
170 175 180

acc cca gtc gat gca ggc cgc gaa gca gtt gtc ggt gaa act ctg aac 691
Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val Gly Glu Thr Leu Asn
185 190 195

cct aag gcc ggc gaa gtt gtt tac ctt gca acc aac tct tcc tca ggc 739
Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr Asn Ser Ser Ser Gly
200 205 210

```
tcc aag ttc tac gac ttc tac gac ttc cag ctc ggc cag cgt tac gac   787
Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu Gly Gln Arg Tyr Asp
    215                 220                 225

acc gga ctg gat ttc cag gaa acc gtc gat cag aag aag atc cgc acc   835
Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln Lys Lys Ile Arg Thr
230                 235                 240                 245

tac acc gca gtc tgg aac cag gac cag gtt cag gac tac acc aac gtt   883
Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln Asp Tyr Thr Asn Val
                250                 255                 260

gaa ctg acc cca gaa ggc ctg act gtg acc act aag gac gca gtc tcc   931
Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr Lys Asp Ala Val Ser
            265                 270                 275

ggc gag ctg gtt gac cag ttc acc ctg agc aag cag gac cgc gac gaa   979
Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys Gln Asp Arg Asp Glu
        280                 285                 290

gaa tct gaa gtc cca gtt gaa gat gac aag gac gga gac aac gcg acc   1027
Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp Gly Asp Asn Ala Thr
    295                 300                 305

ggc tcc tcc aac ctt ggt cta gct gct atc ttg gct cca gtt ctg gcc   1075
Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu Ala Pro Val Leu Ala
310                 315                 320                 325

atc ttc ggt ttc gtc ggt gga ctc ttt gtt ggc ggc ggc tcc ctc gct   1123
Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly Gly Gly Ser Leu Ala
                330                 335                 340

gag ttc ttt gcc aac ctc ggc gtg aag atg cct ttc taatactgtc         1169
Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro Phe
            345                 350

tgagattcaa gca                                                    1182
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20050244-pct

Sequence Listing

<210> 332
<211> 353
<212> PRT
<213> Corynebacterium glutamicum

<400> 332

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Val Gln Lys Lys Ser Arg Thr Gly Gln Thr Thr Trp Asn Gly Gly Pro
  1               5                  10                  15

Pro Ile Glu Asn Pro Gly Thr Ser Phe Ile Leu Ser Ala Gly Asp Gln
             20                  25                  30

Ala Asn His Ser Ser Trp Asp Glu His Ser Ala Tyr Ile Ser Pro Glu
         35                  40                  45

Thr Leu Arg Asn Tyr Arg Leu Ala Val Asn Asn Gly Asn His Asp Gln
     50                  55                  60

Tyr Asn Tyr Asp Ala Tyr Asn Ala Met Tyr Pro Arg Pro Asn Gln Val
 65                  70                  75                  80
```

```
Asp Glu Asn Tyr Phe Phe Glu Tyr Asn Asn Ala Leu Phe Leu Ser Leu
                 85                  90                  95

Asp Ser Asn Asp Tyr Leu Asp Ile Asp Asp Asp Ile Ala Phe Leu Arg
            100                 105                 110

Asp Thr Val Ala Ala His Gly Asp Asp Lys Asp Trp Ile Val Leu Thr
        115                 120                 125

Tyr His His Ser Thr Phe Ser Gln Ala Tyr His Met Asp Asp Ala Arg
    130                 135                 140

Ile Lys Tyr Gln Arg Glu Arg Leu Thr Pro Val Ile Ser Glu Leu Asn
145                 150                 155                 160

Val Asp Leu Val Leu Gly Gly His Asp His Ile Tyr Thr Arg Ser His
                165                 170                 175

Leu Met Asn Gly Phe Thr Pro Val Asp Ala Gly Arg Glu Ala Val Val
            180                 185                 190

Gly Glu Thr Leu Asn Pro Lys Ala Gly Glu Val Val Tyr Leu Ala Thr
        195                 200                 205

Asn Ser Ser Ser Gly Ser Lys Phe Tyr Asp Phe Tyr Asp Phe Gln Leu
    210                 215                 220

Gly Gln Arg Tyr Asp Thr Gly Leu Asp Phe Gln Glu Thr Val Asp Gln
225                 230                 235                 240

Lys Lys Ile Arg Thr Tyr Thr Ala Val Trp Asn Gln Asp Gln Val Gln
                245                 250                 255

Asp Tyr Thr Asn Val Glu Leu Thr Pro Glu Gly Leu Thr Val Thr Thr
            260                 265                 270

Lys Asp Ala Val Ser Gly Glu Leu Val Asp Gln Phe Thr Leu Ser Lys
        275                 280                 285

Gln Asp Arg Asp Glu Glu Ser Glu Val Pro Val Glu Asp Asp Lys Asp
    290                 295                 300

Gly Asp Asn Ala Thr Gly Ser Ser Asn Leu Gly Leu Ala Ala Ile Leu
305                 310                 315                 320

Ala Pro Val Leu Ala Ile Phe Gly Phe Val Gly Gly Leu Phe Val Gly
                325                 330                 335

Gly Gly Ser Leu Ala Glu Phe Phe Ala Asn Leu Gly Val Lys Met Pro
            340                 345                 350

Phe
```

<210> 333
<211> 1266
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (101)..(1243)
<223> RXA01967

<400> 333
gatgccaccg ttgaggcaga caaaaacgtg ggtggaccgc aatgggtccg ctcatgtgga 60

gttgtcgcca accgtgccac cgcaaacccc caaacgtcac atg cgc atc caa agc 115
Met Arg Ile Gln Ser
1 5

ccc atg gaa att tcc tgg agt gaa gcg gtg cgc gaa ggc ggg gag cat 163
Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg Glu Gly Gly Glu His
10 15 20

tcc gct cgc cgc tgt ggt gac atg gct gtg tcc gcg ttg gct aag ccg 211
Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser Ala Leu Ala Lys Pro
25 30 35

aat ccc atc att gac gat gat ccg gaa ggc aac ccc gat gtt tgc atg 259
Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn Pro Asp Val Cys Met
40 45 50

tat acc tgg atc gtt gag tgt ccc ggc gct acc gca gtg ctg cta tgg 307
Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr Ala Val Leu Leu Trp
55 60 65

atc aat ggg gtt ttt gat cac gag cgc att gaa gaa tct gaa atg acc 355
Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu Glu Ser Glu Met Thr
70 75 80 85

cgc ctc gag ggc tct gat ctg tgg att ctc agc ttg cgt atg cct tcc 403
Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser Leu Arg Met Pro Ser
90 95 100

gat tgg cga gcc agc tac acc gtc aac gcc tgg tct ggc gac ggg gtt 451
Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp Ser Gly Asp Gly Val
105 110 115

gcg cca tgg cgt gag gcg ggc gat cgg atg cat atc cgc aaa gcc gcg 499
Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His Ile Arg Lys Ala Ala
120 125 130

atg tcg ggt ggg cgt ccg gat tcc cgc gcg atg ggt cat atc atg gat 547
Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met Gly His Ile Met Asp
135 140 145

tcc tcg ctc gtt gaa ggc cct gat gcg ttg ccg gac tgc tgg gtt gcg 595
Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro Asp Cys Trp Val Ala
150 155 160 165

gcg tcg aca agc gta aaa gtc gtg gaa gaa acc gtc gcc ggc gag cat 643
Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr Val Ala Gly Glu His
170 175 180

ttc tgg ttc tat gag gcg ccg gtc aag gcg ccg ctg ctg gtg ctg ttt 691
Phe Trp Phe Tyr Glu Ala Pro Val Lys Ala Pro Leu Leu Val Leu Phe
185 190 195

gat ggc caa cac tgg aac aac agc atg aat ctg cct gcg cag gtc gat 739
Asp Gly Gln His Trp Asn Asn Ser Met Asn Leu Pro Ala Gln Val Asp

```
        200                 205                 210

gcg gcc atc gcc atc ggc ttg ctg ccg ccg gtc agc ctg ctc atg atc   787
Ala Ala Ile Ala Ile Gly Leu Leu Pro Pro Val Ser Leu Leu Met Ile
    215                 220                 225

gat tcc gtc aac acc gaa cgc cgc tgg gat agt gtc ggc gtg cca ggt   835
Asp Ser Val Asn Thr Glu Arg Arg Trp Asp Ser Val Gly Val Pro Gly
230                 235                 240                 245

ggg cag gtt gat gtg ctt atc gac gcc ctc ctc ccg cac gtc cgc gaa   883
Gly Gln Val Asp Val Leu Ile Asp Ala Leu Leu Pro His Val Arg Glu
                250                 255                 260

acc tac aac gtt tcc gcg cgc ggc gaa gac acc att gtc acc ggt gca   931
Thr Tyr Asn Val Ser Ala Arg Gly Glu Asp Thr Ile Val Thr Gly Ala
            265                 270                 275

agc ttc ggc ggc ctg gcg tcc ctg tgg gct ctt gcg ctt tcc gac ggc   979
Ser Phe Gly Gly Leu Ala Ser Leu Trp Ala Leu Ala Leu Ser Asp Gly
        280                 285                 290

gaa gtc ggc cac gca atc gcg caa tcg cca agc ctg tgg cgc ttc aac   1027
Glu Val Gly His Ala Ile Ala Gln Ser Pro Ser Leu Trp Arg Phe Asn
    295                 300                 305

gtt gcc gac gcg ctt tct gca gca gag cag tgg agc tca atc cac ctg   1075
Val Ala Asp Ala Leu Ser Ala Ala Glu Gln Trp Ser Ser Ile His Leu
310                 315                 320                 325

caa gct gga aaa tac gaa ggt gaa atg ctg cgc ctg tcg cat cag ctc   1123
Gln Ala Gly Lys Tyr Glu Gly Glu Met Leu Arg Leu Ser His Gln Leu
                330                 335                 340

gcc gaa gat ctc tcc ggc gac atc cgc gag gtt cgt gtg cgc ggc gtg   1171
Ala Glu Asp Leu Ser Gly Asp Ile Arg Glu Val Arg Val Arg Gly Val
            345                 350                 355

cat ggc ggc cac gat tgg gcc tgg tgg cgg gtg cat atg ctc acc gaa   1219
His Gly Gly His Asp Trp Ala Trp Trp Arg Val His Met Leu Thr Glu
        360                 365                 370

ctc acc agg ctg ctt aaa acc ctc taatcaaagt agggtgcaaa acg         1266
Leu Thr Arg Leu Leu Lys Thr Leu
    375                 380
```

09054P-2005US

<210> 334
<211> 381
<212> PRT
<213> Corynebacterium glutamicum

<400> 334

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Met Arg Ile Gln Ser Pro Met Glu Ile Ser Trp Ser Glu Ala Val Arg
  1               5                  10                  15

Glu Gly Gly Glu His Ser Ala Arg Arg Cys Gly Asp Met Ala Val Ser
             20                  25                  30

Ala Leu Ala Lys Pro Asn Pro Ile Ile Asp Asp Asp Pro Glu Gly Asn
         35                  40                  45
```

```
Pro Asp Val Cys Met Tyr Thr Trp Ile Val Glu Cys Pro Gly Ala Thr
     50                  55                  60

Ala Val Leu Leu Trp Ile Asn Gly Val Phe Asp His Glu Arg Ile Glu
 65                  70                  75                  80

Glu Ser Glu Met Thr Arg Leu Glu Gly Ser Asp Leu Trp Ile Leu Ser
                 85                  90                  95

Leu Arg Met Pro Ser Asp Trp Arg Ala Ser Tyr Thr Val Asn Ala Trp
            100                 105                 110

Ser Gly Asp Gly Val Ala Pro Trp Arg Glu Ala Gly Asp Arg Met His
        115                 120                 125

Ile Arg Lys Ala Ala Met Ser Gly Gly Arg Pro Asp Ser Arg Ala Met
    130                 135                 140

Gly His Ile Met Asp Ser Ser Leu Val Glu Gly Pro Asp Ala Leu Pro
145                 150                 155                 160

Asp Cys Trp Val Ala Ala Ser Thr Ser Val Lys Val Val Glu Glu Thr
                165                 170                 175

Val Ala Gly Glu His Phe Trp Phe Tyr Glu Ala Pro Val Lys Ala Pro
            180                 185                 190

Leu Leu Val Leu Phe Asp Gly Gln His Trp Asn Asn Ser Met Asn Leu
        195                 200                 205

Pro Ala Gln Val Asp Ala Ala Ile Ala Ile Gly Leu Leu Pro Pro Val
    210                 215                 220

Ser Leu Leu Met Ile Asp Ser Val Asn Thr Glu Arg Arg Trp Asp Ser
225                 230                 235                 240

Val Gly Val Pro Gly Gly Gln Val Asp Val Leu Ile Asp Ala Leu Leu
                245                 250                 255

Pro His Val Arg Glu Thr Tyr Asn Val Ser Ala Arg Gly Glu Asp Thr
            260                 265                 270

Ile Val Thr Gly Ala Ser Phe Gly Gly Leu Ala Ser Leu Trp Ala Leu
        275                 280                 285

Ala Leu Ser Asp Gly Glu Val Gly His Ala Ile Ala Gln Ser Pro Ser
    290                 295                 300

Leu Trp Arg Phe Asn Val Ala Asp Ala Leu Ser Ala Ala Glu Gln Trp
305                 310                 315                 320

Ser Ser Ile His Leu Gln Ala Gly Lys Tyr Glu Gly Glu Met Leu Arg
                325                 330                 335

Leu Ser His Gln Leu Ala Glu Asp Leu Ser Gly Asp Ile Arg Glu Val
            340                 345                 350

Arg Val Arg Gly Val His Gly Gly His Asp Trp Ala Trp Trp Arg Val
        355                 360                 365
```

```
His Met Leu Thr Glu Leu Thr Arg Leu Leu Lys Thr Leu
    370                 375                 380


<210> 335
<211> 555
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(532)
<223> RXA00070

<400> 335
ccactcgtcc tcgacatact tctcctggca ctaaacgcag gggttgacac atctgggtag 60

actatcgaag tacattttgt gtcattgagg aggatcaacg gtg ggt atc aat cgc   115
                                        Val Gly Ile Asn Arg
                                          1               5

atc agc caa ggc tct gcc ccg aag ctg gga gtg cga agc acc aga cag   163
Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val Arg Ser Thr Arg Gln
                10                  15                  20

cga aaa gcc gta att gac gtt ctt gag gaa atc gat aac ttc gct tcc   211
Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile Asp Asn Phe Ala Ser
            25                  30                  35

gcc aaa gaa atc cat cac gag cta tcc acc agg gaa cac aac gtc ggc   259
Ala Lys Glu Ile His His Glu Leu Ser Thr Arg Glu His Asn Val Gly
        40                  45                  50

ctc aca acc gtc tac cga acc ctc caa tcc ctc gcc gac atc gga gca   307
Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu Ala Asp Ile Gly Ala
    55                  60                  65

gtc gac gta ctt acc gtc acg ggt gga gaa act ctg tac cgc caa tgc   355
Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr Leu Tyr Arg Gln Cys
70                  75                  80                  85

cac gac gag gga cac cac cat cac ctg gtc tgc acc aat tgc ggt cgc   403
His Asp Glu Gly His His His His Leu Val Cys Thr Asn Cys Gly Arg
                90                  95                  100

aca gtc gaa atc gat ggc ggt cca gta gag aca tgg gca cag gaa att   451
Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr Trp Ala Gln Glu Ile
            105                 110                 115

gcc act aaa aac ggc ttt gct ctc agt agt cac gag gct gaa atc ttt   499
Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His Glu Ala Glu Ile Phe
        120                 125                 130

gga ctt tgc gct gat tgt aag gaa aaa gtt acg tagttcaagg acatatgaag 552
Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
    135                 140

ctg                                                               555


<210> 336
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<211> 144
<212> PRT
<213> Corynebacterium glutamicum

<400> 336
Val Gly Ile Asn Arg Ile Ser Gln Gly Ser Ala Pro Lys Leu Gly Val
1 5 10 15

Arg Ser Thr Arg Gln Arg Lys Ala Val Ile Asp Val Leu Glu Glu Ile
20 25 30

Asp Asn Phe Ala Ser Ala Lys Glu Ile His His Glu Leu Ser Thr Arg
35 40 45

Glu His Asn Val Gly Leu Thr Thr Val Tyr Arg Thr Leu Gln Ser Leu
50 55 60

Ala Asp Ile Gly Ala Val Asp Val Leu Thr Val Thr Gly Gly Glu Thr
65 70 75 80

Leu Tyr Arg Gln Cys His Asp Glu Gly His His His His Leu Val Cys
85 90 95

Thr Asn Cys Gly Arg Thr Val Glu Ile Asp Gly Gly Pro Val Glu Thr
100 105 110

Trp Ala Gln Glu Ile Ala Thr Lys Asn Gly Phe Ala Leu Ser Ser His
115 120 125

Glu Ala Glu Ile Phe Gly Leu Cys Ala Asp Cys Lys Glu Lys Val Thr
130 135 140

<210> 337
<211> 681
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(658)
<223> RXA01934

<400> 337
ttattgatga tcgcgtgcgt aacattgagg cagcgcgcga agaaggtctc agcacaattc 60

acttcactgg cttagattcc ttaaaagaaa gcattcagga atg aca cct caa cca 115
Met Thr Pro Gln Pro
1 5

ctg att ttg cct ttc ggc gat aaa gtt ccg cgg atc cat gaa agc gca 163
Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg Ile His Glu Ser Ala
10 15 20

tgg att gcc ccg aat gcc acg att atc ggg gat gtc gag att ggc ccg 211
Trp Ile Ala Pro Asn Ala Thr Ile Ile Gly Asp Val Glu Ile Gly Pro
25 30 35

```
gat gcg tcc att ttt tat ggc gtt gtc ctg cgc ggt gac gtc aac aaa   259
Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg Gly Asp Val Asn Lys
         40                  45                  50

atc acc atc ggc gcc cgc acc aac gtc cag gac aat tgt gtt ctc cac   307
Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp Asn Cys Val Leu His
     55                  60                  65

gtc gat ggc gat gcg ccg tgc acc ctc ggc gac gat gtc acg gtc ggc   355
Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp Asp Val Thr Val Gly
 70                  75                  80                  85

cac atg gcg ctt gtt cac ggc gcg acg gtg ggc aac ggc acg ctt gtc   403
His Met Ala Leu Val His Gly Ala Thr Val Gly Asn Gly Thr Leu Val
                90                  95                 100

ggc atg aaa tct gcg ctg ctt tcc ggc agc cac gtc ggc gcc ggc gca   451
Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His Val Gly Ala Gly Ala
            105                 110                 115

ctc att gcc gct ggt gcg gtg gtg ctg gag ggc cat gaa atc ccg gcg   499
Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly His Glu Ile Pro Ala
        120                 125                 130

aaa gct tta gcg gcc ggg gtt ccg gcc aaa gtg cgc aga ttg ctt gac   547
Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val Arg Arg Leu Leu Asp
    135                 140                 145

gac gcc cag tcc cag tca ttt atc ccc cac gcg ggc cgc tat gta gaa   595
Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala Gly Arg Tyr Val Glu
150                 155                 160                 165

aca tca aaa gcc cag gct tcc atc gcg gaa gca ctg agc tta gat gag   643
Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala Leu Ser Leu Asp Glu
                170                 175                 180

gtt agg gta cga gag taagtggctc gttgagtagt cga                    681
Val Arg Val Arg Glu
            185
```

<210> 338
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 338

```
Met Thr Pro Gln Pro Leu Ile Leu Pro Phe Gly Asp Lys Val Pro Arg
  1               5                  10                  15

Ile His Glu Ser Ala Trp Ile Ala Pro Asn Ala Thr Ile Ile Gly Asp
             20                  25                  30

Val Glu Ile Gly Pro Asp Ala Ser Ile Phe Tyr Gly Val Val Leu Arg
         35                  40                  45

Gly Asp Val Asn Lys Ile Thr Ile Gly Ala Arg Thr Asn Val Gln Asp
     50                  55                  60

Asn Cys Val Leu His Val Asp Gly Asp Ala Pro Cys Thr Leu Gly Asp
 65                  70                  75                  80
```

```
Asp Val Thr Val Gly His Met Ala Leu Val His Gly Ala Thr Val Gly
                 85                  90                  95

Asn Gly Thr Leu Val Gly Met Lys Ser Ala Leu Leu Ser Gly Ser His
            100                 105                 110

Val Gly Ala Gly Ala Leu Ile Ala Ala Gly Ala Val Val Leu Glu Gly
        115                 120                 125

His Glu Ile Pro Ala Lys Ala Leu Ala Ala Gly Val Pro Ala Lys Val
    130                 135                 140

Arg Arg Leu Leu Asp Asp Ala Gln Ser Gln Ser Phe Ile Pro His Ala
145                 150                 155                 160

Gly Arg Tyr Val Glu Thr Ser Lys Ala Gln Ala Ser Ile Ala Glu Ala
                165                 170                 175

Leu Ser Leu Asp Glu Val Arg Val Arg Glu
            180                 185
```

Sequence Listing

<210> 339
<211> 609
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(586)
<223> RXN01997

<400> 339

```
aaaaaggtgg gaaacttagc caatccaaag cccaaaaatg cgggttatgc tgcgctaacc 60

tatgctgaca gccttgcgga agttgtgtac gttaggggcc atg aca atc aac gag   115
                                            Met Thr Ile Asn Glu
                                              1               5

aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct   163
Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
                10                  15                  20

tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc   211
Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
            25                  30                  35

acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa   259
Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu
        40                  45                  50

cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca   307
His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro
    55                  60                  65

cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc   355
Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile
70                  75                  80                  85

gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg   403
```

```
Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu
                 90                  95                 100

atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc   451
Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser
            105                 110                 115

cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa gaa gaa gca   499
Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu Glu Glu Ala
        120                 125                 130

acc gtc ggc gag atc atc gac cgc ctc cgt atc gct ggt gat tcc ggt   547
Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile Ala Gly Asp Ser Gly
    135                 140                 145

tcc gga atc ctg cgc atc gac ggc gaa ctc ggc tcc cgc taaattcccc    596
Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly Ser Arg
150                 155                 160

gcagttttta atg                                                   609
```

Sequence Listing

<210> 340
<211> 162
<212> PRT
<213> Corynebacterium glutamicum

<400> 340

```
Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
  1               5                  10                  15

Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu
             20                  25                  30

Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
         35                  40                  45

Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
     50                  55                  60

Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp
 65                  70                  75                  80

Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln
                 85                  90                  95

Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu
            100                 105                 110

Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln
        115                 120                 125

Ile Glu Glu Glu Ala Thr Val Gly Glu Ile Ile Asp Arg Leu Arg Ile
    130                 135                 140

Ala Gly Asp Ser Gly Ser Gly Ile Leu Arg Ile Asp Gly Glu Leu Gly
145                 150                 155                 160

Ser Arg
```

<210> 341
<211> 490
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(490)
<223> FRXA01997

<400> 341
aaaaaggtgg gaaacttagc caatccaaag cccaaaaatg cgggttatgc tgcgctaacc 60

tatgctgaca gccttgcgga agttgtgtac gttaggggcc atg aca atc aac gag 115
Met Thr Ile Asn Glu
1 5

aag atc gca tca gct ttc aac aac caa gtg act gca gag ctt gaa gct 163
Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr Ala Glu Leu Glu Ala
10 15 20

tca atg gtg tac ctt cag ctc tcc tac gtt cta gac gat ctg ggc ctc 211
Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu Asp Asp Leu Gly Leu
25 30 35

acc ggc atg cgc gac tgg atg aag gca cag agc aaa gaa gag ctc gaa 259
Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser Lys Glu Glu Leu Glu
40 45 50

cac gca cag aag ttc gct cag cac ctt ctt gac cgt gac tac acc cca 307
His Ala Gln Lys Phe Ala Gln His Leu Leu Asp Arg Asp Tyr Thr Pro
55 60 65

cag atc ggt gac att gca cca cca aag ctt gat gtc acc tcc gct atc 355
Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp Val Thr Ser Ala Ile
70 75 80 85

gag gct ttc gag gct tcc ctg gca cac gag cag aag atc tcc ggc ctg 403
Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln Lys Ile Ser Gly Leu
90 95 100

atc cgc gag ctc gct gcc atc cag gac gct gag aag gac tac gat tcc 451
Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu Lys Asp Tyr Asp Ser
105 110 115

cgc gca ctg atc gac tgg ttc ctc aac gag cag atc gaa 490
Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln Ile Glu
120 125 130

<210> 342
<211> 130
<212> PRT
<213> Corynebacterium glutamicum

<400> 342
Met Thr Ile Asn Glu Lys Ile Ala Ser Ala Phe Asn Asn Gln Val Thr
1 5 10 15

Ala Glu Leu Glu Ala Ser Met Val Tyr Leu Gln Leu Ser Tyr Val Leu

```
            20                  25                  30

Asp Asp Leu Gly Leu Thr Gly Met Arg Asp Trp Met Lys Ala Gln Ser
         35                  40                  45

Lys Glu Glu Leu Glu His Ala Gln Lys Phe Ala Gln His Leu Leu Asp
     50                  55                  60

Arg Asp Tyr Thr Pro Gln Ile Gly Asp Ile Ala Pro Pro Lys Leu Asp
 65                  70                  75                  80

Val Thr Ser Ala Ile Glu Ala Phe Glu Ala Ser Leu Ala His Glu Gln
                 85                  90                  95

Lys Ile Ser Gly Leu Ile Arg Glu Leu Ala Ala Ile Gln Asp Ala Glu
            100                 105                 110

Lys Asp Tyr Asp Ser Arg Ala Leu Ile Asp Trp Phe Leu Asn Glu Gln
        115                 120                 125

Ile Glu
    130
```

09693454.090305

<210> 343
<211> 783
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> RXA01082

<400> 343
ggccttgctt gcgttagttg cagtgcttcc tgaatatgct tctgaaacgg ttgtcgagca 60

```
cacttatcaa acatcggcgg cgaattaaga aggtgaacag ttg acg cag tgg ggt   115
                                            Leu Thr Gln Trp Gly
                                              1               5

aat tcg aat gtt gtg gag gac tat ctc aca gca ctt ttc cgt gca gaa   163
Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala Leu Phe Arg Ala Glu
                 10                  15                  20

gaa tgg gat gag gaa cca aca aca gga aaa ctc gct gaa gta att gga   211
Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu Ala Glu Val Ile Gly
             25                  30                  35

gtt acc gca tca acg gtg tcg gcg acg ctc aaa aaa ctc aac cct gag   259
Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys Lys Leu Asn Pro Glu
         40                  45                  50

ggc ttc gtc aat tac cgt ccc tac ggg gac atc gag ctg acg ccc gca   307
Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile Glu Leu Thr Pro Ala
     55                  60                  65

ggt cga gac atc gcc atc aac gtg atc agg cgg cgc cgg atc att gag   355
Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg Arg Arg Ile Ile Glu
 70                  75                  80                  85
```

```
acc tat ctg tct gag aag ctt gga tta ggc gct cat gaa cta cac ggc   403
Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala His Glu Leu His Gly
                 90                  95                 100

gag gca gat tta tta gag cac gca gtg tct cca ctg gtg ttg gag aag   451
Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro Leu Val Leu Glu Lys
            105                 110                 115

atg ttt cag gca gtg ggc tat cca acg ttg gat cct cac ggg gat ccc   499
Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp Pro His Gly Asp Pro
        120                 125                 130

atc ccc acc gaa tct ggg gag atg acc atc aat gat gga ctc atg ctt   547
Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn Asp Gly Leu Met Leu
    135                 140                 145

ttg gga cta aaa gct ggc gca tct gcc acg gtt aca cgt gtt agg gac   595
Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val Thr Arg Val Arg Asp
150                 155                 160                 165

gga aac cca tca gtg gtt cgg tac ctc act gga gtg gga att acc gtg   643
Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly Val Gly Ile Thr Val
                170                 175                 180

ggc aca acg gtc acg gtc gtt gaa gct ctt agc gat att gcc aca ctg   691
Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser Asp Ile Ala Thr Leu
            185                 190                 195

cgc ctg cag atc ggg gaa atg ttt caa gac att ccc ctt gca gtg gca   739
Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile Pro Leu Ala Val Ala
        200                 205                 210

aac gca gtg cgc gta tca cgt tagttcagcg tgcccagcgc gct             783
Asn Ala Val Arg Val Ser Arg
    215                 220
```

Applicant's Copy

<210> 344
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 344

```
Leu Thr Gln Trp Gly Asn Ser Asn Val Val Glu Asp Tyr Leu Thr Ala
  1               5                  10                  15

Leu Phe Arg Ala Glu Glu Trp Asp Glu Glu Pro Thr Thr Gly Lys Leu
             20                  25                  30

Ala Glu Val Ile Gly Val Thr Ala Ser Thr Val Ser Ala Thr Leu Lys
         35                  40                  45

Lys Leu Asn Pro Glu Gly Phe Val Asn Tyr Arg Pro Tyr Gly Asp Ile
     50                  55                  60

Glu Leu Thr Pro Ala Gly Arg Asp Ile Ala Ile Asn Val Ile Arg Arg
 65                  70                  75                  80

Arg Arg Ile Ile Glu Thr Tyr Leu Ser Glu Lys Leu Gly Leu Gly Ala
                 85                  90                  95
```

```
His Glu Leu His Gly Glu Ala Asp Leu Leu Glu His Ala Val Ser Pro
            100                 105                 110

Leu Val Leu Glu Lys Met Phe Gln Ala Val Gly Tyr Pro Thr Leu Asp
        115                 120                 125

Pro His Gly Asp Pro Ile Pro Thr Glu Ser Gly Glu Met Thr Ile Asn
    130                 135                 140

Asp Gly Leu Met Leu Leu Gly Leu Lys Ala Gly Ala Ser Ala Thr Val
145                 150                 155                 160

Thr Arg Val Arg Asp Gly Asn Pro Ser Val Val Arg Tyr Leu Thr Gly
                165                 170                 175

Val Gly Ile Thr Val Gly Thr Thr Val Thr Val Val Glu Ala Leu Ser
            180                 185                 190

Asp Ile Ala Thr Leu Arg Leu Gln Ile Gly Glu Met Phe Gln Asp Ile
        195                 200                 205

Pro Leu Ala Val Ala Asn Ala Val Arg Val Ser Arg
    210                 215                 220
```

Sequence Page

<210> 345
<211> 1068
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1045)
<223> RXA01236

<400> 345

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tttccaccag ttaagatgtt gtgagacaaa tccaaacata gaagggctgt gcattctcat 60

ggtttcaacc acaacatctc gctcaatcgc tggactgtca gtg ctt gtg gca aca   115
                                            Val Leu Val Ala Thr
                                              1               5

gca cta atc gct ggc tgt agt tcc gca gag gat ggg acg gtt gac tcg   163
Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp Gly Thr Val Asp Ser
                 10                  15                  20

ggg agc agc aca gag gtc acc aca acc caa agc aag gaa ggt ttt cct   211
Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser Lys Glu Gly Phe Pro
             25                  30                  35

gtc acc gtc acg ttt gcc cca gaa gca cct gtg acc att gag gat caa   259
Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val Thr Ile Glu Asp Gln
         40                  45                  50

cca gag cgc atc gtc agt ttg tcc cca gcg att aca gaa acc ttg ttc   307
Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile Thr Glu Thr Leu Phe
     55                  60                  65

gct gtc ggg gca ggg gat cat gtc gtc gca gtg gat gaa tac tca aac   355
Ala Val Gly Ala Gly Asp His Val Val Ala Val Asp Glu Tyr Ser Asn
 70                  75                  80                  85
```

```
tac cca gag gac gca ccg ctg gtg cag ggt ctg tct ggt ttt act ccc   403
Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu Ser Gly Phe Thr Pro
                 90                  95                 100

aat gtg gag tcc atc ttg gat tac gat cct gac ctg gtc gtg ttg atg   451
Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp Leu Val Val Leu Met
            105                 110                 115

tct gca gat gat tcc att ttg acc ggc ctg gat gct gca gga gtg gat   499
Ser Ala Asp Asp Ser Ile Leu Thr Gly Leu Asp Ala Ala Gly Val Asp
        120                 125                 130

act tta gtg atc ccc gca gca gag aac ttg gat gag acc tac tcc cag   547
Thr Leu Val Ile Pro Ala Ala Glu Asn Leu Asp Glu Thr Tyr Ser Gln
    135                 140                 145

att gaa caa gta ggt cga gcc acc gga ttt gaa gat caa gca aca acg   595
Ile Glu Gln Val Gly Arg Ala Thr Gly Phe Glu Asp Gln Ala Thr Thr
150                 155                 160                 165

gtt gtt gat cag atg aaa acc gcc att gat gct gca gtt gcc aca gtt   643
Val Val Asp Gln Met Lys Thr Ala Ile Asp Ala Ala Val Ala Thr Val
                170                 175                 180

cct gaa gag gta aaa gag cag ggc tta acc tac ttc cac gag ctg ggc   691
Pro Glu Glu Val Lys Glu Gln Gly Leu Thr Tyr Phe His Glu Leu Gly
            185                 190                 195

agt gat ttg ttc act gtg tca gag caa acc tac atc ggt cag att tac   739
Ser Asp Leu Phe Thr Val Ser Glu Gln Thr Tyr Ile Gly Gln Ile Tyr
        200                 205                 210

gac atg ttt ggt ctc acc tct att gct gac ggt ggc gac gct tac tcg   787
Asp Met Phe Gly Leu Thr Ser Ile Ala Asp Gly Gly Asp Ala Tyr Ser
    215                 220                 225

cag cta tcc aac gaa gca atc att gcg gca aac cct gat ctg att ttc   835
Gln Leu Ser Asn Glu Ala Ile Ile Ala Ala Asn Pro Asp Leu Ile Phe
230                 235                 240                 245

ctc agc gat gcc aag gcc gaa aac ctc act gca gaa gat att gcg gcg   883
Leu Ser Asp Ala Lys Ala Glu Asn Leu Thr Ala Glu Asp Ile Ala Ala
                250                 255                 260

cgt cca ggc tgg gac acc att gat gca gta gcc aat gga cgt atc tac   931
Arg Pro Gly Trp Asp Thr Ile Asp Ala Val Ala Asn Gly Arg Ile Tyr
            265                 270                 275

att ttg gac gat gat att gct tcc agg tgg gga cct cgc gta tcc cag   979
Ile Leu Asp Asp Asp Ile Ala Ser Arg Trp Gly Pro Arg Val Ser Gln
        280                 285                 290

ctg gtg gaa gaa atc gca gcg cag ttg aat cag ctt gct tct tct gaa   1027
Leu Val Glu Glu Ile Ala Ala Gln Leu Asn Gln Leu Ala Ser Ser Glu
    295                 300                 305

gct gtg ccg gcc gct gct taagttttcg tgctgaagag aat                1068
Ala Val Pro Ala Ala Ala
310                 315
```

<210> 346
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 346

```
Val Leu Val Ala Thr Ala Leu Ile Ala Gly Cys Ser Ser Ala Glu Asp
  1               5                  10                  15

Gly Thr Val Asp Ser Gly Ser Ser Thr Glu Val Thr Thr Thr Gln Ser
            20                  25                  30

Lys Glu Gly Phe Pro Val Thr Val Thr Phe Ala Pro Glu Ala Pro Val
         35                  40                  45

Thr Ile Glu Asp Gln Pro Glu Arg Ile Val Ser Leu Ser Pro Ala Ile
     50                  55                  60

Thr Glu Thr Leu Phe Ala Val Gly Ala Gly Asp His Val Val Ala Val
 65                  70                  75                  80

Asp Glu Tyr Ser Asn Tyr Pro Glu Asp Ala Pro Leu Val Gln Gly Leu
                85                  90                  95

Ser Gly Phe Thr Pro Asn Val Glu Ser Ile Leu Asp Tyr Asp Pro Asp
            100                 105                 110

Leu Val Val Leu Met Ser Ala Asp Asp Ser Ile Leu Thr Gly Leu Asp
        115                 120                 125

Ala Ala Gly Val Asp Thr Leu Val Ile Pro Ala Ala Glu Asn Leu Asp
    130                 135                 140

Glu Thr Tyr Ser Gln Ile Glu Gln Val Gly Arg Ala Thr Gly Phe Glu
145                 150                 155                 160

Asp Gln Ala Thr Thr Val Val Asp Gln Met Lys Thr Ala Ile Asp Ala
                165                 170                 175

Ala Val Ala Thr Val Pro Glu Glu Val Lys Glu Gln Gly Leu Thr Tyr
            180                 185                 190

Phe His Glu Leu Gly Ser Asp Leu Phe Thr Val Ser Glu Gln Thr Tyr
        195                 200                 205

Ile Gly Gln Ile Tyr Asp Met Phe Gly Leu Thr Ser Ile Ala Asp Gly
    210                 215                 220

Gly Asp Ala Tyr Ser Gln Leu Ser Asn Glu Ala Ile Ile Ala Ala Asn
225                 230                 235                 240

Pro Asp Leu Ile Phe Leu Ser Asp Ala Lys Ala Glu Asn Leu Thr Ala
                245                 250                 255

Glu Asp Ile Ala Ala Arg Pro Gly Trp Asp Thr Ile Asp Ala Val Ala
            260                 265                 270

Asn Gly Arg Ile Tyr Ile Leu Asp Asp Asp Ile Ala Ser Arg Trp Gly
        275                 280                 285
```

```
Pro Arg Val Ser Gln Leu Val Glu Glu Ile Ala Ala Gln Leu Asn Gln
    290                 295                 300

Leu Ala Ser Ser Glu Ala Val Pro Ala Ala Ala
305                 310                 315


<210> 347
<211> 1059
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1036)
<223> RXA01354

<400> 347
tcggcgccat gcgccttcca aaaaggcatt gcttttcgac gtccccctac gcttcgattt 60

tgcaaaatta tttaggcaag gctacctttt gcctatgcat atg aag att agc cgg   115
                                            Met Lys Ile Ser Arg
                                              1               5

cgc gca ttc ctc ggc aca ctg ctc ggc gcc acc acc ctt gct gta act   163
Arg Ala Phe Leu Gly Thr Leu Leu Gly Ala Thr Thr Leu Ala Val Thr
                 10                  15                  20

gcc tgc gcg caa tcc tct caa aac caa aac tcc tcc gct tcc tca tct   211
Ala Cys Ala Gln Ser Ser Gln Asn Gln Asn Ser Ser Ala Ser Ser Ser
             25                  30                  35

tct tca tcc tca gcg gaa tca agc acc tct tca tcc tcc tcc gat gaa   259
Ser Ser Ser Ser Ala Glu Ser Ser Thr Ser Ser Ser Ser Ser Asp Glu
         40                  45                  50

cag cgc atc gtc gcc ctc aac acc ggt cag ttg gac aac ctc ctc ctt   307
Gln Arg Ile Val Ala Leu Asn Thr Gly Gln Leu Asp Asn Leu Leu Leu
     55                  60                  65

ctc ggc atc acc cca gtg ggc gtc gcc gct gca aaa aac tct gac ctg   355
Leu Gly Ile Thr Pro Val Gly Val Ala Ala Ala Lys Asn Ser Asp Leu
 70                  75                  80                  85

atc cca cag ttc ctc aag gat cgc ttc ggt gca gac atg gac ttg gac   403
Ile Pro Gln Phe Leu Lys Asp Arg Phe Gly Ala Asp Met Asp Leu Asp
                 90                  95                 100

agc atc gcc gac tgc ggt ctc cgc caa tct cca gac atc gaa gcc atc   451
Ser Ile Ala Asp Cys Gly Leu Arg Gln Ser Pro Asp Ile Glu Ala Ile
            105                 110                 115

gcg aac ctc aac ccc acc ctg atc tgc gca aac tcc cgc gcc gac gaa   499
Ala Asn Leu Asn Pro Thr Leu Ile Cys Ala Asn Ser Arg Ala Asp Glu
        120                 125                 130

gag gtc ctc aac aaa ctc cgc acg atc gcc ccc gtg gtc acc ggc gaa   547
Glu Val Leu Asn Lys Leu Arg Thr Ile Ala Pro Val Val Thr Gly Glu
    135                 140                 145

ggt ggc ggt gaa aac tgg aag caa gac ctc ctc acc atc gca gag gca   595
```

```
Gly Gly Gly Glu Asn Trp Lys Gln Asp Leu Leu Thr Ile Ala Glu Ala
150                 155                 160                 165

gca ggc cag aag gaa aag gct gaa acc ctc ctg aaa tca tac gag gac   643
Ala Gly Gln Lys Glu Lys Ala Glu Thr Leu Leu Lys Ser Tyr Glu Asp
                170                 175                 180

tca gca gcc gaa atc gcc gca aac cag cct gcg aac cca cca acc gtt   691
Ser Ala Ala Glu Ile Ala Ala Asn Gln Pro Ala Asn Pro Pro Thr Val
            185                 190                 195

tcc ttc ctg cgc acc aaa gat cag gaa ttc cag atg tac ggc gca caa   739
Ser Phe Leu Arg Thr Lys Asp Gln Glu Phe Gln Met Tyr Gly Ala Gln
        200                 205                 210

tcc atg gcc gga acg gtt gct gcc gat tgc ggt tac gcc cgc cca gaa   787
Ser Met Ala Gly Thr Val Ala Ala Asp Cys Gly Tyr Ala Arg Pro Glu
    215                 220                 225

aac cag cag ttc acc gac acg gca ggt caa gac ctc tcc gct gag ctc   835
Asn Gln Gln Phe Thr Asp Thr Ala Gly Gln Asp Leu Ser Ala Glu Leu
230                 235                 240                 245

att gcc caa gct gat gcc gac tgg ctt ttc tac ggc atc aaa gaa ggc   883
Ile Ala Gln Ala Asp Ala Asp Trp Leu Phe Tyr Gly Ile Lys Glu Gly
                250                 255                 260

aac atc aac cct gaa gac acc cca ttg tgg act tca ctc aaa gcg gtt   931
Asn Ile Asn Pro Glu Asp Thr Pro Leu Trp Thr Ser Leu Lys Ala Val
            265                 270                 275

cag tcc aac caa gca atc cca gtt gac ggc gat tcc tgg tac ctc aac   979
Gln Ser Asn Gln Ala Ile Pro Val Asp Gly Asp Ser Trp Tyr Leu Asn
        280                 285                 290

gca tcc ctc gtg tcg gct gaa atc atc ctc caa ggc ctc aaa gac aac   1027
Ala Ser Leu Val Ser Ala Glu Ile Ile Leu Gln Gly Leu Lys Asp Asn
    295                 300                 305

gtc acc gtc taagccgatt taagggcctc aaa                            1059
Val Thr Val
310
```

<210> 348
<211> 312
<212> PRT
<213> Corynebacterium glutamicum

<400> 348

```
Met Lys Ile Ser Arg Arg Ala Phe Leu Gly Thr Leu Leu Gly Ala Thr
  1               5                  10                  15

Thr Leu Ala Val Thr Ala Cys Ala Gln Ser Ser Gln Asn Gln Asn Ser
             20                  25                  30

Ser Ala Ser Ser Ser Ser Ser Ser Ser Ala Glu Ser Ser Thr Ser Ser
         35                  40                  45

Ser Ser Ser Asp Glu Gln Arg Ile Val Ala Leu Asn Thr Gly Gln Leu
     50                  55                  60
```

```
Asp Asn Leu Leu Leu Leu Gly Ile Thr Pro Val Gly Val Ala Ala Ala
 65                  70                  75                  80

Lys Asn Ser Asp Leu Ile Pro Gln Phe Leu Lys Asp Arg Phe Gly Ala
                 85                  90                  95

Asp Met Asp Leu Asp Ser Ile Ala Asp Cys Gly Leu Arg Gln Ser Pro
            100                 105                 110

Asp Ile Glu Ala Ile Ala Asn Leu Asn Pro Thr Leu Ile Cys Ala Asn
        115                 120                 125

Ser Arg Ala Asp Glu Glu Val Leu Asn Lys Leu Arg Thr Ile Ala Pro
    130                 135                 140

Val Val Thr Gly Glu Gly Gly Gly Glu Asn Trp Lys Gln Asp Leu Leu
145                 150                 155                 160

Thr Ile Ala Glu Ala Ala Gly Gln Lys Glu Lys Ala Glu Thr Leu Leu
                165                 170                 175

Lys Ser Tyr Glu Asp Ser Ala Ala Glu Ile Ala Ala Asn Gln Pro Ala
            180                 185                 190

Asn Pro Pro Thr Val Ser Phe Leu Arg Thr Lys Asp Gln Glu Phe Gln
        195                 200                 205

Met Tyr Gly Ala Gln Ser Met Ala Gly Thr Val Ala Ala Asp Cys Gly
    210                 215                 220

Tyr Ala Arg Pro Glu Asn Gln Gln Phe Thr Asp Thr Ala Gly Gln Asp
225                 230                 235                 240

Leu Ser Ala Glu Leu Ile Ala Gln Ala Asp Ala Asp Trp Leu Phe Tyr
                245                 250                 255

Gly Ile Lys Glu Gly Asn Ile Asn Pro Glu Asp Thr Pro Leu Trp Thr
            260                 265                 270

Ser Leu Lys Ala Val Gln Ser Asn Gln Ala Ile Pro Val Asp Gly Asp
        275                 280                 285

Ser Trp Tyr Leu Asn Ala Ser Leu Val Ser Ala Glu Ile Ile Leu Gln
    290                 295                 300

Gly Leu Lys Asp Asn Val Thr Val
305                 310
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<210> 349
<211> 1071
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1048)
<223> RXA01620

<400> 349

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cggccgagca gtaaacttgc aggtcaatgc aacttttaa ccgtagaaag ttatggccaa 60

agactggcaa taggttaaga acttgcgtta ggatagccta atg caa tct att cga   115
                                            Met Gln Ser Ile Arg
                                              1               5

acg acc ttc agg tcg ctt tca cgc agc gca gtt atc gtg ggt acc gtt   163
Thr Thr Phe Arg Ser Leu Ser Arg Ser Ala Val Ile Val Gly Thr Val
                 10                  15                  20

ttg gct ttg ggt atc gca gga tgt tcc acg gcc agt gat gaa gcc aca   211
Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala Ser Asp Glu Ala Thr
             25                  30                  35

agc acc agc gac gat gta gct gtc ggc ggc cgc cta ttt tct aca gcg   259
Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg Leu Phe Ser Thr Ala
         40                  45                  50

gat tcc gcc acc gcc gct ctg gga agc gac gcc gaa cca ggc caa ttc   307
Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala Glu Pro Gly Gln Phe
     55                  60                  65

ccc cgc acc gtt gtg cat tca cgc ggc gaa act acc ctt gag cag cag   355
Pro Arg Thr Val Val His Ser Arg Gly Glu Thr Thr Leu Glu Gln Gln
 70                  75                  80                  85

cca caa cga gtc gtg gtt ctc gac agc ggt gaa atc gac cag gtt ttg   403
Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu Ile Asp Gln Val Leu
                 90                  95                 100

agc ctc ggc gtg act ccc gtc ggc atc gcc agc ccg aaa gac gcc tcc   451
Ser Leu Gly Val Thr Pro Val Gly Ile Ala Ser Pro Lys Asp Ala Ser
             105                 110                 115

agc cag ccc gct tac ctc gaa aat cag ctg gca gat gta caa act gtg   499
Ser Gln Pro Ala Tyr Leu Glu Asn Gln Leu Ala Asp Val Gln Thr Val
         120                 125                 130

ggc acc acg agt gag ctc aat ttc gaa gcc atc gcc gcc ctc aag cct   547
Gly Thr Thr Ser Glu Leu Asn Phe Glu Ala Ile Ala Ala Leu Lys Pro
     135                 140                 145

gac ctg att ctg ggc agc aag ctg cgc gtc gac gaa tcc tac gat cag   595
Asp Leu Ile Leu Gly Ser Lys Leu Arg Val Asp Glu Ser Tyr Asp Gln
150                 155                 160                 165

ctc tcc caa atc gca cca acc gtg ctg agt att cgc ccc gga ttc ccc   643
Leu Ser Gln Ile Ala Pro Thr Val Leu Ser Ile Arg Pro Gly Phe Pro
                 170                 175                 180

tgg aag gaa aac ttc ctc ctc acc gcc gac gcg ctc ggt ctc gag ggc   691
Trp Lys Glu Asn Phe Leu Leu Thr Ala Asp Ala Leu Gly Leu Glu Gly
             185                 190                 195

aaa gcc gtc gag gtt ctc aac gag tac caa acc cat gtc gat gca gtc   739
Lys Ala Val Glu Val Leu Asn Glu Tyr Gln Thr His Val Asp Ala Val
         200                 205                 210

cgc gag acc atc gac ggc agc cca gaa atc tca ctc gtc cgc ttc atg   787
Arg Glu Thr Ile Asp Gly Ser Pro Glu Ile Ser Leu Val Arg Phe Met
     215                 220                 225
```

```
cct ggt cgc acc cgc ctg tac gga aac ctc tct ttc atc ggt gca atc   835
Pro Gly Arg Thr Arg Leu Tyr Gly Asn Leu Ser Phe Ile Gly Ala Ile
230                 235                 240                 245

ctt aag gac ctg ggg ctt tct cgc cca gag atc caa aat atc gac gat   883
Leu Lys Asp Leu Gly Leu Ser Arg Pro Glu Ile Gln Asn Ile Asp Asp
                250                 255                 260

ctt gcc gtg gag atc tcc ccc gaa aac atc acc gat gcc aac ggc gac   931
Leu Ala Val Glu Ile Ser Pro Glu Asn Ile Thr Asp Ala Asn Gly Asp
            265                 270                 275

tgg att ttc tac tcc acc tac ggc aag ccc gag gcc acc gag cag gac   979
Trp Ile Phe Tyr Ser Thr Tyr Gly Lys Pro Glu Ala Thr Glu Gln Asp
        280                 285                 290

aac att ttg tcc aac gag ctg tgg cac aac ctt ccc cgc cgt cca aga   1027
Asn Ile Leu Ser Asn Glu Leu Trp His Asn Leu Pro Arg Arg Pro Arg
    295                 300                 305

agg tca tgc cct gga ggt caa tgacgagagc tggttcatgg ggt             1071
Arg Ser Cys Pro Gly Gly Gln
310                 315
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<210> 350
<211> 316
<212> PRT
<213> Corynebacterium glutamicum

<400> 350

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Met Gln Ser Ile Arg Thr Thr Phe Arg Ser Leu Ser Arg Ser Ala Val
  1               5                  10                  15

Ile Val Gly Thr Val Leu Ala Leu Gly Ile Ala Gly Cys Ser Thr Ala
             20                  25                  30

Ser Asp Glu Ala Thr Ser Thr Ser Asp Asp Val Ala Val Gly Gly Arg
         35                  40                  45

Leu Phe Ser Thr Ala Asp Ser Ala Thr Ala Ala Leu Gly Ser Asp Ala
     50                  55                  60

Glu Pro Gly Gln Phe Pro Arg Thr Val Val His Ser Arg Gly Glu Thr
 65                  70                  75                  80

Thr Leu Glu Gln Gln Pro Gln Arg Val Val Val Leu Asp Ser Gly Glu
                 85                  90                  95

Ile Asp Gln Val Leu Ser Leu Gly Val Thr Pro Val Gly Ile Ala Ser
            100                 105                 110

Pro Lys Asp Ala Ser Ser Gln Pro Ala Tyr Leu Glu Asn Gln Leu Ala
        115                 120                 125

Asp Val Gln Thr Val Gly Thr Thr Ser Glu Leu Asn Phe Glu Ala Ile
    130                 135                 140

Ala Ala Leu Lys Pro Asp Leu Ile Leu Gly Ser Lys Leu Arg Val Asp
145                 150                 155                 160
```

```
Glu Ser Tyr Asp Gln Leu Ser Gln Ile Ala Pro Thr Val Leu Ser Ile
                165                 170                 175

Arg Pro Gly Phe Pro Trp Lys Glu Asn Phe Leu Leu Thr Ala Asp Ala
            180                 185                 190

Leu Gly Leu Glu Gly Lys Ala Val Glu Val Leu Asn Glu Tyr Gln Thr
        195                 200                 205

His Val Asp Ala Val Arg Glu Thr Ile Asp Gly Ser Pro Glu Ile Ser
    210                 215                 220

Leu Val Arg Phe Met Pro Gly Arg Thr Arg Leu Tyr Gly Asn Leu Ser
225                 230                 235                 240

Phe Ile Gly Ala Ile Leu Lys Asp Leu Gly Leu Ser Arg Pro Glu Ile
                245                 250                 255

Gln Asn Ile Asp Asp Leu Ala Val Glu Ile Ser Pro Glu Asn Ile Thr
            260                 265                 270

Asp Ala Asn Gly Asp Trp Ile Phe Tyr Ser Thr Tyr Gly Lys Pro Glu
        275                 280                 285

Ala Thr Glu Gln Asp Asn Ile Leu Ser Asn Glu Leu Trp His Asn Leu
    290                 295                 300

Pro Arg Arg Pro Arg Arg Ser Cys Pro Gly Gly Gln
305                 310                 315


<210> 351
<211> 915
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(892)
<223> RXA02052

<400> 351
cctcggcgtc gcactccttc taagctcctg ttcttcaaca tcttccgatg aatcaatcca 60

acctgaagtt gccagcactg gatattcagt ggagcacgca atg ggc acc acc gaa   115
                                              Met Gly Thr Thr Glu
                                                1               5

atc cct gaa acc cca acg cgt gtg gtc gtc att gat tcc cca cac ctc   163
Ile Pro Glu Thr Pro Thr Arg Val Val Val Ile Asp Ser Pro His Leu
                10                  15                  20

gac gca ctt ttg gct ttg gga att act cca gtc gga gct acg gaa tct   211
Asp Ala Leu Leu Ala Leu Gly Ile Thr Pro Val Gly Ala Thr Glu Ser
            25                  30                  35

gga tcc gaa aat ggt ttc ccc gcc tac ttg gct gac gag cta aaa gac   259
Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala Asp Glu Leu Lys Asp
        40                  45                  50
```

```
acc gaa tct gtt ggg ctg aca tct gag cca aat ttg gaa aag atc gcc   307
Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn Leu Glu Lys Ile Ala
     55                  60                  65

gca ctg gat ccg gat ttg atc att ggc gca aag gtc cgc cac gag gct   355
Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys Val Arg His Glu Ala
 70                  75                  80                  85

att tat gat cag ctt tca gac atc gca cca acc gtg atg tcc gaa ggt   403
Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr Val Met Ser Glu Gly
                 90                  95                 100

tcc ggc aca aac tgg aat gaa cag gca gaa atc act gcg gca gca gta   451
Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile Thr Ala Ala Ala Val
            105                 110                 115

aac aag tct gat gag atg gac aaa ctg atc tca gac ttg gac acc cgt   499
Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser Asp Leu Asp Thr Arg
        120                 125                 130

gcc aca gag ctt ggt gaa gag atc ggt gct gac gga caa acc gct tca   547
Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp Gly Gln Thr Ala Ser
    135                 140                 145

atg gtt cga ttc cgc acg gac aac ttc agg ctc tat ggt ccc gag acc   595
Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu Tyr Gly Pro Glu Thr
150                 155                 160                 165

ttc tct ggt tca gtt ctg gaa caa gtt gga ttt gac ctg ggg gaa cgt   643
Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe Asp Leu Gly Glu Arg
                170                 175                 180

gat tgg aat gag tac tcc atg atg gag cta tcc tca gaa aac ttt ggg   691
Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser Ser Glu Asn Phe Gly
            185                 190                 195

cag atc gat gga gac ctt att ttc tac acc atc cca gga tcc cct gaa   739
Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile Pro Gly Ser Pro Glu
        200                 205                 210

gca acc act tat cca aag att tcc gaa ctg tgg gtt gat tca cca gca   787
Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp Val Asp Ser Pro Ala
    215                 220                 225

gtt cgg caa ggt aga act tac gag ttt gaa gac gaa acc tgg atg gtc   835
Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp Glu Thr Trp Met Val
230                 235                 240                 245

ggc atc ggt gta tta ggt gcc aat gaa atc ttg gat gac ctg gaa gaa   883
Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu Asp Asp Leu Glu Glu
                250                 255                 260

act ctg agc tagtttcctt taggccaagc aac                            915
Thr Leu Ser
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<210> 352
<211> 264
<212> PRT
<213> Corynebacterium glutamicum

<400> 352
Met Gly Thr Thr Glu Ile Pro Glu Thr Pro Thr Arg Val Val Val Ile
1 5 10 15

Asp Ser Pro His Leu Asp Ala Leu Leu Ala Leu Gly Ile Thr Pro Val
20 25 30

Gly Ala Thr Glu Ser Gly Ser Glu Asn Gly Phe Pro Ala Tyr Leu Ala
35 40 45

Asp Glu Leu Lys Asp Thr Glu Ser Val Gly Leu Thr Ser Glu Pro Asn
50 55 60

Leu Glu Lys Ile Ala Ala Leu Asp Pro Asp Leu Ile Ile Gly Ala Lys
65 70 75 80

Val Arg His Glu Ala Ile Tyr Asp Gln Leu Ser Asp Ile Ala Pro Thr
85 90 95

Val Met Ser Glu Gly Ser Gly Thr Asn Trp Asn Glu Gln Ala Glu Ile
100 105 110

Thr Ala Ala Ala Val Asn Lys Ser Asp Glu Met Asp Lys Leu Ile Ser
115 120 125

Asp Leu Asp Thr Arg Ala Thr Glu Leu Gly Glu Glu Ile Gly Ala Asp
130 135 140

Gly Gln Thr Ala Ser Met Val Arg Phe Arg Thr Asp Asn Phe Arg Leu
145 150 155 160

Tyr Gly Pro Glu Thr Phe Ser Gly Ser Val Leu Glu Gln Val Gly Phe
165 170 175

Asp Leu Gly Glu Arg Asp Trp Asn Glu Tyr Ser Met Met Glu Leu Ser
180 185 190

Ser Glu Asn Phe Gly Gln Ile Asp Gly Asp Leu Ile Phe Tyr Thr Ile
195 200 205

Pro Gly Ser Pro Glu Ala Thr Thr Tyr Pro Lys Ile Ser Glu Leu Trp
210 215 220

Val Asp Ser Pro Ala Val Arg Gln Gly Arg Thr Tyr Glu Phe Glu Asp
225 230 235 240

Glu Thr Trp Met Val Gly Ile Gly Val Leu Gly Ala Asn Glu Ile Leu
245 250 255

Asp Asp Leu Glu Glu Thr Leu Ser
260

<210> 353
<211> 1200
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS

<222> (101)..(1177)
<223> RXA00372

<400> 353
gcagacattt ccataagtcc tgcgaaatgc gcccattcat gtaaagatgt tatttcctcc 60

cccaaacact ccttaaaatt tcaagaaggg ccttattttc atg tct tcg aag cac 115
Met Ser Ser Lys His
1 5

cct ttg aag cgc act gcc gtt act gtt ttt gca ctc ggc gct tcc gct 163
Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala Leu Gly Ala Ser Ala
10 15 20

gct ctc ctc gtg gct tgc tct gaa cct tct gag gac gtt tcc acc gca 211
Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu Asp Val Ser Thr Ala
25 30 35

gag acc acc act gca agc tct tcc gct aac gca tcc gat gca gcc ggt 259
Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala Ser Asp Ala Ala Gly
40 45 50

gaa aaa gta acc atc acc gtc tac acc tct gag cct gag gaa aag gtc 307
Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu Pro Glu Glu Lys Val
55 60 65

gat gag atc aac aag gcg ttc atg gaa gcc aac cca gat att gag gtt 355
Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn Pro Asp Ile Glu Val
70 75 80 85

gag gtg tac cgc gct ggt act ggc gat ctg act gct cgc att gaa gct 403
Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr Ala Arg Ile Glu Ala
90 95 100

gaa aag gca tcc ggt tct atc gag gct gat gtg ttg tgg gct gcg gat 451
Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val Leu Trp Ala Ala Asp
105 110 115

gct gca acc ttt gaa act tat gca gca cag ggc gac ctt gca gag ctg 499
Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly Asp Leu Ala Glu Leu
120 125 130

gaa gat gtt gag act tcc gac atc att gaa gag gct ctg gat gct gag 547
Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu Ala Leu Asp Ala Glu
135 140 145

aac ttt tat gta ggc acc cgc atc atc cca acc gtg att gca tac aac 595
Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr Val Ile Ala Tyr Asn
150 155 160 165

act gaa gtt gtt gat cag gct gag ctt cct acg tct tgg gct gat ctg 643
Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr Ser Trp Ala Asp Leu
170 175 180

act gat cct aag tat gca ggc caa ctg gtc atg ccg gat cca gct gtg 691
Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met Pro Asp Pro Ala Val
185 190 195

tct ggt gct gca gcc ttc aat gct tct gtg tgg aag aac gac cct gcg 739
Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp Lys Asn Asp Pro Ala
200 205 210

```
ctt ggc gaa gcc tgg atc acc gcc ttg ggt gaa aac caa cca atg atc   787
Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu Asn Gln Pro Met Ile
    215                 220                 225

gct cag tcc aac ggc cca acc tcc cag gag atc gct ggc ggt ggc cac   835
Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile Ala Gly Gly Gly His
230                 235                 240                 245

cca gtg ggc atc gtg gtg gac tac ttg gtg cgc gac ttg gct gct gct   883
Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg Asp Leu Ala Ala Ala
                250                 255                 260

gga tct cca atc gac acc atc tac gca tcg gag ggt tct cct tac atc   931
Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu Gly Ser Pro Tyr Ile
            265                 270                 275

act gag cct gca ggt gtg ttc gct gat tct gaa aag aag gaa gca gcc   979
Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu Lys Lys Glu Ala Ala
        280                 285                 290

gag cgc tac atc aac ttc ctg ctg tct gtt gaa ggc cag gaa atc gca   1027
Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu Gly Gln Glu Ile Ala
    295                 300                 305

gtt gag cag gca tac ctg cca gtg cgt gaa gat gtc gga act cca gag   1075
Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp Val Gly Thr Pro Glu
310                 315                 320                 325

ggc acc ccc gag ttg gct gac atc gag ctc atg acc cct gac ctg gag   1123
Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met Thr Pro Asp Leu Glu
                330                 335                 340

gtt gta acc gct gat aag gcg gct gct gtt gag ttc ttc caa aac gca   1171
Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu Phe Phe Gln Asn Ala
            345                 350                 355

atg aac tagttttcct atgcagttat ctc                                1200
Met Asn
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Applicant's Copy

<210> 354
<211> 359
<212> PRT
<213> Corynebacterium glutamicum

<400> 354

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Met Ser Ser Lys His Pro Leu Lys Arg Thr Ala Val Thr Val Phe Ala
  1               5                  10                  15

Leu Gly Ala Ser Ala Ala Leu Leu Val Ala Cys Ser Glu Pro Ser Glu
             20                  25                  30

Asp Val Ser Thr Ala Glu Thr Thr Thr Ala Ser Ser Ser Ala Asn Ala
         35                  40                  45

Ser Asp Ala Ala Gly Glu Lys Val Thr Ile Thr Val Tyr Thr Ser Glu
     50                  55                  60

Pro Glu Glu Lys Val Asp Glu Ile Asn Lys Ala Phe Met Glu Ala Asn
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 65                  70                  75                  80

Pro Asp Ile Glu Val Glu Val Tyr Arg Ala Gly Thr Gly Asp Leu Thr
                 85                  90                  95

Ala Arg Ile Glu Ala Glu Lys Ala Ser Gly Ser Ile Glu Ala Asp Val
            100                 105                 110

Leu Trp Ala Ala Asp Ala Ala Thr Phe Glu Thr Tyr Ala Ala Gln Gly
        115                 120                 125

Asp Leu Ala Glu Leu Glu Asp Val Glu Thr Ser Asp Ile Ile Glu Glu
    130                 135                 140

Ala Leu Asp Ala Glu Asn Phe Tyr Val Gly Thr Arg Ile Ile Pro Thr
145                 150                 155                 160

Val Ile Ala Tyr Asn Thr Glu Val Val Asp Gln Ala Glu Leu Pro Thr
                165                 170                 175

Ser Trp Ala Asp Leu Thr Asp Pro Lys Tyr Ala Gly Gln Leu Val Met
            180                 185                 190

Pro Asp Pro Ala Val Ser Gly Ala Ala Ala Phe Asn Ala Ser Val Trp
        195                 200                 205

Lys Asn Asp Pro Ala Leu Gly Glu Ala Trp Ile Thr Ala Leu Gly Glu
    210                 215                 220

Asn Gln Pro Met Ile Ala Gln Ser Asn Gly Pro Thr Ser Gln Glu Ile
225                 230                 235                 240

Ala Gly Gly Gly His Pro Val Gly Ile Val Val Asp Tyr Leu Val Arg
                245                 250                 255

Asp Leu Ala Ala Ala Gly Ser Pro Ile Asp Thr Ile Tyr Ala Ser Glu
            260                 265                 270

Gly Ser Pro Tyr Ile Thr Glu Pro Ala Gly Val Phe Ala Asp Ser Glu
        275                 280                 285

Lys Lys Glu Ala Ala Glu Arg Tyr Ile Asn Phe Leu Leu Ser Val Glu
    290                 295                 300

Gly Gln Glu Ile Ala Val Glu Gln Ala Tyr Leu Pro Val Arg Glu Asp
305                 310                 315                 320

Val Gly Thr Pro Glu Gly Thr Pro Glu Leu Ala Asp Ile Glu Leu Met
                325                 330                 335

Thr Pro Asp Leu Glu Val Val Thr Ala Asp Lys Ala Ala Ala Val Glu
            340                 345                 350

Phe Phe Gln Asn Ala Met Asn
        355
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<210> 355
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXA00088

<400> 355
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agttttggtg gattattttt atagactttc aaaggacgac atg gtg aaa aac cga 115
Met Val Lys Asn Arg
1 5

ttc aag cta gtt tca atc gca act gtt gcg gcc ctg gcg ctc gtt ggc 163
Phe Lys Leu Val Ser Ile Ala Thr Val Ala Ala Leu Ala Leu Val Gly
10 15 20

tgc tct tcc acc gac agc acc tct tcc gag tct tct tcc gct gca gag 211
Cys Ser Ser Thr Asp Ser Thr Ser Ser Glu Ser Ser Ser Ala Ala Glu
25 30 35

tca acc gct gca gct agc acc ctg act atc gaa gac aac cac ggc acc 259
Ser Thr Ala Ala Ala Ser Thr Leu Thr Ile Glu Asp Asn His Gly Thr
40 45 50

gaa ggg atc tcc ctg cca atc gag ggc gtc gct gcg acc gac aac cgc 307
Glu Gly Ile Ser Leu Pro Ile Glu Gly Val Ala Ala Thr Asp Asn Arg
55 60 65

gca ttc gaa ctg ctt gat cgc tgg ggt gta gag ctc gtt gca gct cca 355
Ala Phe Glu Leu Leu Asp Arg Trp Gly Val Glu Leu Val Ala Ala Pro
70 75 80 85

ctt cag ctg gtt cca ttt acc gtt acg ggc tac acc gaa gag ggc ggc 403
Leu Gln Leu Val Pro Phe Thr Val Thr Gly Tyr Thr Glu Glu Gly Gly
90 95 100

gtc gct aac ctt ggc tcc cac cgc gag cca gac ctg gaa gca ctt gct 451
Val Ala Asn Leu Gly Ser His Arg Glu Pro Asp Leu Glu Ala Leu Ala
105 110 115

gct gca cag cct tcc ctg atc atc aac ggc cag cgc ttc gct cag tac 499
Ala Ala Gln Pro Ser Leu Ile Ile Asn Gly Gln Arg Phe Ala Gln Tyr
120 125 130

tac gat gac atc att gcc ctg aac cct gac gca acc gtt gtt gag cta 547
Tyr Asp Asp Ile Ile Ala Leu Asn Pro Asp Ala Thr Val Val Glu Leu
135 140 145

gac cca cgc gat ggc gag cca ctt gac cag gag ctt atc cgc cag gct 595
Asp Pro Arg Asp Gly Glu Pro Leu Asp Gln Glu Leu Ile Arg Gln Ala
150 155 160 165

gaa acc ctc ggt gag atc ttc ggc gaa gaa gaa gat gct gca aag atc 643
Glu Thr Leu Gly Glu Ile Phe Gly Glu Glu Glu Asp Ala Ala Lys Ile
170 175 180

gtt gct gat ttc gag tcc gca ctt gag cgc gct aag acc gca tac gca 691
Val Ala Asp Phe Glu Ser Ala Leu Glu Arg Ala Lys Thr Ala Tyr Ala
185 190 195

```
gca atc tcc gac cag acc gtc atg gca gtt aac gtt tcc ggc gga aac   739
Ala Ile Ser Asp Gln Thr Val Met Ala Val Asn Val Ser Gly Gly Asn
        200                 205                 210

att ggc tac atc gct cct tcc gtt gga cgc acc tac ggt cca atc ttc   787
Ile Gly Tyr Ile Ala Pro Ser Val Gly Arg Thr Tyr Gly Pro Ile Phe
    215                 220                 225

gac ctg gtt gga ctc acc cca gca ctc gag gtt ggc aac gcg tcc tcc   835
Asp Leu Val Gly Leu Thr Pro Ala Leu Glu Val Gly Asn Ala Ser Ser
230                 235                 240                 245

gac cac gag ggc gac gac att aac gtc gaa gca atc gca gct gca aac   883
Asp His Glu Gly Asp Asp Ile Asn Val Glu Ala Ile Ala Ala Ala Asn
                250                 255                 260

cca gac ctg atc ctg gtc atg gac cgc gat ggt ggc acc agc acc cgc   931
Pro Asp Leu Ile Leu Val Met Asp Arg Asp Gly Gly Thr Ser Thr Arg
            265                 270                 275

aac gaa gct gat tac gtt cca gca gag cag atc gtc tcc gac aat gaa   979
Asn Glu Ala Asp Tyr Val Pro Ala Glu Gln Ile Val Ser Asp Asn Glu
        280                 285                 290

gca ctg gca aac gtc aag gct gtc acc gac gga tac gtt tac tac gca   1027
Ala Leu Ala Asn Val Lys Ala Val Thr Asp Gly Tyr Val Tyr Tyr Ala
    295                 300                 305

cct gca gat acc tac acc aac gaa aac atc atc acc tac acc gag atc   1075
Pro Ala Asp Thr Tyr Thr Asn Glu Asn Ile Ile Thr Tyr Thr Glu Ile
310                 315                 320                 325

ctc aac ggc atg gca gat atg ttc gag aag gca gct cag taggggatcg    1124
Leu Asn Gly Met Ala Asp Met Phe Glu Lys Ala Ala Gln
                330                 335

atcccacact gac                                                   1137


<210> 356
<211> 338
<212> PRT
<213> Corynebacterium glutamicum

<400> 356
Met Val Lys Asn Arg Phe Lys Leu Val Ser Ile Ala Thr Val Ala Ala
  1               5                  10                  15

Leu Ala Leu Val Gly Cys Ser Ser Thr Asp Ser Thr Ser Ser Glu Ser
            20                  25                  30

Ser Ser Ala Ala Glu Ser Thr Ala Ala Ala Ser Thr Leu Thr Ile Glu
        35                  40                  45

Asp Asn His Gly Thr Glu Gly Ile Ser Leu Pro Ile Glu Gly Val Ala
    50                  55                  60

Ala Thr Asp Asn Arg Ala Phe Glu Leu Leu Asp Arg Trp Gly Val Glu
65                  70                  75                  80

Leu Val Ala Ala Pro Leu Gln Leu Val Pro Phe Thr Val Thr Gly Tyr
```

```
                85                  90                  95

Thr Glu Glu Gly Gly Val Ala Asn Leu Gly Ser His Arg Glu Pro Asp
            100                 105                 110

Leu Glu Ala Leu Ala Ala Ala Gln Pro Ser Leu Ile Ile Asn Gly Gln
        115                 120                 125

Arg Phe Ala Gln Tyr Tyr Asp Asp Ile Ile Ala Leu Asn Pro Asp Ala
    130                 135                 140

Thr Val Val Glu Leu Asp Pro Arg Asp Gly Glu Pro Leu Asp Gln Glu
145                 150                 155                 160

Leu Ile Arg Gln Ala Glu Thr Leu Gly Glu Ile Phe Gly Glu Glu Glu
                165                 170                 175

Asp Ala Ala Lys Ile Val Ala Asp Phe Glu Ser Ala Leu Glu Arg Ala
            180                 185                 190

Lys Thr Ala Tyr Ala Ala Ile Ser Asp Gln Thr Val Met Ala Val Asn
        195                 200                 205

Val Ser Gly Gly Asn Ile Gly Tyr Ile Ala Pro Ser Val Gly Arg Thr
    210                 215                 220

Tyr Gly Pro Ile Phe Asp Leu Val Gly Leu Thr Pro Ala Leu Glu Val
225                 230                 235                 240

Gly Asn Ala Ser Ser Asp His Glu Gly Asp Asp Ile Asn Val Glu Ala
                245                 250                 255

Ile Ala Ala Ala Asn Pro Asp Leu Ile Leu Val Met Asp Arg Asp Gly
            260                 265                 270

Gly Thr Ser Thr Arg Asn Glu Ala Asp Tyr Val Pro Ala Glu Gln Ile
        275                 280                 285

Val Ser Asp Asn Glu Ala Leu Ala Asn Val Lys Ala Val Thr Asp Gly
    290                 295                 300

Tyr Val Tyr Tyr Ala Pro Ala Asp Thr Tyr Thr Asn Glu Asn Ile Ile
305                 310                 315                 320

Thr Tyr Thr Glu Ile Leu Asn Gly Met Ala Asp Met Phe Glu Lys Ala
                325                 330                 335

Ala Gln
```

<210> 357
<211> 1233
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1210)
<223> RXS00156

<400> 357
accgagagcg tggtacgcct catttagttt cctcctatga atcttgatgt ggttcatgcg 60

```
ttttttatgca atatcaacca aaagttggta cgatcctcat atg aat gaa cgc aca   115
                                            Met Asn Glu Arg Thr
                                              1               5

tcg gat gca ttt gac gcc ctc ctt gtg ctc tcc ttc ggt ggt ccc gaa   163
Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser Phe Gly Gly Pro Glu
                 10                  15                  20

ggg cac gag gag gtt cgt ccg ttt ttg gag aat gtc act cac gga agg   211
Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn Val Thr His Gly Arg
             25                  30                  35

ggg att ccg ccg gaa cgt cta gat gaa gtg gcg gtt cat tac cac cac   259
Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala Val His Tyr His His
         40                  45                  50

ttc ggt ggt atc agc ccc atc aat gcg ctg aac agg gaa att atc gcc   307
Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn Arg Glu Ile Ile Ala
     55                  60                  65

aat gtg gaa aaa gaa ttg gcg tct cgc gat cac aag ctg cct gtt tat   355
Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His Lys Leu Pro Val Tyr
 70                  75                  80                  85

ttt ggt aac cgc aac tgg aag ccg ttt gat aat gag gcc gct gaa caa   403
Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn Glu Ala Ala Glu Gln
                 90                  95                 100

atg gct gat gac ggc gtg aaa aac gcg ctg gtg ttg gca act tcc gct   451
Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val Leu Ala Thr Ser Ala
             105                 110                 115

tgg ggt ggc tac tcc ggt tgt cgg cag tac cag gaa gat att cag ggc   499
Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln Glu Asp Ile Gln Gly
         120                 125                 130

atg atc aag cac ctg gag tct cag ggg cag tcg atc acg ttc acc aag   547
Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser Ile Thr Phe Thr Lys
     135                 140                 145

ctg cgt cag ttc tac gat cac cct cgt ttt gtc tcc acc atg gct caa   595
Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val Ser Thr Met Ala Gln
150                 155                 160                 165

ttg gtt cag gat tcc tac gcg aag ctt ccc gat gag ctg cga gat gag   643
Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp Glu Leu Arg Asp Glu
                 170                 175                 180

gcg cgt ctg gtc ttc acc gcg cac tcc att cca ctg act gcg gac aat   691
Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro Leu Thr Ala Asp Asn
             185                 190                 195

gct gcg gga acc cct gag gat ggc tcc ttg tat tcc aca cag gtc aag   739
Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr Ser Thr Gln Val Lys
         200                 205                 210

gaa gcg tca gca ctg att gct gag gct gtt ggt gtg tca gat ttt gat   787
Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly Val Ser Asp Phe Asp
```

```
    215                 220                 225

gtg gtg tgg cag tcc cgc tcg ggt agc ccg cac act ccg tgg ctg gag   835
Val Val Trp Gln Ser Arg Ser Gly Ser Pro His Thr Pro Trp Leu Glu
230                 235                 240                 245

cct gac atc gtg gat cac gca gtg gag ctc aac gag aag ggt caa aaa   883
Pro Asp Ile Val Asp His Ala Val Glu Leu Asn Glu Lys Gly Gln Lys
                250                 255                 260

gcg ctc gtt gtc tgc cct gta ggc ttt att tct gat cat atg gaa gtc   931
Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser Asp His Met Glu Val
            265                 270                 275

att tgg gat ctt gat tcc gag ctg atg gaa gaa gcc gag aag cgc aac   979
Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu Ala Glu Lys Arg Asn
        280                 285                 290

atg gtg gtc gag cgt gtc gct acc gtt ggc ccc acc gat gaa ttc gca   1027
Met Val Val Glu Arg Val Ala Thr Val Gly Pro Thr Asp Glu Phe Ala
    295                 300                 305

gcc ctt gtg gtt gat ctc atc gag gag gca gag ctc aag cgc gtt atc   1075
Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu Leu Lys Arg Val Ile
310                 315                 320                 325

gag cgc ctt gga aag ctg cca gca cgc gga agt tcc gtc aac ggc gca   1123
Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser Ser Val Asn Gly Ala
                330                 335                 340

ccg tgt ggc gac ggc tgc tgt ggt acc gcc aag cat aaa acc gcg cgg   1171
Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys His Lys Thr Ala Arg
            345                 350                 355

gtg aac ccc aac gct cgc tca gcg gcg cca gct gcc aac taggagtgat    1220
Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala Ala Asn
        360                 365                 370

agtccctcgc aaa                                                   1233
```

<210> 358
<211> 370
<212> PRT
<213> Corynebacterium glutamicum

<400> 358

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Met Asn Glu Arg Thr Ser Asp Ala Phe Asp Ala Leu Leu Val Leu Ser
  1               5                  10                  15

Phe Gly Gly Pro Glu Gly His Glu Glu Val Arg Pro Phe Leu Glu Asn
             20                  25                  30

Val Thr His Gly Arg Gly Ile Pro Pro Glu Arg Leu Asp Glu Val Ala
         35                  40                  45

Val His Tyr His His Phe Gly Gly Ile Ser Pro Ile Asn Ala Leu Asn
     50                  55                  60

Arg Glu Ile Ile Ala Asn Val Glu Lys Glu Leu Ala Ser Arg Asp His
 65                  70                  75                  80
```

```
Lys Leu Pro Val Tyr Phe Gly Asn Arg Asn Trp Lys Pro Phe Asp Asn
                 85                  90                  95

Glu Ala Ala Glu Gln Met Ala Asp Asp Gly Val Lys Asn Ala Leu Val
            100                 105                 110

Leu Ala Thr Ser Ala Trp Gly Gly Tyr Ser Gly Cys Arg Gln Tyr Gln
        115                 120                 125

Glu Asp Ile Gln Gly Met Ile Lys His Leu Glu Ser Gln Gly Gln Ser
    130                 135                 140

Ile Thr Phe Thr Lys Leu Arg Gln Phe Tyr Asp His Pro Arg Phe Val
145                 150                 155                 160

Ser Thr Met Ala Gln Leu Val Gln Asp Ser Tyr Ala Lys Leu Pro Asp
                165                 170                 175

Glu Leu Arg Asp Glu Ala Arg Leu Val Phe Thr Ala His Ser Ile Pro
            180                 185                 190

Leu Thr Ala Asp Asn Ala Ala Gly Thr Pro Glu Asp Gly Ser Leu Tyr
        195                 200                 205

Ser Thr Gln Val Lys Glu Ala Ser Ala Leu Ile Ala Glu Ala Val Gly
    210                 215                 220

Val Ser Asp Phe Asp Val Val Trp Gln Ser Arg Ser Gly Ser Pro His
225                 230                 235                 240

Thr Pro Trp Leu Glu Pro Asp Ile Val Asp His Ala Val Glu Leu Asn
                245                 250                 255

Glu Lys Gly Gln Lys Ala Leu Val Val Cys Pro Val Gly Phe Ile Ser
            260                 265                 270

Asp His Met Glu Val Ile Trp Asp Leu Asp Ser Glu Leu Met Glu Glu
        275                 280                 285

Ala Glu Lys Arg Asn Met Val Val Glu Arg Val Ala Thr Val Gly Pro
    290                 295                 300

Thr Asp Glu Phe Ala Ala Leu Val Val Asp Leu Ile Glu Glu Ala Glu
305                 310                 315                 320

Leu Lys Arg Val Ile Glu Arg Leu Gly Lys Leu Pro Ala Arg Gly Ser
                325                 330                 335

Ser Val Asn Gly Ala Pro Cys Gly Asp Gly Cys Cys Gly Thr Ala Lys
            340                 345                 350

His Lys Thr Ala Arg Val Asn Pro Asn Ala Arg Ser Ala Ala Pro Ala
        355                 360                 365

Ala Asn
    370
```

<210> 359
<211> 810

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(787)
<223> RXS00624

<400> 359
tccatgacgt tttgaatgga aaatctccat ttgtggagtt agaagaagac cactagtttt 60

caacaggacg acaacggccg gacatgcgac aatacaatgc atg tcc ggc cgt ctt 115
Met Ser Gly Arg Leu
1 5

ctt gtt tca gtt tct agt att ttc gac cag acc cga tcg gcg gct gac 163
Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr Arg Ser Ala Ala Asp
10 15 20

agg ctc att tca gac ctg cga gcc gac ggc atc gag gtc tca tta ctt 211
Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile Glu Val Ser Leu Leu
25 30 35

gtc gca ccc cgc atc gat ggg gac tgg cgt ctc gcc aaa gac aaa ggg 259
Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu Ala Lys Asp Lys Gly
40 45 50

acc ctc gcg tgg atg gaa caa caa cgc gaa cgc ggc cac gaa ctc atc 307
Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg Gly His Glu Leu Ile
55 60 65

ctc aac ggt ttc gac caa gca gtt cag gga cgt cgc tca gaa ttc gcc 355
Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg Arg Ser Glu Phe Ala
70 75 80 85

aac ctt gaa cgg cac gaa gca cgt ctt cgc ctt acc ggt gcc att agg 403
Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu Thr Gly Ala Ile Arg
90 95 100

caa atg cag aaa att ggc ttc gaa ttc caa atc ttt gcc cca cct cgt 451
Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile Phe Ala Pro Pro Arg
105 110 115

tgg aga atg tca gaa ggc acc ttc gcg gta ctc cca gaa ttt gat ttc 499
Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu Pro Glu Phe Asp Phe
120 125 130

aac gtc gcc gcc tcg acc agg gga tta cat aac ctc gac acc ggc gaa 547
Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn Leu Asp Thr Gly Glu
135 140 145

ttc ttg gcg tgt aga aac ctc tcc gtg ggt gaa ggt ttt ggt gct gca 595
Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu Gly Phe Gly Ala Ala
150 155 160 165

aaa tgg tgg cgc aag aat gtc atc aag gct gtc act cgt gga gcg gaa 643
Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val Thr Arg Gly Ala Glu
170 175 180

aaa gga aat aca gtg cgc ttg tcc gca tcg gcg cga aat ctc acc aac 691
Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala Arg Asn Leu Thr Asn

```
            185                 190                 195

cct aaa gtc gca gct gac ttc cgg gaa gct gca tta gct gcc ttg gat   739
Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala Leu Ala Ala Leu Asp
        200                 205                 210

ttg ggt gct cag gtg caa acc tat tct cag gcg gcc gca caa ctg gcc   787
Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala Ala Ala Gln Leu Ala
    215                 220                 225

tagttgggga ggttcggggc acc                                        810


<210> 360
<211> 229
<212> PRT
<213> Corynebacterium glutamicum

<400> 360
Met Ser Gly Arg Leu Leu Val Ser Val Ser Ser Ile Phe Asp Gln Thr
  1               5                  10                  15

Arg Ser Ala Ala Asp Arg Leu Ile Ser Asp Leu Arg Ala Asp Gly Ile
             20                  25                  30

Glu Val Ser Leu Leu Val Ala Pro Arg Ile Asp Gly Asp Trp Arg Leu
         35                  40                  45

Ala Lys Asp Lys Gly Thr Leu Ala Trp Met Glu Gln Gln Arg Glu Arg
     50                  55                  60

Gly His Glu Leu Ile Leu Asn Gly Phe Asp Gln Ala Val Gln Gly Arg
 65                  70                  75                  80

Arg Ser Glu Phe Ala Asn Leu Glu Arg His Glu Ala Arg Leu Arg Leu
                 85                  90                  95

Thr Gly Ala Ile Arg Gln Met Gln Lys Ile Gly Phe Glu Phe Gln Ile
            100                 105                 110

Phe Ala Pro Pro Arg Trp Arg Met Ser Glu Gly Thr Phe Ala Val Leu
        115                 120                 125

Pro Glu Phe Asp Phe Asn Val Ala Ala Ser Thr Arg Gly Leu His Asn
    130                 135                 140

Leu Asp Thr Gly Glu Phe Leu Ala Cys Arg Asn Leu Ser Val Gly Glu
145                 150                 155                 160

Gly Phe Gly Ala Ala Lys Trp Trp Arg Lys Asn Val Ile Lys Ala Val
                165                 170                 175

Thr Arg Gly Ala Glu Lys Gly Asn Thr Val Arg Leu Ser Ala Ser Ala
            180                 185                 190

Arg Asn Leu Thr Asn Pro Lys Val Ala Ala Asp Phe Arg Glu Ala Ala
        195                 200                 205

Leu Ala Ala Leu Asp Leu Gly Ala Gln Val Gln Thr Tyr Ser Gln Ala
    210                 215                 220
```

Ala Ala Gln Leu Ala
225

<210> 361
<211> 1068
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1045)
<223> RXA00024

<400> 361
ttaagacatc aacatatggc ttgtgctact gaaagatttt tcttctgaaa ttctgtagaa 60

acgctcctat gctcggggca gtaagttgtg agcataggaa atg gag cac ggc gtg 115
Met Glu His Gly Val
1 5

acc gtt att aaa ggc act gaa ttt gat gtt ttc cca cta aac ctc ggt 163
Thr Val Ile Lys Gly Thr Glu Phe Asp Val Phe Pro Leu Asn Leu Gly
10 15 20

gga aat acc ttt ggc tgg acc tcg aat agg gaa cag acc ttc gcg gtt 211
Gly Asn Thr Phe Gly Trp Thr Ser Asn Arg Glu Gln Thr Phe Ala Val
25 30 35

ttg gat gca ttc gtg gca gcg gga gga aac ttt gtt gac acc gcc gat 259
Leu Asp Ala Phe Val Ala Ala Gly Gly Asn Phe Val Asp Thr Ala Asp
40 45 50

tct tat tct gca tgg gtt gaa ggc aat gag ggt ggc gag tcg gag cgg 307
Ser Tyr Ser Ala Trp Val Glu Gly Asn Glu Gly Gly Glu Ser Glu Arg
55 60 65

gag ctc ggc gcg tgg att aag gaa cgt ggc gca gac aag ctg atc att 355
Glu Leu Gly Ala Trp Ile Lys Glu Arg Gly Ala Asp Lys Leu Ile Ile
70 75 80 85

gct acc aag tct ggt gcg ttg gag cct gtt gct ggt cgt tcc cgt gag 403
Ala Thr Lys Ser Gly Ala Leu Glu Pro Val Ala Gly Arg Ser Arg Glu
90 95 100

gca act ttc aag gct gtc gag ggt tcc ctg gag cgt ttg ggc gtg gaa 451
Ala Thr Phe Lys Ala Val Glu Gly Ser Leu Glu Arg Leu Gly Val Glu
105 110 115

tcg atc gat att ttt tac tac cac tac gac gat gag gca gtc agc att 499
Ser Ile Asp Ile Phe Tyr Tyr His Tyr Asp Asp Glu Ala Val Ser Ile
120 125 130

gat gag cag gtt gct atc gct aat gat ctg att gca cag ggc aag att 547
Asp Glu Gln Val Ala Ile Ala Asn Asp Leu Ile Ala Gln Gly Lys Ile
135 140 145

aag cac ctc gca ttg tct aac tac agc gcg gag cgt tta gct gag ttc 595
Lys His Leu Ala Leu Ser Asn Tyr Ser Ala Glu Arg Leu Ala Glu Phe
150 155 160 165

```
ttt gag aag tct gta ggc act cca gcg cag ccg gtt gct ctg caa ccg   643
Phe Glu Lys Ser Val Gly Thr Pro Ala Gln Pro Val Ala Leu Gln Pro
                170                 175                 180

cac tac aac ctg gtg tcg agg aag gat tat gag gag aac gtg cag cca   691
His Tyr Asn Leu Val Ser Arg Lys Asp Tyr Glu Glu Asn Val Gln Pro
            185                 190                 195

ctc gcc gag aag cat ggc gtt gca gtc ttc cct tat ttc gcg ctt gcc   739
Leu Ala Glu Lys His Gly Val Ala Val Phe Pro Tyr Phe Ala Leu Ala
        200                 205                 210

gcg ggt ctt ttg acc gga aag tac acc tcc aag gag gat att tcg ggt   787
Ala Gly Leu Leu Thr Gly Lys Tyr Thr Ser Lys Glu Asp Ile Ser Gly
    215                 220                 225

aaa gcg cgt gcg ggg cag ttg gat cgt tac gcc agc gat gag gcg ttt   835
Lys Ala Arg Ala Gly Gln Leu Asp Arg Tyr Ala Ser Asp Glu Ala Phe
230                 235                 240                 245

gcc gtg gtg aca gag ttg cgt gct gtt gcc gat gag ttg ggt gtt gcg   883
Ala Val Val Thr Glu Leu Arg Ala Val Ala Asp Glu Leu Gly Val Ala
                250                 255                 260

cca acg act gtg gcg ctt gcg tgg ttg gtt gcg cat ggt gtg acc gca   931
Pro Thr Thr Val Ala Leu Ala Trp Leu Val Ala His Gly Val Thr Ala
            265                 270                 275

ccg att gcg tcc gtg tcc aag gta gag cag ttg aag gat ttg atg gct   979
Pro Ile Ala Ser Val Ser Lys Val Glu Gln Leu Lys Asp Leu Met Ala
        280                 285                 290

gtg aag gat gtg gag ctg agc gct gag cag ctt gca cgt ttg gat aag   1027
Val Lys Asp Val Glu Leu Ser Ala Glu Gln Leu Ala Arg Leu Asp Lys
    295                 300                 305

gtt tcg gag cct ttc gct taagctctcc tcaaaagtaa gtg                 1068
Val Ser Glu Pro Phe Ala
310                 315
```

<210> 362
<211> 315
<212> PRT
<213> Corynebacterium glutamicum

<400> 362

```
Met Glu His Gly Val Thr Val Ile Lys Gly Thr Glu Phe Asp Val Phe
  1               5                  10                  15

Pro Leu Asn Leu Gly Gly Asn Thr Phe Gly Trp Thr Ser Asn Arg Glu
             20                  25                  30

Gln Thr Phe Ala Val Leu Asp Ala Phe Val Ala Ala Gly Gly Asn Phe
         35                  40                  45

Val Asp Thr Ala Asp Ser Tyr Ser Ala Trp Val Glu Gly Asn Glu Gly
     50                  55                  60

Gly Glu Ser Glu Arg Glu Leu Gly Ala Trp Ile Lys Glu Arg Gly Ala
 65                  70                  75                  80
```

```
Asp Lys Leu Ile Ile Ala Thr Lys Ser Gly Ala Leu Glu Pro Val Ala
                 85                  90                  95

Gly Arg Ser Arg Glu Ala Thr Phe Lys Ala Val Glu Gly Ser Leu Glu
            100                 105                 110

Arg Leu Gly Val Glu Ser Ile Asp Ile Phe Tyr Tyr His Tyr Asp Asp
        115                 120                 125

Glu Ala Val Ser Ile Asp Glu Gln Val Ala Ile Ala Asn Asp Leu Ile
    130                 135                 140

Ala Gln Gly Lys Ile Lys His Leu Ala Leu Ser Asn Tyr Ser Ala Glu
145                 150                 155                 160

Arg Leu Ala Glu Phe Phe Glu Lys Ser Val Gly Thr Pro Ala Gln Pro
                165                 170                 175

Val Ala Leu Gln Pro His Tyr Asn Leu Val Ser Arg Lys Asp Tyr Glu
            180                 185                 190

Glu Asn Val Gln Pro Leu Ala Glu Lys His Gly Val Ala Val Phe Pro
        195                 200                 205

Tyr Phe Ala Leu Ala Ala Gly Leu Leu Thr Gly Lys Tyr Thr Ser Lys
    210                 215                 220

Glu Asp Ile Ser Gly Lys Ala Arg Ala Gly Gln Leu Asp Arg Tyr Ala
225                 230                 235                 240

Ser Asp Glu Ala Phe Ala Val Val Thr Glu Leu Arg Ala Val Ala Asp
                245                 250                 255

Glu Leu Gly Val Ala Pro Thr Thr Val Ala Leu Ala Trp Leu Val Ala
            260                 265                 270

His Gly Val Thr Ala Pro Ile Ala Ser Val Ser Lys Val Glu Gln Leu
        275                 280                 285

Lys Asp Leu Met Ala Val Lys Asp Val Glu Leu Ser Ala Glu Gln Leu
    290                 295                 300

Ala Arg Leu Asp Lys Val Ser Glu Pro Phe Ala
305                 310                 315
```

<210> 363
<211> 1329
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1306)
<223> RXA02526

<400> 363
aggaaatgac actcaactag aaatcttttc ttcagatgcc acaatcgaaa gctggttggc 60

tgcggagaga gcactctcaa ctgctcaagc ccgccatggt gtg atc act gaa gac 115

```
                                                    Val Ile Thr Glu Asp
                                                      1               5

gat gct gca cag atc aac cag gcg gca gtc ctt tcc aac att gac cgc   163
Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu Ser Asn Ile Asp Arg
                10                  15                  20

gag aag ctg tgg gaa gat gcc aaa aat gtc ggc tac ccc atc ctt ggc   211
Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly Tyr Pro Ile Leu Gly
            25                  30                  35

ttg gta aga caa atc gcc agt cac ctt cca gaa ggc ccc aac ggg cga   259
Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu Gly Pro Asn Gly Arg
        40                  45                  50

gtc cac tac ggc gcc acg acc caa gtc atc atg gac act gga ctg gtg   307
Val His Tyr Gly Ala Thr Thr Gln Val Ile Met Asp Thr Gly Leu Val
    55                  60                  65

ttg caa atg act gcc tct ttg aac gcc ctt gat aaa cag atc gtg cgt   355
Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp Lys Gln Ile Val Arg
70                  75                  80                  85

ctg ggg aat gca ctg gca gca cgg gct gaa gag cac aaa gac acc gtg   403
Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu His Lys Asp Thr Val
                90                  95                  100

atg ccg gga cgc acc cat gct cag cag gca att ccc act aca ttt gga   451
Met Pro Gly Arg Thr His Ala Gln Gln Ala Ile Pro Thr Thr Phe Gly
            105                 110                 115

gca acc ctc gct acc ttt ttg gat caa atc cgc agg cag agg gaa cga   499
Ala Thr Leu Ala Thr Phe Leu Asp Gln Ile Arg Arg Gln Arg Glu Arg
        120                 125                 130

ctt gag gaa gca ctc gag cgc gtg cga gtc att tcg ctg ttt ggt gct   547
Leu Glu Glu Ala Leu Glu Arg Val Arg Val Ile Ser Leu Phe Gly Ala
    135                 140                 145

ggt gga aac aac gca gca caa ggc gaa caa gcg gca acg gtt cgt gca   595
Gly Gly Asn Asn Ala Ala Gln Gly Glu Gln Ala Ala Thr Val Arg Ala
150                 155                 160                 165

gag atg gcc cgc ctg ttg gat ctg aag gac ccg gtg gtg tca tgg cat   643
Glu Met Ala Arg Leu Leu Asp Leu Lys Asp Pro Val Val Ser Trp His
                170                 175                 180

gtg gaa cgc gat gtg ctt ggg gac ttc gga tgg gtg tgc tca acg ctg   691
Val Glu Arg Asp Val Leu Gly Asp Phe Gly Trp Val Cys Ser Thr Leu
            185                 190                 195

tgt gga tcg atg gca aaa ttt ggc cga aac atc gtg gat ctt tcc cga   739
Cys Gly Ser Met Ala Lys Phe Gly Arg Asn Ile Val Asp Leu Ser Arg
        200                 205                 210

act gaa atc gga gaa gtt ttt gag cct tac aac tcc cat cgg ggt gca   787
Thr Glu Ile Gly Glu Val Phe Glu Pro Tyr Asn Ser His Arg Gly Ala
    215                 220                 225

tct tcc atg atg cct cag aaa gtc aac ccg att tct tcc gag ctc atg   835
Ser Ser Met Met Pro Gln Lys Val Asn Pro Ile Ser Ser Glu Leu Met
```

```
230                 235                 240                 245

att ggt att tca gtg gtg gcg ggt gcc ttg acc tcg act ttg cca cgg   883
Ile Gly Ile Ser Val Val Ala Gly Ala Leu Thr Ser Thr Leu Pro Arg
                250                 255                 260

ctt cag gaa tcg gga cat gaa cga gca gca gga gag tgg cag gga gaa   931
Leu Gln Glu Ser Gly His Glu Arg Ala Ala Gly Glu Trp Gln Gly Glu
            265                 270                 275

tgg ctt gtc att cca acg ttg gcc aat cta gct ggc gct gca ctc gat   979
Trp Leu Val Ile Pro Thr Leu Ala Asn Leu Ala Gly Ala Ala Leu Asp
        280                 285                 290

gaa gcc att gtg gtg gct gaa gga atg cga gtg gat aca gat cgt atg   1027
Glu Ala Ile Val Val Ala Glu Gly Met Arg Val Asp Thr Asp Arg Met
    295                 300                 305

tcc tcg aac ttg gct ttt gct ggt gga ttg atc atg gcg gaa gct cag   1075
Ser Ser Asn Leu Ala Phe Ala Gly Gly Leu Ile Met Ala Glu Ala Gln
310                 315                 320                 325

atg att caa cta gct cca gct ctg ggg cgt gag aaa gct cat gac ttg   1123
Met Ile Gln Leu Ala Pro Ala Leu Gly Arg Glu Lys Ala His Asp Leu
                330                 335                 340

gtt tat gaa gca tcc aca aag act cgt gaa gag cac acc acg ctg gca   1171
Val Tyr Glu Ala Ser Thr Lys Thr Arg Glu Glu His Thr Thr Leu Ala
            345                 350                 355

gaa gaa ctg ccg ata att gca gtt caa cat ggg gtc gaa gac ctg ttg   1219
Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly Val Glu Asp Leu Leu
        360                 365                 370

cct aag aat ttt gcg cag cct gca gac tac gtc ggc gaa gca caa tcc   1267
Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val Gly Glu Ala Gln Ser
    375                 380                 385

atg gtg aat gca gct gtc gcc gcc tgg aat gcc caa ctt taacaaccca    1316
Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala Gln Leu
390                 395                 400

aaactttaac aac                                                   1329
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<210> 364
<211> 402
<212> PRT
<213> Corynebacterium glutamicum

<400> 364

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Val Ile Thr Glu Asp Asp Ala Ala Gln Ile Asn Gln Ala Ala Val Leu
  1               5                  10                  15

Ser Asn Ile Asp Arg Glu Lys Leu Trp Glu Asp Ala Lys Asn Val Gly
            20                  25                  30

Tyr Pro Ile Leu Gly Leu Val Arg Gln Ile Ala Ser His Leu Pro Glu
        35                  40                  45

Gly Pro Asn Gly Arg Val His Tyr Gly Ala Thr Thr Gln Val Ile Met
```

```
     50                  55                  60

Asp Thr Gly Leu Val Leu Gln Met Thr Ala Ser Leu Asn Ala Leu Asp
 65                  70                  75                  80

Lys Gln Ile Val Arg Leu Gly Asn Ala Leu Ala Ala Arg Ala Glu Glu
                 85                  90                  95

His Lys Asp Thr Val Met Pro Gly Arg Thr His Ala Gln Gln Ala Ile
            100                 105                 110

Pro Thr Thr Phe Gly Ala Thr Leu Ala Thr Phe Leu Asp Gln Ile Arg
        115                 120                 125

Arg Gln Arg Glu Arg Leu Glu Glu Ala Leu Glu Arg Val Arg Val Ile
    130                 135                 140

Ser Leu Phe Gly Ala Gly Gly Asn Asn Ala Ala Gln Gly Glu Gln Ala
145                 150                 155                 160

Ala Thr Val Arg Ala Glu Met Ala Arg Leu Leu Asp Leu Lys Asp Pro
                165                 170                 175

Val Val Ser Trp His Val Glu Arg Asp Val Leu Gly Asp Phe Gly Trp
            180                 185                 190

Val Cys Ser Thr Leu Cys Gly Ser Met Ala Lys Phe Gly Arg Asn Ile
        195                 200                 205

Val Asp Leu Ser Arg Thr Glu Ile Gly Glu Val Phe Glu Pro Tyr Asn
    210                 215                 220

Ser His Arg Gly Ala Ser Ser Met Met Pro Gln Lys Val Asn Pro Ile
225                 230                 235                 240

Ser Ser Glu Leu Met Ile Gly Ile Ser Val Val Ala Gly Ala Leu Thr
                245                 250                 255

Ser Thr Leu Pro Arg Leu Gln Glu Ser Gly His Glu Arg Ala Ala Gly
            260                 265                 270

Glu Trp Gln Gly Glu Trp Leu Val Ile Pro Thr Leu Ala Asn Leu Ala
        275                 280                 285

Gly Ala Ala Leu Asp Glu Ala Ile Val Val Ala Glu Gly Met Arg Val
    290                 295                 300

Asp Thr Asp Arg Met Ser Ser Asn Leu Ala Phe Ala Gly Gly Leu Ile
305                 310                 315                 320

Met Ala Glu Ala Gln Met Ile Gln Leu Ala Pro Ala Leu Gly Arg Glu
                325                 330                 335

Lys Ala His Asp Leu Val Tyr Glu Ala Ser Thr Lys Thr Arg Glu Glu
            340                 345                 350

His Thr Thr Leu Ala Glu Glu Leu Pro Ile Ile Ala Val Gln His Gly
        355                 360                 365

Val Glu Asp Leu Leu Pro Lys Asn Phe Ala Gln Pro Ala Asp Tyr Val
    370                 375                 380
```

Confidential - Pfizer

```
Gly Glu Ala Gln Ser Met Val Asn Ala Ala Val Ala Ala Trp Asn Ala
385                 390                 395                 400

Gln Leu
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<210> 365
<211> 1108
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1099)
<223> RXN02813

<400> 365

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ggactctaaa ttgacccgat ctttatactc cgaccttgct ggtagtggag aacacctcag 60

cagcctttcc gacgagactt tcctaaagaa tcttcttgtc gtg gag gcc gct ttg   115
                                            Val Glu Ala Ala Leu
                                              1               5

gcg gtt gca gct gcc ccc gag cac gca gca atg gcg aag gcc acc att   163
Ala Val Ala Ala Ala Pro Glu His Ala Ala Met Ala Lys Ala Thr Ile
                 10                  15                  20

gat tct tat cag ttg gat gtg gag gag ctt tcc cgt cgc gca gcc gag   211
Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser Arg Arg Ala Ala Glu
             25                  30                  35

ggc ggt aat ccg ctc att ccg ctg gtc act gac ctc aag gcc atc aat   259
Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp Leu Lys Ala Ile Asn
         40                  45                  50

ccg gca ggc atc cac att ggc gca acg agc cag gac atc att gat tct   307
Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln Asp Ile Ile Asp Ser
     55                  60                  65

gcg tta atg ctg tgc atg aag gaa ggg gtg ggg gag gtc gtc gac aag   355
Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly Glu Val Val Asp Lys
 70                  75                  80                  85

ctt aaa aag ctt gcg cga gat ttg gcc gag ctc acc gcg gag cat aaa   403
Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu Thr Ala Glu His Lys
                 90                  95                 100

gca acc ccg atc atg ggg cgc acg ttg ggg cag atc gcg acg ccg acg   451
Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln Ile Ala Thr Pro Thr
            105                 110                 115

acg ttc ggc gcg ctg acc ggc ggc tgg ctg gtt gcg gtg gac aat gcg   499
Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala
        120                 125                 130

gca cgc gcc ctg gag gcg ctg gag ttt ccg gtg tcg tat ggc ggt gcc   547
Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala
    135                 140                 145
```

```
agc gga aat atg acg gcg gtg cac ccg cgt ggc ttc gag att cag gcg   595
Ser Gly Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala
150                 155                 160                 165

aag ctg gcc gag gag ttg ggc ctt ttt gat ccg cag tgg gtg tgg cat   643
Lys Leu Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His
                170                 175                 180

tcc gat cgc acg ccg atc act gcg atc gcg tcg gcg ctg gca acg gcc   691
Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala
            185                 190                 195

gct ggt gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa   739
Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln
        200                 205                 210

acc gag gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg   787
Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala
    215                 220                 225

atg ccc cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac   835
Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr
230                 235                 240                 245

gcg cgc cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac   883
Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp
                250                 255                 260

tgc cgt ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg   931
Cys Arg Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr
            265                 270                 275

ctg cgc gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca   979
Leu Arg Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala
        280                 285                 290

acc agc atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc   1027
Thr Ser Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg
    295                 300                 305

gtc aat gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta   1075
Val Asn Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu
310                 315                 320                 325

gaa att tat gga aaa gga cgc agt taatggatc                        1108
Glu Ile Tyr Gly Lys Gly Arg Ser
                330
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<210> 366
<211> 333
<212> PRT
<213> Corynebacterium glutamicum

<400> 366

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Val Glu Ala Ala Leu Ala Val Ala Ala Ala Pro Glu His Ala Ala Met
  1               5                  10                  15

Ala Lys Ala Thr Ile Asp Ser Tyr Gln Leu Asp Val Glu Glu Leu Ser
             20                  25                  30
```

```
Arg Arg Ala Ala Glu Gly Gly Asn Pro Leu Ile Pro Leu Val Thr Asp
          35                  40                  45

Leu Lys Ala Ile Asn Pro Ala Gly Ile His Ile Gly Ala Thr Ser Gln
     50                  55                  60

Asp Ile Ile Asp Ser Ala Leu Met Leu Cys Met Lys Glu Gly Val Gly
 65                  70                  75                  80

Glu Val Val Asp Lys Leu Lys Lys Leu Ala Arg Asp Leu Ala Glu Leu
                 85                  90                  95

Thr Ala Glu His Lys Ala Thr Pro Ile Met Gly Arg Thr Leu Gly Gln
            100                 105                 110

Ile Ala Thr Pro Thr Thr Phe Gly Ala Leu Thr Gly Gly Trp Leu Val
        115                 120                 125

Ala Val Asp Asn Ala Ala Arg Ala Leu Glu Ala Leu Glu Phe Pro Val
    130                 135                 140

Ser Tyr Gly Gly Ala Ser Gly Asn Met Thr Ala Val His Pro Arg Gly
145                 150                 155                 160

Phe Glu Ile Gln Ala Lys Leu Ala Glu Glu Leu Gly Leu Phe Asp Pro
                165                 170                 175

Gln Trp Val Trp His Ser Asp Arg Thr Pro Ile Thr Ala Ile Ala Ser
            180                 185                 190

Ala Leu Ala Thr Ala Ala Gly Val Val Arg Lys Ile Ala Gly Asp Val
        195                 200                 205

Val Phe Tyr Ser Gln Thr Glu Val Gly Glu Leu Arg Glu Lys Ser Pro
    210                 215                 220

Gly Gly Ser Ser Ala Met Pro His Lys Ala Asn Pro Ala Ala Ala Ile
225                 230                 235                 240

Ala Cys Asp Gly Tyr Ala Arg Arg Ala Pro Gly Leu Leu Ala Thr Leu
                245                 250                 255

Phe Asp Ala Leu Asp Cys Arg Leu Gln Arg Gly Thr Gly Ser Trp His
            260                 265                 270

Ala Glu Trp Ala Thr Leu Arg Glu Leu Ala Ala Val Thr His Ser Ala
        275                 280                 285

Val Ser Arg Ala Ala Thr Ser Ile Asp Gly Ile Thr Val Asn Val Asp
    290                 295                 300

Val Met Ala Ser Arg Val Asn Gly Pro Thr Gly His Ala Glu Asp Leu
305                 310                 315                 320

Ala Glu Arg Ala Leu Glu Ile Tyr Gly Lys Gly Arg Ser
                325                 330
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Applicant's Copy

<210> 367
<211> 651
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(642)
<223> FRXA02813

<400> 367

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ggc gcg ctg acc ggc ggc tgg ctg gtt gcg gtg gac aat gcg gca cgc   48
Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala Ala Arg
  1               5                  10                  15

gcc ctg gag gcg ctg gag ttt ccg gtg tcg tat ggc ggt gcc agc gga   96
Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala Ser Gly
             20                  25                  30

aat atg acg gcg gtg cac ccg cgt ggc ttc gag att cag gcg aag ctg   144
Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala Lys Leu
         35                  40                  45

gcc gag gag ttg ggc ctt ttt gat ccg cag tgg gtg tgg cat tcc gat   192
Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His Ser Asp
     50                  55                  60

cgc acg ccg atc act gcg atc gcg tcg gcg ctg gca acg gcc gct ggt   240
Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala Ala Gly
 65                  70                  75                  80

gtg gta cgc aaa att gct ggt gac gtg gtg ttt tac tca caa acc gag   288
Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu
                 85                  90                  95

gtc ggc gag ttg cgg gag aaa tcc ccc ggc ggc agc tcc gcg atg ccc   336
Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala Met Pro
            100                 105                 110

cac aaa gcc aat ccg gcc gct gcg att gcg tgc gac ggt tac gcg cgc   384
His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr Ala Arg
        115                 120                 125

cgg gca cct ggc ctt ctt gca acg ctt ttc gac gcc ctc gac tgc cgt   432
Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp Cys Arg
    130                 135                 140

ttg cag cgc ggc acc ggc agc tgg cac gcg gag tgg gca acg ctg cgc   480
Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr Leu Arg
145                 150                 155                 160

gag ttg gct gct gtc act cac tca gca gtg agc agg gct gca acc agc   528
Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala Thr Ser
                165                 170                 175

atc gat ggc atc acc gtc aac gtt gat gtg atg gca agt cgc gtc aat   576
Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg Val Asn
            180                 185                 190

gga cca acc ggg cac gcc gaa gat ttg gcg gag cgg gca cta gaa att   624
Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu Glu Ile
        195                 200                 205

tat gga aaa gga cgc agt taatggatc                                651
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Tyr Gly Lys Gly Arg Ser
210

<210> 368
<211> 214
<212> PRT
<213> Corynebacterium glutamicum

<400> 368
Gly Ala Leu Thr Gly Gly Trp Leu Val Ala Val Asp Asn Ala Ala Arg
1 5 10 15

Ala Leu Glu Ala Leu Glu Phe Pro Val Ser Tyr Gly Gly Ala Ser Gly
20 25 30

Asn Met Thr Ala Val His Pro Arg Gly Phe Glu Ile Gln Ala Lys Leu
35 40 45

Ala Glu Glu Leu Gly Leu Phe Asp Pro Gln Trp Val Trp His Ser Asp
50 55 60

Arg Thr Pro Ile Thr Ala Ile Ala Ser Ala Leu Ala Thr Ala Ala Gly
65 70 75 80

Val Val Arg Lys Ile Ala Gly Asp Val Val Phe Tyr Ser Gln Thr Glu
85 90 95

Val Gly Glu Leu Arg Glu Lys Ser Pro Gly Gly Ser Ser Ala Met Pro
100 105 110

His Lys Ala Asn Pro Ala Ala Ala Ile Ala Cys Asp Gly Tyr Ala Arg
115 120 125

Arg Ala Pro Gly Leu Leu Ala Thr Leu Phe Asp Ala Leu Asp Cys Arg
130 135 140

Leu Gln Arg Gly Thr Gly Ser Trp His Ala Glu Trp Ala Thr Leu Arg
145 150 155 160

Glu Leu Ala Ala Val Thr His Ser Ala Val Ser Arg Ala Ala Thr Ser
165 170 175

Ile Asp Gly Ile Thr Val Asn Val Asp Val Met Ala Ser Arg Val Asn
180 185 190

Gly Pro Thr Gly His Ala Glu Asp Leu Ala Glu Arg Ala Leu Glu Ile
195 200 205

Tyr Gly Lys Gly Arg Ser
210

<210> 369
<211> 260
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(237)

<223> RXA01113

<400> 369
ggc gat att tgg gaa cgt cca ggc ctt gat cac act cag cgt cgc ctg 48
Gly Asp Ile Trp Glu Arg Pro Gly Leu Asp His Thr Gln Arg Arg Leu
1 5 10 15

ctc acc atc gcg att ttg acc gcg gtg ggc aat gac ggc gag ttg gac 96
Leu Thr Ile Ala Ile Leu Thr Ala Val Gly Asn Asp Gly Glu Leu Asp
20 25 30

atg cac att cgt gct gct ctg cgc gct ggc gtg gat cag gaa acc atc 144
Met His Ile Arg Ala Ala Leu Arg Ala Gly Val Asp Gln Glu Thr Ile
35 40 45

ggc gag gtc atc ctg cac act gcg gtg tat gcg ggt gtg ccg aac tcc 192
Gly Glu Val Ile Leu His Thr Ala Val Tyr Ala Gly Val Pro Asn Ser
50 55 60

aac cat ggt ttc aag ctg ctg aac aac gct gtg tca gac ctt cag 237
Asn His Gly Phe Lys Leu Leu Asn Asn Ala Val Ser Asp Leu Gln
65 70 75

taattctcga agctctccac ggg 260

<210> 370
<211> 79
<212> PRT
<213> Corynebacterium glutamicum

<400> 370
Gly Asp Ile Trp Glu Arg Pro Gly Leu Asp His Thr Gln Arg Arg Leu
1 5 10 15

Leu Thr Ile Ala Ile Leu Thr Ala Val Gly Asn Asp Gly Glu Leu Asp
20 25 30

Met His Ile Arg Ala Ala Leu Arg Ala Gly Val Asp Gln Glu Thr Ile
35 40 45

Gly Glu Val Ile Leu His Thr Ala Val Tyr Ala Gly Val Pro Asn Ser
50 55 60

Asn His Gly Phe Lys Leu Leu Asn Asn Ala Val Ser Asp Leu Gln
65 70 75

<210> 371
<211> 444
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(421)
<223> RXA02126

<400> 371
tccgaggaag acatggcggc acttcaagaa gtgaccgccc gcgattatgg cgagcacagc 60

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ggttttcctg tgtattccgg caagtagaaa gatttttatc atg gga caa aaa gta   115
                                            Met Gly Gln Lys Val
                                              1               5

acc gca ggt cgt gac atc cta gga gag ttt gca cct aag tcc gct gaa   163
Thr Ala Gly Arg Asp Ile Leu Gly Glu Phe Ala Pro Lys Ser Ala Glu
                10                  15                  20

ctc aac gat gat gtc ctc ttt ggc cag gtg tgg tcg agg gaa tca gag   211
Leu Asn Asp Asp Val Leu Phe Gly Gln Val Trp Ser Arg Glu Ser Glu
            25                  30                  35

ctt tcc cca cgt gac cga agc atc gtg atc gtg aca atg ttg atg gca   259
Leu Ser Pro Arg Asp Arg Ser Ile Val Ile Val Thr Met Leu Met Ala
        40                  45                  50

agt ggc gtg ctg gat agt gct ttt gaa agc cac gtt cag cga gcc aaa   307
Ser Gly Val Leu Asp Ser Ala Phe Glu Ser His Val Gln Arg Ala Lys
    55                  60                  65

gac aac ggt gtc act gct gaa gaa atc gca gag atc atc acc cac gtg   355
Asp Asn Gly Val Thr Ala Glu Glu Ile Ala Glu Ile Ile Thr His Val
70                  75                  80                  85

gcc ttt tat gca ggt tgg cca aag gct tgg gct gcg ttc cgc atc gca   403
Ala Phe Tyr Ala Gly Trp Pro Lys Ala Trp Ala Ala Phe Arg Ile Ala
                90                  95                  100

aag gac att tac acc aag taatagcgag gcagaaaaca cat                444
Lys Asp Ile Tyr Thr Lys
            105
```

<210> 372
<211> 107
<212> PRT
<213> Corynebacterium glutamicum

<400> 372

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Met Gly Gln Lys Val Thr Ala Gly Arg Asp Ile Leu Gly Glu Phe Ala
  1               5                  10                  15

Pro Lys Ser Ala Glu Leu Asn Asp Asp Val Leu Phe Gly Gln Val Trp
            20                  25                  30

Ser Arg Glu Ser Glu Leu Ser Pro Arg Asp Arg Ser Ile Val Ile Val
        35                  40                  45

Thr Met Leu Met Ala Ser Gly Val Leu Asp Ser Ala Phe Glu Ser His
    50                  55                  60

Val Gln Arg Ala Lys Asp Asn Gly Val Thr Ala Glu Glu Ile Ala Glu
65                  70                  75                  80

Ile Ile Thr His Val Ala Phe Tyr Ala Gly Trp Pro Lys Ala Trp Ala
                85                  90                  95

Ala Phe Arg Ile Ala Lys Asp Ile Tyr Thr Lys
            100                 105
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<210> 373
<211> 1284
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1261)
<223> RXA01465

<400> 373
gagactggcg aggatggtaa ccacgttcac tacccattcg tcctggataa ggaagactag 60

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ttttttctacc tagctagcat tgaagtcccg accacatctt gtg gcg gga ctt ttc   115
                                            Val Ala Gly Leu Phe
                                              1               5

cca ctt aac cag aaa gcc ata gaa aaa ttg tct gat tta acc atc caa   163
Pro Leu Asn Gln Lys Ala Ile Glu Lys Leu Ser Asp Leu Thr Ile Gln
                 10                  15                  20

aaa gtc gaa tcc cgt atc ctc gac gtt ccc ctc att cgc cca cac ggc   211
Lys Val Glu Ser Arg Ile Leu Asp Val Pro Leu Ile Arg Pro His Gly
             25                  30                  35

ttc gca act acc acc tcc act gag cag cac att ctg ctg gtc agc gtg   259
Phe Ala Thr Thr Thr Ser Thr Glu Gln His Ile Leu Leu Val Ser Val
         40                  45                  50

cac tta gaa aac ggt gtc atc ggc tac ggt gag ggc gtt gtg ccc ggc   307
His Leu Glu Asn Gly Val Ile Gly Tyr Gly Glu Gly Val Val Pro Gly
     55                  60                  65

ggt cca tgg tgg ggc ggc gag tcg gtt gag acc atg aag gcg ctt gtc   355
Gly Pro Trp Trp Gly Gly Glu Ser Val Glu Thr Met Lys Ala Leu Val
 70                  75                  80                  85

gac ggc tac ctc gcc cca gtg ctc atc ggc cgt gct gtc tcc gag ctt   403
Asp Gly Tyr Leu Ala Pro Val Leu Ile Gly Arg Ala Val Ser Glu Leu
                 90                  95                 100

gca gga att atg gca gac ctt gag cgt gtt gtt gca cgt gcg cgt tat   451
Ala Gly Ile Met Ala Asp Leu Glu Arg Val Val Ala Arg Ala Arg Tyr
            105                 110                 115

gcc aag gcg gct gtt gac gtc gca atg cat gat gcc tgg gca cgc agc   499
Ala Lys Ala Ala Val Asp Val Ala Met His Asp Ala Trp Ala Arg Ser
        120                 125                 130

ctc aat gtg ccc gtc cgc gac ctg ctt ggt ggc acc gtg cgc gac aag   547
Leu Asn Val Pro Val Arg Asp Leu Leu Gly Gly Thr Val Arg Asp Lys
    135                 140                 145

gtg gat gtc acc tgg gcg ctg ggc gtt ttg ccg ctt gat gtt gcg gtg   595
Val Asp Val Thr Trp Ala Leu Gly Val Leu Pro Leu Asp Val Ala Val
150                 155                 160                 165

gcg gaa att gaa gag cgc atc gag gag ttt ggt aac cgt tcc ttc aag   643
Ala Glu Ile Glu Glu Arg Ile Glu Glu Phe Gly Asn Arg Ser Phe Lys
                170                 175                 180
```

```
ttg aag atg ggt gct ggc gat cct gcg gaa gat act cgc cgt gta gca   691
Leu Lys Met Gly Ala Gly Asp Pro Ala Glu Asp Thr Arg Arg Val Ala
            185                 190                 195

gaa ttg gcg cgc gaa gtt ggc gac cgc gtt tct ctg cgc att gat att   739
Glu Leu Ala Arg Glu Val Gly Asp Arg Val Ser Leu Arg Ile Asp Ile
        200                 205                 210

aac gca cgt tgg gat cgc cgc acc gct ctg cat tac ttg ccg att ctc   787
Asn Ala Arg Trp Asp Arg Arg Thr Ala Leu His Tyr Leu Pro Ile Leu
    215                 220                 225

gcg gag gct ggc gtc gag ctg ttc gag cag ccc acc ccg gcc gac gac   835
Ala Glu Ala Gly Val Glu Leu Phe Glu Gln Pro Thr Pro Ala Asp Asp
230                 235                 240                 245

ctg gaa acc ctg cgc gaa atc acc cgc cgc acc aac gtt tcg gtc atg   883
Leu Glu Thr Leu Arg Glu Ile Thr Arg Arg Thr Asn Val Ser Val Met
                250                 255                 260

gca gat gaa tcc gtg tgg acc cca gct gaa gct ctc gcg gtg gtg aaa   931
Ala Asp Glu Ser Val Trp Thr Pro Ala Glu Ala Leu Ala Val Val Lys
            265                 270                 275

gcc cag gct gcg gat gtt atc gca ctg aaa acc act aag cac ggt ggt   979
Ala Gln Ala Ala Asp Val Ile Ala Leu Lys Thr Thr Lys His Gly Gly
        280                 285                 290

ctg ctg gaa tcc aag aag atc gcc gct atc gcc gaa gcc ggc ggg ctg   1027
Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala Glu Ala Gly Gly Leu
    295                 300                 305

gcc tgc cat ggt gca acc agt ctg gaa ggt cca atc ggc acc gca gca   1075
Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro Ile Gly Thr Ala Ala
310                 315                 320                 325

tcc ctg cag ttt gcg gca tcc acc aag gcg atc tcc tac ggt aca gaa   1123
Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile Ser Tyr Gly Thr Glu
                330                 335                 340

ctg ttc gga ccg cag ttg ctc aaa gat acc tat att gtc caa gaa ttt   1171
Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr Ile Val Gln Glu Phe
            345                 350                 355

gag tac aag gac ggc cag gtt gct att cca caa ggc cca ggt ttg ggc   1219
Glu Tyr Lys Asp Gly Gln Val Ala Ile Pro Gln Gly Pro Gly Leu Gly
        360                 365                 370

gtc gat gtg gac atg gac aaa gtc aac ttc tac acc cgt aaa           1261
Val Asp Val Asp Met Asp Lys Val Asn Phe Tyr Thr Arg Lys
    375                 380                 385

taaggagaat tatcgatgct gtt                                        1284
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<210> 374
<211> 387
<212> PRT
<213> Corynebacterium glutamicum

<400> 374

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Val Ala Gly Leu Phe Pro Leu Asn Gln Lys Ala Ile Glu Lys Leu Ser
 1               5                  10                  15

Asp Leu Thr Ile Gln Lys Val Glu Ser Arg Ile Leu Asp Val Pro Leu
            20                  25                  30

Ile Arg Pro His Gly Phe Ala Thr Thr Thr Ser Thr Glu Gln His Ile
        35                  40                  45

Leu Leu Val Ser Val His Leu Glu Asn Gly Val Ile Gly Tyr Gly Glu
    50                  55                  60

Gly Val Val Pro Gly Gly Pro Trp Trp Gly Gly Glu Ser Val Glu Thr
65                  70                  75                  80

Met Lys Ala Leu Val Asp Gly Tyr Leu Ala Pro Val Leu Ile Gly Arg
                85                  90                  95

Ala Val Ser Glu Leu Ala Gly Ile Met Ala Asp Leu Glu Arg Val Val
            100                 105                 110

Ala Arg Ala Arg Tyr Ala Lys Ala Ala Val Asp Val Ala Met His Asp
        115                 120                 125

Ala Trp Ala Arg Ser Leu Asn Val Pro Val Arg Asp Leu Leu Gly Gly
    130                 135                 140

Thr Val Arg Asp Lys Val Asp Val Thr Trp Ala Leu Gly Val Leu Pro
145                 150                 155                 160

Leu Asp Val Ala Val Ala Glu Ile Glu Glu Arg Ile Glu Glu Phe Gly
                165                 170                 175

Asn Arg Ser Phe Lys Leu Lys Met Gly Ala Gly Asp Pro Ala Glu Asp
            180                 185                 190

Thr Arg Arg Val Ala Glu Leu Ala Arg Glu Val Gly Asp Arg Val Ser
        195                 200                 205

Leu Arg Ile Asp Ile Asn Ala Arg Trp Asp Arg Arg Thr Ala Leu His
    210                 215                 220

Tyr Leu Pro Ile Leu Ala Glu Ala Gly Val Glu Leu Phe Glu Gln Pro
225                 230                 235                 240

Thr Pro Ala Asp Asp Leu Glu Thr Leu Arg Glu Ile Thr Arg Arg Thr
                245                 250                 255

Asn Val Ser Val Met Ala Asp Glu Ser Val Trp Thr Pro Ala Glu Ala
            260                 265                 270

Leu Ala Val Val Lys Ala Gln Ala Ala Asp Val Ile Ala Leu Lys Thr
        275                 280                 285

Thr Lys His Gly Gly Leu Leu Glu Ser Lys Lys Ile Ala Ala Ile Ala
    290                 295                 300

Glu Ala Gly Gly Leu Ala Cys His Gly Ala Thr Ser Leu Glu Gly Pro
305                 310                 315                 320

Ile Gly Thr Ala Ala Ser Leu Gln Phe Ala Ala Ser Thr Lys Ala Ile
```

```
                325                 330                 335

Ser Tyr Gly Thr Glu Leu Phe Gly Pro Gln Leu Leu Lys Asp Thr Tyr
            340                 345                 350

Ile Val Gln Glu Phe Glu Tyr Lys Asp Gly Gln Val Ala Ile Pro Gln
        355                 360                 365

Gly Pro Gly Leu Gly Val Asp Val Asp Met Asp Lys Val Asn Phe Tyr
    370                 375                 380

Thr Arg Lys
385
```

<210> 375
<211> 1137
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1114)
<223> RXA02316

<400> 375

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tgcgcaccta cggcgccgaa ttcccgctgg tcctgcttaa agatggacag gcactgctta 60

tcgacgacca cggcgtccac ctaatttagg atggttcccc atg agc acc cca act   115
                                             Met Ser Thr Pro Thr
                                               1               5

gtt gat gag att cta gag cgc gcc cac gtg gtg tcg ctg ccg atg cgt   163
Val Asp Glu Ile Leu Glu Arg Ala His Val Val Ser Leu Pro Met Arg
                  10                  15                  20

gtg aag ttt cgt ggc gtc acc acc agg gag gct ttg ctg att gaa ggc   211
Val Lys Phe Arg Gly Val Thr Thr Arg Glu Ala Leu Leu Ile Glu Gly
              25                  30                  35

cct gct ggt tgg gga gag ttc gcg ccc ttc ctt gag tat gac ccg caa   259
Pro Ala Gly Trp Gly Glu Phe Ala Pro Phe Leu Glu Tyr Asp Pro Gln
          40                  45                  50

gaa tcg gcc agt tgg cta aag tcc ggc att gaa gca gcg tgg gag ggt   307
Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu Ala Ala Trp Glu Gly
      55                  60                  65

ttt ccg gcg ccg ttg cgt gat cgc gtg gaa gtc aat gcc acc atc cca   355
Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val Asn Ala Thr Ile Pro
  70                  75                  80                  85

gct gtt ccg gcc gat caa gtg gca gaa gtt ttg gac cgt ttc cca ggc   403
Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu Asp Arg Phe Pro Gly
                  90                  95                 100

tgt cgc acc atc aaa gta aag gtc gcg gaa cca ggc cag acc ttg gct   451
Cys Arg Thr Ile Lys Val Lys Val Ala Glu Pro Gly Gln Thr Leu Ala
              105                 110                 115

gat gac atc gcg cga gtt gcc gct gcc cgt gag gca cgc ccc ggc gcg   499
```

```
Asp Asp Ile Ala Arg Val Ala Ala Ala Arg Glu Ala Arg Pro Gly Ala
        120                 125                 130

atc atc cgt gtt gat gcc aat tgt ggg tgg agt gtg gag cag gcg gtg   547
Ile Ile Arg Val Asp Ala Asn Cys Gly Trp Ser Val Glu Gln Ala Val
    135                 140                 145

gag gcg gct cag gcg ttg gcg ccg ttg gat tat tta gag cag ccg tgt   595
Glu Ala Ala Gln Ala Leu Ala Pro Leu Asp Tyr Leu Glu Gln Pro Cys
150                 155                 160                 165

gcc acc gtg gag gaa ctg gcg gaa gtg cgc atg acg gtg cag cgg cgc   643
Ala Thr Val Glu Glu Leu Ala Glu Val Arg Met Thr Val Gln Arg Arg
                170                 175                 180

gga ctt ttt gtg cgc gtt gca gcg gat gaa tcg atc aga aaa tct gat   691
Gly Leu Phe Val Arg Val Ala Ala Asp Glu Ser Ile Arg Lys Ser Asp
            185                 190                 195

gat cct tat cgg gtg gcg gat ctg cgt gct gcg gat gtg gct gtg gtg   739
Asp Pro Tyr Arg Val Ala Asp Leu Arg Ala Ala Asp Val Ala Val Val
        200                 205                 210

aag gtt gct cct ttg ggt ggt gtg aaa agg gta ctt gag gtg gtg caa   787
Lys Val Ala Pro Leu Gly Gly Val Lys Arg Val Leu Glu Val Val Gln
    215                 220                 225

cat ttg cgg gcg cgc acg atg gac atc act gta gca agt gcg ttg gac   835
His Leu Arg Ala Arg Thr Met Asp Ile Thr Val Ala Ser Ala Leu Asp
230                 235                 240                 245

acg gtt gtg ggg atg aat gct ggg ttg gct gcg gtg gcg gcg ttg ccg   883
Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala Val Ala Ala Leu Pro
                250                 255                 260

aag ttg gat gat gac gat ctc att gat gtg cca cca gcg gcg gcg ggt   931
Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro Pro Ala Ala Ala Gly
            265                 270                 275

ctt gcg act tcg cag ttg ttc ctg gag gat gtc gcg acc ccg cac gca   979
Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val Ala Thr Pro His Ala
        280                 285                 290

atc act gat ggg ttc atg gaa acg cgt gta att gcc ccg gaa atg gat   1027
Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile Ala Pro Glu Met Asp
    295                 300                 305

cgt ttg gaa acg ctt gct gcc agc aaa gat agg cgt gat tgg tgg ttt   1075
Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg Arg Asp Trp Trp Phe
310                 315                 320                 325

gag cgc gtg cgt gaa tcg tat ccg tac ctg gag acg atc tagactgttg    1124
Glu Arg Val Arg Glu Ser Tyr Pro Tyr Leu Glu Thr Ile
                330                 335

tgcatgtcca gca                                                   1137
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<210> 376
<211> 338
<212> PRT

<213> Corynebacterium glutamicum

<400> 376

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Met Ser Thr Pro Thr Val Asp Glu Ile Leu Glu Arg Ala His Val Val
  1               5                  10                  15

Ser Leu Pro Met Arg Val Lys Phe Arg Gly Val Thr Thr Arg Glu Ala
            20                  25                  30

Leu Leu Ile Glu Gly Pro Ala Gly Trp Gly Glu Phe Ala Pro Phe Leu
        35                  40                  45

Glu Tyr Asp Pro Gln Glu Ser Ala Ser Trp Leu Lys Ser Gly Ile Glu
    50                  55                  60

Ala Ala Trp Glu Gly Phe Pro Ala Pro Leu Arg Asp Arg Val Glu Val
65                  70                  75                  80

Asn Ala Thr Ile Pro Ala Val Pro Ala Asp Gln Val Ala Glu Val Leu
                85                  90                  95

Asp Arg Phe Pro Gly Cys Arg Thr Ile Lys Val Lys Val Ala Glu Pro
            100                 105                 110

Gly Gln Thr Leu Ala Asp Asp Ile Ala Arg Val Ala Ala Ala Arg Glu
        115                 120                 125

Ala Arg Pro Gly Ala Ile Ile Arg Val Asp Ala Asn Cys Gly Trp Ser
    130                 135                 140

Val Glu Gln Ala Val Glu Ala Ala Gln Ala Leu Ala Pro Leu Asp Tyr
145                 150                 155                 160

Leu Glu Gln Pro Cys Ala Thr Val Glu Glu Leu Ala Glu Val Arg Met
                165                 170                 175

Thr Val Gln Arg Arg Gly Leu Phe Val Arg Val Ala Ala Asp Glu Ser
            180                 185                 190

Ile Arg Lys Ser Asp Asp Pro Tyr Arg Val Ala Asp Leu Arg Ala Ala
        195                 200                 205

Asp Val Ala Val Val Lys Val Ala Pro Leu Gly Gly Val Lys Arg Val
    210                 215                 220

Leu Glu Val Val Gln His Leu Arg Ala Arg Thr Met Asp Ile Thr Val
225                 230                 235                 240

Ala Ser Ala Leu Asp Thr Val Val Gly Met Asn Ala Gly Leu Ala Ala
                245                 250                 255

Val Ala Ala Leu Pro Lys Leu Asp Asp Asp Asp Leu Ile Asp Val Pro
            260                 265                 270

Pro Ala Ala Ala Gly Leu Ala Thr Ser Gln Leu Phe Leu Glu Asp Val
        275                 280                 285

Ala Thr Pro His Ala Ile Thr Asp Gly Phe Met Glu Thr Arg Val Ile
    290                 295                 300

Ala Pro Glu Met Asp Arg Leu Glu Thr Leu Ala Ala Ser Lys Asp Arg
```

```
305                 310                 315                 320

Arg Asp Trp Trp Phe Glu Arg Val Arg Glu Ser Tyr Pro Tyr Leu Glu
                325                 330                 335

Thr Ile
```

<210> 377
<211> 414
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(391)
<223> RXA01464

<400> 377

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caaggacggc caggttgcta ttccacaagg cccaggtttg ggcgtcgatg tggacatgga 60

caaagtcaac ttctacaccc gtaaataagg agaattatcg atg ctg ttt cta gca   115
                                            Met Leu Phe Leu Ala
                                              1               5

cgc atg gac gtc gtc ttc cct gat tcc atg gac gcc gat gtg atg gca   163
Arg Met Asp Val Val Phe Pro Asp Ser Met Asp Ala Asp Val Met Ala
                 10                  15                  20

gat ttc cag gct aag gaa aag gcc tac tcc gga gac ctg caa tcc cgt   211
Asp Phe Gln Ala Lys Glu Lys Ala Tyr Ser Gly Asp Leu Gln Ser Arg
             25                  30                  35

gga atc atg aaa gca atc tgg cga gtc gtc ggc gag tat gca aac tac   259
Gly Ile Met Lys Ala Ile Trp Arg Val Val Gly Glu Tyr Ala Asn Tyr
         40                  45                  50

tcc att ttc gat gtc gat gac cac gac gag ctg cat gca att ctt agt   307
Ser Ile Phe Asp Val Asp Asp His Asp Glu Leu His Ala Ile Leu Ser
     55                  60                  65

ggc ttt ccg atg ttc aaa tac atg aat gtc aag atc act cca ctg gca   355
Gly Phe Pro Met Phe Lys Tyr Met Asn Val Lys Ile Thr Pro Leu Ala
 70                  75                  80                  85

aaa cac ccc aat gct ctg gag tat tac ctc aag gga tagttgaggt        401
Lys His Pro Asn Ala Leu Glu Tyr Tyr Leu Lys Gly
                 90                  95

tctaaccgct cta                                                   414
```

<210> 378
<211> 97
<212> PRT
<213> Corynebacterium glutamicum

<400> 378

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Met Leu Phe Leu Ala Arg Met Asp Val Val Phe Pro Asp Ser Met Asp
  1               5                  10                  15
```

```
Ala Asp Val Met Ala Asp Phe Gln Ala Lys Glu Lys Ala Tyr Ser Gly
            20                  25                  30

Asp Leu Gln Ser Arg Gly Ile Met Lys Ala Ile Trp Arg Val Val Gly
        35                  40                  45

Glu Tyr Ala Asn Tyr Ser Ile Phe Asp Val Asp Asp His Asp Glu Leu
    50                  55                  60

His Ala Ile Leu Ser Gly Phe Pro Met Phe Lys Tyr Met Asn Val Lys
65                  70                  75                  80

Ile Thr Pro Leu Ala Lys His Pro Asn Ala Leu Glu Tyr Tyr Leu Lys
                85                  90                  95

Gly
```

<210> 379
<211> 1119
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1096)
<223> RXA02603

<400> 379

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gcatggtgct tggcgtgcat tacccaaccg atgtgctagc cggcgcgttg ttgggagcag 60

cgaccgcaga ggccgtccat aagatcgaaa gggctacgaa gtg agc gaa cac gcc   115
                                        Val Ser Glu His Ala
                                          1               5

gct gaa cat cac cgc gat acc caa aat ttc tta acc tcc gaa ccg cac   163
Ala Glu His His Arg Asp Thr Gln Asn Phe Leu Thr Ser Glu Pro His
                10                  15                  20

acc acg gca atc gaa gac aac aag aag cgc caa ccg ccg aaa aac ctt   211
Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln Pro Pro Lys Asn Leu
            25                  30                  35

gct gac ggc atg atc aag gcg ctg cgc ccc aag cag tgg gtc aag aac   259
Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys Gln Trp Val Lys Asn
        40                  45                  50

gtt ctt gtg cta gca gca cca ctt gct gct ggt gca gat gcg atc ttc   307
Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly Ala Asp Ala Ile Phe
    55                  60                  65

aac cag cgc acg atc atc gac gtt gct atc gca ttc gta gtg ttc tgc   355
Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala Phe Val Val Phe Cys
70                  75                  80                  85

ttc ggt gca tca gcc att tac ttg gtt aat gat gcc cgt gac gtg gaa   403
Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp Ala Arg Asp Val Glu
                90                  95                  100
```

```
gct gac cgc gag cac cca acc aag cgt ttc cgc ccc atc gct gca gga   451
Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg Pro Ile Ala Ala Gly
            105                 110                 115

gtc ctg cca gta gga atg gca tac ggc atg gcc gtg gcg ctc att gca   499
Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala Val Ala Leu Ile Ala
        120                 125                 130

cta tcc atc gga ctg tct ttc ctc gcc acc gac ggc gtg gca ctt gcc   547
Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp Gly Val Ala Leu Ala
    135                 140                 145

tgc gtg att ggc gtg tac att gcg ctg cag ctg gga tac tgc ttc ggt   595
Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu Gly Tyr Cys Phe Gly
150                 155                 160                 165

tgg aag cac atg cca gtg atc gat att gcg ctt gtc tcc tcc gga ttc   643
Trp Lys His Met Pro Val Ile Asp Ile Ala Leu Val Ser Ser Gly Phe
                170                 175                 180

atg ctc cgc gca atg gca ggt ggt gtc gca gca ggc atc gag cta tcc   691
Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala Gly Ile Glu Leu Ser
            185                 190                 195

cag tgg ttc ctg cta gtc gct gcg ttt ggt tcc ctg ttc atg gca tct   739
Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser Leu Phe Met Ala Ser
        200                 205                 210

gga aag cgc tac gca gaa atc ctt ctg cac gag cgc acc ggc gct aag   787
Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu Arg Thr Gly Ala Lys
    215                 220                 225

atc cgc aag tcc ctg gaa agc tac acc ccc acc tac ctg cgc ttc gtt   835
Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr Tyr Leu Arg Phe Val
230                 235                 240                 245

tgg acc atg gca gca aca gca gtg gtc atg tcc tac gca ctg tgg ggc   883
Trp Thr Met Ala Ala Thr Ala Val Val Met Ser Tyr Ala Leu Trp Gly
                250                 255                 260

ttc gac ctt tcc caa cac tcc acc gac gca ggt ccg tgg tac caa atc   931
Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly Pro Trp Tyr Gln Ile
            265                 270                 275

tcc atg gtt cca ttc acc atc gcc atc ctg cgc tac gca gcc ggc gta   979
Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg Tyr Ala Ala Gly Val
        280                 285                 290

gac acc ggc gac ggc ggt gcc cct gac gaa gtg gca ctc agc gac aaa   1027
Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val Ala Leu Ser Asp Lys
    295                 300                 305

gtt ctg cag gta cta gcc cta gca tgg gtt ttc tgc atc gtg atg gct   1075
Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe Cys Ile Val Met Ala
310                 315                 320                 325

gtg tac atc atg ccg atg ttt tgaatattta ccaatgaaca tgc            1119
Val Tyr Ile Met Pro Met Phe
                330
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<210> 380
<211> 332
<212> PRT
<213> Corynebacterium glutamicum

<400> 380
Val Ser Glu His Ala Ala Glu His His Arg Asp Thr Gln Asn Phe Leu
1 5 10 15

Thr Ser Glu Pro His Thr Thr Ala Ile Glu Asp Asn Lys Lys Arg Gln
20 25 30

Pro Pro Lys Asn Leu Ala Asp Gly Met Ile Lys Ala Leu Arg Pro Lys
35 40 45

Gln Trp Val Lys Asn Val Leu Val Leu Ala Ala Pro Leu Ala Ala Gly
50 55 60

Ala Asp Ala Ile Phe Asn Gln Arg Thr Ile Ile Asp Val Ala Ile Ala
65 70 75 80

Phe Val Val Phe Cys Phe Gly Ala Ser Ala Ile Tyr Leu Val Asn Asp
85 90 95

Ala Arg Asp Val Glu Ala Asp Arg Glu His Pro Thr Lys Arg Phe Arg
100 105 110

Pro Ile Ala Ala Gly Val Leu Pro Val Gly Met Ala Tyr Gly Met Ala
115 120 125

Val Ala Leu Ile Ala Leu Ser Ile Gly Leu Ser Phe Leu Ala Thr Asp
130 135 140

Gly Val Ala Leu Ala Cys Val Ile Gly Val Tyr Ile Ala Leu Gln Leu
145 150 155 160

Gly Tyr Cys Phe Gly Trp Lys His Met Pro Val Ile Asp Ile Ala Leu
165 170 175

Val Ser Ser Gly Phe Met Leu Arg Ala Met Ala Gly Gly Val Ala Ala
180 185 190

Gly Ile Glu Leu Ser Gln Trp Phe Leu Leu Val Ala Ala Phe Gly Ser
195 200 205

Leu Phe Met Ala Ser Gly Lys Arg Tyr Ala Glu Ile Leu Leu His Glu
210 215 220

Arg Thr Gly Ala Lys Ile Arg Lys Ser Leu Glu Ser Tyr Thr Pro Thr
225 230 235 240

Tyr Leu Arg Phe Val Trp Thr Met Ala Ala Thr Ala Val Val Met Ser
245 250 255

Tyr Ala Leu Trp Gly Phe Asp Leu Ser Gln His Ser Thr Asp Ala Gly
260 265 270

Pro Trp Tyr Gln Ile Ser Met Val Pro Phe Thr Ile Ala Ile Leu Arg
275 280 285

Tyr Ala Ala Gly Val Asp Thr Gly Asp Gly Gly Ala Pro Asp Glu Val

```
    290                 295                 300

Ala Leu Ser Asp Lys Val Leu Gln Val Leu Ala Leu Ala Trp Val Phe
305                 310                 315                 320

Cys Ile Val Met Ala Val Tyr Ile Met Pro Met Phe
                325                 330


<210> 381
<211> 470
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(447)
<223> RXN02839

<400> 381
tgt gtg gtg aat gat tat gct gac cgc aag ttt gat ggt cat gtt aag   48
Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
  1               5                  10                  15

cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag   96
Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
             20                  25                  30

gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg   144
Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
         35                  40                  45

ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg   192
Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
     50                  55                  60

ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa   240
Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65                  70                  75                  80

gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc   288
Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
                 85                  90                  95

gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc   336
Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
            100                 105                 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac   384
Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
        115                 120                 125

cgc gat gat gat gtg aag att ggc att aaa tcc acg gca atc ctg ttg   432
Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
    130                 135                 140

gcc aat acg ata aat tgatattggg attttgcaga ttg                    470
Ala Asn Thr Ile Asn
145
```

<210> 382
<211> 149
<212> PRT
<213> Corynebacterium glutamicum

<400> 382
Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
1 5 10 15

Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
20 25 30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
35 40 45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
50 55 60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
65 70 75 80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
85 90 95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
100 105 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
115 120 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser Thr Ala Ile Leu Leu
130 135 140

Ala Asn Thr Ile Asn
145

<210> 383
<211> 417
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(417)
<223> FRXA02839

<400> 383
tgt gtg gtg aat gat tat gct gac cgc aag ttt gat ggt cat gtt aag 48
Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
1 5 10 15

cgc acg gcg aac cga cca ctt ccc agc ggc gcg gta aca gag aaa gag 96
Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
20 25 30

gcg cgc gcg ctg ttt gtc gtg ctg gta ctg att tcg ttt tta ctg gtg 144
Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
35 40 45

ctg acg ctg aat acg atg acc att ctg ttg tcg att gcc gcg cta gcg 192

```
Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
     50                  55                  60

ctg gcg tgg gtg tac ccg ttt atg aag cgg tat acc cat cta ccg caa   240
Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65                  70                  75                  80

gtg gtg ctg ggc gcg gcg ttt ggc tgg tcg att cca atg gct ttt gcc   288
Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
                85                  90                  95

gct gtg agt gag tcg gtg cca ttg agt tgc tgg tta atg ttc ctc gcc   336
Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
            100                 105                 110

aat att ctc tgg gcg gtg gct tac gac acg cag tat gcg atg gtt gac   384
Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
        115                 120                 125

cgc gat gat gat gtg aag att ggc att aaa tcc                       417
Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
    130                 135
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SEQUENCE LISTING

<210> 384
<211> 139
<212> PRT
<213> Corynebacterium glutamicum

<400> 384

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Cys Val Val Asn Asp Tyr Ala Asp Arg Lys Phe Asp Gly His Val Lys
  1               5                  10                  15

Arg Thr Ala Asn Arg Pro Leu Pro Ser Gly Ala Val Thr Glu Lys Glu
             20                  25                  30

Ala Arg Ala Leu Phe Val Val Leu Val Leu Ile Ser Phe Leu Leu Val
         35                  40                  45

Leu Thr Leu Asn Thr Met Thr Ile Leu Leu Ser Ile Ala Ala Leu Ala
     50                  55                  60

Leu Ala Trp Val Tyr Pro Phe Met Lys Arg Tyr Thr His Leu Pro Gln
 65                  70                  75                  80

Val Val Leu Gly Ala Ala Phe Gly Trp Ser Ile Pro Met Ala Phe Ala
                85                  90                  95

Ala Val Ser Glu Ser Val Pro Leu Ser Cys Trp Leu Met Phe Leu Ala
            100                 105                 110

Asn Ile Leu Trp Ala Val Ala Tyr Asp Thr Gln Tyr Ala Met Val Asp
        115                 120                 125

Arg Asp Asp Asp Val Lys Ile Gly Ile Lys Ser
    130                 135
```

<210> 385
<211> 1356
<212> DNA

<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1333)
<223> RXA01502

<400> 385
gctcgccgag ggtttcggcc ttttaactag catggtgtat agatccatgc ggtcgacctt 60

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gcgcctgacc gtccactttt ttagggacta ggagtacagc atg agc aca cca caa   115
                                            Met Ser Thr Pro Gln
                                              1               5

agc atc gtc att atc ggc ggc ggt tta gcc gga gcg aaa acc gca gag   163
Ser Ile Val Ile Ile Gly Gly Gly Leu Ala Gly Ala Lys Thr Ala Glu
                 10                  15                  20

gca cta cgt gta aac ggg tat gaa ggc tcc atc acg ctc atc gca gca   211
Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile Thr Leu Ile Ala Ala
             25                  30                  35

gag gat tat ctg cca tat gag cgc cca ccg ctg tca aag gag tac atg   259
Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu Ser Lys Glu Tyr Met
         40                  45                  50

gct gga aaa gtg ggc ttt gac aag gcg att gtt cac ccg gcg gag tgg   307
Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val His Pro Ala Glu Trp
     55                  60                  65

tac aaa gaa aac aat gtc acg ctg cgt caa ggt gtg cgt gca acg gca   355
Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly Val Arg Ala Thr Ala
 70                  75                  80                  85

att gat gcg ggt tca cgc caa gtc acc gtt gat gat ggc gga aac act   403
Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp Asp Gly Gly Asn Thr
                 90                  95                 100

gag acc att aac tac gac aaa cta gtt ctt gct act gga tca gca gtg   451
Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala Thr Gly Ser Ala Val
            105                 110                 115

cgc aaa ctt cca att ccg gga gcc gac gcc tct aat gtg cac tac ctg   499
Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser Asn Val His Tyr Leu
        120                 125                 130

cgc acc gtg gaa gac tct gac gcg atc aag gca acc ttc ggt gaa ggt   547
Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala Thr Phe Gly Glu Gly
    135                 140                 145

aaa aag ctg gtc ctc atc ggt ggt ggc tgg atc gga ctc gaa gtc gca   595
Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile Gly Leu Glu Val Ala
150                 155                 160                 165

tca gcg gca cga gga gct ggc act gac gtc act gtt ttg gaa ggt gga   643
Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr Val Leu Glu Gly Gly
                170                 175                 180

aag ctc cca ctt ttg aaa gtc ctt ggt gaa acg gtc gcg caa gtc ttt   691
Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr Val Ala Gln Val Phe
            185                 190                 195
```

```
gcc gat ctg cat gtg gca aac ggc gtt gac ctg cgc acc gaa gtg aaa   739
Ala Asp Leu His Val Ala Asn Gly Val Asp Leu Arg Thr Glu Val Lys
        200                 205                 210

att acg gac atc gtc acc gaa gat gga cgt gca gtt ggc gtg cga ctt   787
Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala Val Gly Val Arg Leu
    215                 220                 225

gat gac ggc gaa gtg gtt ccc gca gac gca gta gtc att ggc atc ggt   835
Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val Val Ile Gly Ile Gly
230                 235                 240                 245

gtc acc cca gtg att gac cta gcg gaa act gct gga ctg gaa atc gac   883
Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala Gly Leu Glu Ile Asp
                250                 255                 260

aat ggt gtt ttg gtg gac gca gca ctg cgt acc agc gac ccg gat atc   931
Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr Ser Asp Pro Asp Ile
            265                 270                 275

tac gca gtt gga gac att gcg aac cac gat cac cca gtt cta gga cac   979
Tyr Ala Val Gly Asp Ile Ala Asn His Asp His Pro Val Leu Gly His
        280                 285                 290

cgc atc cgc gtg gag cac tgg gcc acc gcg ttg aat caa cct gcg gct  1027
Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu Asn Gln Pro Ala Ala
    295                 300                 305

gcg gtg aaa tcc cta ctt ggc aaa gac gcc gag ttt acc aac ctt ccg  1075
Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu Phe Thr Asn Leu Pro
310                 315                 320                 325

tac ttc ttt aca gat caa ttc gat ctg ggt tgt gaa tac gtc ggc cac  1123
Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys Glu Tyr Val Gly His
                330                 335                 340

gcc acc ggt tcg cag gag aag gta ttc atc cgt gga aac ctt gaa aca  1171
Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg Gly Asn Leu Glu Thr
            345                 350                 355

cga gaa ttt gtc gcc ttc tgg gtt gat act gaa aac cga att ctc gcc  1219
Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu Asn Arg Ile Leu Ala
        360                 365                 370

gca atg aac gtg aat gtg tgg gat gtt cct gat caa atc aag cct ctc  1267
Ala Met Asn Val Asn Val Trp Asp Val Pro Asp Gln Ile Lys Pro Leu
    375                 380                 385

atc gca tca gga aag agc gtt gac acc gag aag cta gtg gat cca gaa  1315
Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys Leu Val Asp Pro Glu
390                 395                 400                 405

gtt ccg tat tca gag ctc taagcagtgt gtttgatggc cgc                1356
Val Pro Tyr Ser Glu Leu
                410
```

<210> 386
<211> 411
<212> PRT

<213> Corynebacterium glutamicum

<400> 386

```
Met Ser Thr Pro Gln Ser Ile Val Ile Ile Gly Gly Gly Leu Ala Gly
  1               5                  10                  15

Ala Lys Thr Ala Glu Ala Leu Arg Val Asn Gly Tyr Glu Gly Ser Ile
             20                  25                  30

Thr Leu Ile Ala Ala Glu Asp Tyr Leu Pro Tyr Glu Arg Pro Pro Leu
         35                  40                  45

Ser Lys Glu Tyr Met Ala Gly Lys Val Gly Phe Asp Lys Ala Ile Val
     50                  55                  60

His Pro Ala Glu Trp Tyr Lys Glu Asn Asn Val Thr Leu Arg Gln Gly
 65                  70                  75                  80

Val Arg Ala Thr Ala Ile Asp Ala Gly Ser Arg Gln Val Thr Val Asp
                 85                  90                  95

Asp Gly Gly Asn Thr Glu Thr Ile Asn Tyr Asp Lys Leu Val Leu Ala
            100                 105                 110

Thr Gly Ser Ala Val Arg Lys Leu Pro Ile Pro Gly Ala Asp Ala Ser
        115                 120                 125

Asn Val His Tyr Leu Arg Thr Val Glu Asp Ser Asp Ala Ile Lys Ala
    130                 135                 140

Thr Phe Gly Glu Gly Lys Lys Leu Val Leu Ile Gly Gly Gly Trp Ile
145                 150                 155                 160

Gly Leu Glu Val Ala Ser Ala Ala Arg Gly Ala Gly Thr Asp Val Thr
                165                 170                 175

Val Leu Glu Gly Gly Lys Leu Pro Leu Leu Lys Val Leu Gly Glu Thr
            180                 185                 190

Val Ala Gln Val Phe Ala Asp Leu His Val Ala Asn Gly Val Asp Leu
        195                 200                 205

Arg Thr Glu Val Lys Ile Thr Asp Ile Val Thr Glu Asp Gly Arg Ala
    210                 215                 220

Val Gly Val Arg Leu Asp Asp Gly Glu Val Val Pro Ala Asp Ala Val
225                 230                 235                 240

Val Ile Gly Ile Gly Val Thr Pro Val Ile Asp Leu Ala Glu Thr Ala
                245                 250                 255

Gly Leu Glu Ile Asp Asn Gly Val Leu Val Asp Ala Ala Leu Arg Thr
            260                 265                 270

Ser Asp Pro Asp Ile Tyr Ala Val Gly Asp Ile Ala Asn His Asp His
        275                 280                 285

Pro Val Leu Gly His Arg Ile Arg Val Glu His Trp Ala Thr Ala Leu
    290                 295                 300

Asn Gln Pro Ala Ala Ala Val Lys Ser Leu Leu Gly Lys Asp Ala Glu
```

```
305                 310                 315                 320

Phe Thr Asn Leu Pro Tyr Phe Phe Thr Asp Gln Phe Asp Leu Gly Cys
                325                 330                 335

Glu Tyr Val Gly His Ala Thr Gly Ser Gln Glu Lys Val Phe Ile Arg
            340                 345                 350

Gly Asn Leu Glu Thr Arg Glu Phe Val Ala Phe Trp Val Asp Thr Glu
        355                 360                 365

Asn Arg Ile Leu Ala Ala Met Asn Val Asn Val Trp Asp Val Pro Asp
    370                 375                 380

Gln Ile Lys Pro Leu Ile Ala Ser Gly Lys Ser Val Asp Thr Glu Lys
385                 390                 395                 400

Leu Val Asp Pro Glu Val Pro Tyr Ser Glu Leu
                405                 410
```

<210> 387
<211> 572
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (15)..(572)
<223> RXA02828

<400> 387

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agtcaggatt tatgatg aaa cga cgt gac ttc ctg tcg gcg ctt tct gcc    50
                Met Lys Arg Arg Asp Phe Leu Ser Ala Leu Ser Ala
                  1               5                  10

ggc acc ctc tcg ctg ggc ggn ttt gcg ccc caa ctg ctg ctg gcc caa   98
Gly Thr Leu Ser Leu Gly Gly Phe Ala Pro Gln Leu Leu Leu Ala Gln
          15                  20                  25

ggg atg aat cag cca atg cgc gcg ccc att cat gtg ggt aaa tcg ggc   146
Gly Met Asn Gln Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly
      30                  35                  40

ctg cgc gcc cgc gac gcc gag gcg ctt gcc acc tgg tac caa agc cac   194
Leu Arg Ala Arg Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His
  45                  50                  55                  60

gtc ggc ctg caa gaa att ggc cgc gac ggc gcg acg atc cac atg ggt   242
Val Gly Leu Gln Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly
                  65                  70                  75

gcg ggc ggc acc gtg ctg ctg gaa atc acg cag tac gac ggt atc gtg   290
Ala Gly Gly Thr Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val
              80                  85                  90

ctg gcg ccc atg cgc gtc gcg ggc ctt tat cac aac gcg ttc ctg ctg   338
Leu Ala Pro Met Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu
          95                  100                 105

ccc gcg cgc gcg gat ctg gcg cgg tgg gtg ctg gac gcc tcg gca cgg   386
```

```
Pro Ala Arg Ala Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg
    110                 115                 120

caa ctg cgg atc gac ggc tat gcc gac cac ctt gtc agc gag gcg atg   434
Gln Leu Arg Ile Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met
125                 130                 135                 140

tac ctg acc gac ccc gaa ggc aac ggc gtc gaa atc tac gcc gac cgc   482
Tyr Leu Thr Asp Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg
                145                 150                 155

ccc gcc agc gac tgg gtc tgg cgc aat ggt cag gtc gag atg gac agc   530
Pro Ala Ser Asp Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser
            160                 165                 170

ctg caa atc gac ttc tac agc atg atc gcc acg ctt gac ggc           572
Leu Gln Ile Asp Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
        175                 180                 185


<210> 388
<211> 186
<212> PRT
<213> Corynebacterium glutamicum

<400> 388
Met Lys Arg Arg Asp Phe Leu Ser Ala Leu Ser Ala Gly Thr Leu Ser
  1               5                  10                  15

Leu Gly Gly Phe Ala Pro Gln Leu Leu Leu Ala Gln Gly Met Asn Gln
            20                  25                  30

Pro Met Arg Ala Pro Ile His Val Gly Lys Ser Gly Leu Arg Ala Arg
        35                  40                  45

Asp Ala Glu Ala Leu Ala Thr Trp Tyr Gln Ser His Val Gly Leu Gln
    50                  55                  60

Glu Ile Gly Arg Asp Gly Ala Thr Ile His Met Gly Ala Gly Gly Thr
65                  70                  75                  80

Val Leu Leu Glu Ile Thr Gln Tyr Asp Gly Ile Val Leu Ala Pro Met
                85                  90                  95

Arg Val Ala Gly Leu Tyr His Asn Ala Phe Leu Leu Pro Ala Arg Ala
            100                 105                 110

Asp Leu Ala Arg Trp Val Leu Asp Ala Ser Ala Arg Gln Leu Arg Ile
        115                 120                 125

Asp Gly Tyr Ala Asp His Leu Val Ser Glu Ala Met Tyr Leu Thr Asp
    130                 135                 140

Pro Glu Gly Asn Gly Val Glu Ile Tyr Ala Asp Arg Pro Ala Ser Asp
145                 150                 155                 160

Trp Val Trp Arg Asn Gly Gln Val Glu Met Asp Ser Leu Gln Ile Asp
                165                 170                 175

Phe Tyr Ser Met Ile Ala Thr Leu Asp Gly
            180                 185
```

<210> 389
<211> 762
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(739)
<223> RXA02064

<400> 389
ctagattaca tcctgtgcat cttctggcaa ttgtgaattc atttgcactt aatgcgtgta 60

ggtacttcac atctcgcctg ctcgctctag actataacgc gtg agt aac gcc ttc 115
Val Ser Asn Ala Phe
1 5

gag tat ctt cgc act tat gtc gag tcc act act gaa acc gac gct gct 163
Glu Tyr Leu Arg Thr Tyr Val Glu Ser Thr Thr Glu Thr Asp Ala Ala
10 15 20

gta gcg cgc gct cgt gaa gac gcc gcc gag ttc ggt ctc ccc gcc ccg 211
Val Ala Arg Ala Arg Glu Asp Ala Ala Glu Phe Gly Leu Pro Ala Pro
25 30 35

gat gaa atg act ggc cag ctg cta acc act ttg gct gcc acc acc aat 259
Asp Glu Met Thr Gly Gln Leu Leu Thr Thr Leu Ala Ala Thr Thr Asn
40 45 50

ggc aac ggc tcc act ggt gcc atc gcg att acc ccg gct gcc ggg ttg 307
Gly Asn Gly Ser Thr Gly Ala Ile Ala Ile Thr Pro Ala Ala Gly Leu
55 60 65

gtg ggt ctg tat atc ctg aac gga ctg gcc gat aac acc aca ctg acc 355
Val Gly Leu Tyr Ile Leu Asn Gly Leu Ala Asp Asn Thr Thr Leu Thr
70 75 80 85

tgc att gat cct gaa tca gag cat cag cgc cag gcc aaa gca ctc ttc 403
Cys Ile Asp Pro Glu Ser Glu His Gln Arg Gln Ala Lys Ala Leu Phe
90 95 100

cgc gag gcc ggc tat tcc ccc agc cgc gta cgc ttc ttg ctc tcg cgc 451
Arg Glu Ala Gly Tyr Ser Pro Ser Arg Val Arg Phe Leu Leu Ser Arg
105 110 115

ccg ctc gac gtg atg agt cgc ctt gcc aac gac agc tat cag ctt gtc 499
Pro Leu Asp Val Met Ser Arg Leu Ala Asn Asp Ser Tyr Gln Leu Val
120 125 130

ttc ggc caa gtc tcc ccc atg gat tta aag gcg ctt gtc gac gcc gcc 547
Phe Gly Gln Val Ser Pro Met Asp Leu Lys Ala Leu Val Asp Ala Ala
135 140 145

tgg ccg ctt ctt cga cga ggc ggt gcg ctg gtg ctc gcc gat gcg ctc 595
Trp Pro Leu Leu Arg Arg Gly Gly Ala Leu Val Leu Ala Asp Ala Leu
150 155 160 165

ctt gac ggc acc att gcg gat caa acc cgc aag gat cgt gac acc caa 643
Leu Asp Gly Thr Ile Ala Asp Gln Thr Arg Lys Asp Arg Asp Tnr Gln

```
                170                 175                 180

gca gca cgt gac gcc gat gaa tat att cgt tcc att gaa ggc gca cac   691
Ala Ala Arg Asp Ala Asp Glu Tyr Ile Arg Ser Ile Glu Gly Ala His
            185                 190                 195

gtt gct cgc ctg ccc ctt ggt gca ggc tta acc gtg gtg act aaa gcc   739
Val Ala Arg Leu Pro Leu Gly Ala Gly Leu Thr Val Val Thr Lys Ala
        200                 205                 210

tagaggggga cgtcgagaag cga                                        762


<210> 390
<211> 213
<212> PRT
<213> Corynebacterium glutamicum

<400> 390
Val Ser Asn Ala Phe Glu Tyr Leu Arg Thr Tyr Val Glu Ser Thr Thr
  1               5                  10                  15

Glu Thr Asp Ala Ala Val Ala Arg Ala Arg Glu Asp Ala Ala Glu Phe
             20                  25                  30

Gly Leu Pro Ala Pro Asp Glu Met Thr Gly Gln Leu Leu Thr Thr Leu
         35                  40                  45

Ala Ala Thr Thr Asn Gly Asn Gly Ser Thr Gly Ala Ile Ala Ile Thr
     50                  55                  60

Pro Ala Ala Gly Leu Val Gly Leu Tyr Ile Leu Asn Gly Leu Ala Asp
 65                  70                  75                  80

Asn Thr Thr Leu Thr Cys Ile Asp Pro Glu Ser Glu His Gln Arg Gln
                 85                  90                  95

Ala Lys Ala Leu Phe Arg Glu Ala Gly Tyr Ser Pro Ser Arg Val Arg
            100                 105                 110

Phe Leu Leu Ser Arg Pro Leu Asp Val Met Ser Arg Leu Ala Asn Asp
        115                 120                 125

Ser Tyr Gln Leu Val Phe Gly Gln Val Ser Pro Met Asp Leu Lys Ala
    130                 135                 140

Leu Val Asp Ala Ala Trp Pro Leu Leu Arg Arg Gly Gly Ala Leu Val
145                 150                 155                 160

Leu Ala Asp Ala Leu Leu Asp Gly Thr Ile Ala Asp Gln Thr Arg Lys
                165                 170                 175

Asp Arg Asp Thr Gln Ala Ala Arg Asp Ala Asp Glu Tyr Ile Arg Ser
            180                 185                 190

Ile Glu Gly Ala His Val Ala Arg Leu Pro Leu Gly Ala Gly Leu Thr
        195                 200                 205

Val Val Thr Lys Ala
    210
```

<210> 391
<211> 978
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(955)
<223> RXN00639

<400> 391
agtgttgtta tcgagttcag ccgatcacaa agatttttcc gctaggcagt gatccgactc 60

gcacccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa 115
Met Thr Ser Ala Glu
1 5

cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac 163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
10 15 20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca 211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
25 30 35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac 259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His
40 45 50

aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg 307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met
55 60 65

atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc 355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe
70 75 80 85

gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc 403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr
90 95 100

gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg 451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro
105 110 115

aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca 499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala
120 125 130

tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac 547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn
135 140 145

ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga 595
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly
150 155 160 165

tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc 643
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly
170 175 180

```
acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag   691
Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys Ile Lys Thr Leu Gln
            185                 190                 195

cct gcg cct tac cag atc cct cat gat ggc cca acc ggt tgg ttc att   739
Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro Thr Gly Trp Phe Ile
        200                 205                 210

gag tct tac ggt ggg cac cca tgg cgc cca gcc cac ctc cac ttg cgc   787
Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala His Leu His Leu Arg
    215                 220                 225

gtt tcc cac ccg ggc tac cgc acc atc acc acc cag ctt tac ttc gag   835
Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr Gln Leu Tyr Phe Glu
230                 235                 240                 245

ggt ggc gag tgg gtc gaa aac gac gtt gca acc gct gtg aag cca gaa   883
Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr Ala Val Lys Pro Glu
                250                 255                 260

ctg gtc ctg cac cct gag act ggc gag gat ggt aac cac gtt cac tac   931
Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly Asn His Val His Tyr
            265                 270                 275

cca ttc gtc ctg gat aag gaa gac tagtttttct acctagctag cat         978
Pro Phe Val Leu Asp Lys Glu Asp
        280                 285
```

<210> 392
<211> 285
<212> PRT
<213> Corynebacterium glutamicum

<400> 392

```
Met Thr Ser Ala Glu Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly
  1               5                  10                  15

Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
             20                  25                  30

Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
         35                  40                  45

Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
     50                  55                  60

Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65                  70                  75                  80

Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
                 85                  90                  95

Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
            100                 105                 110

Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
        115                 120                 125

Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
```

```
    130                 135                 140

Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His
145                 150                 155                 160

Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu
                165                 170                 175

Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys
            180                 185                 190

Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro
        195                 200                 205

Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro Trp Arg Pro Ala
    210                 215                 220

His Leu His Leu Arg Val Ser His Pro Gly Tyr Arg Thr Ile Thr Thr
225                 230                 235                 240

Gln Leu Tyr Phe Glu Gly Gly Glu Trp Val Glu Asn Asp Val Ala Thr
                245                 250                 255

Ala Val Lys Pro Glu Leu Val Leu His Pro Glu Thr Gly Glu Asp Gly
            260                 265                 270

Asn His Val His Tyr Pro Phe Val Leu Asp Lys Glu Asp
        275                 280                 285


<210> 393
<211> 760
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(760)
<223> FRXA00639

<400> 393
agtgttgtta tcgagttcag ccgatcacaa agatttttcc gctaggcagt gatccgactc 60

gcacccccta cttcaccccc aaagtctcta ggagtatgac atg act tca gct gaa   115
                                            Met Thr Ser Ala Glu
                                              1               5

cag atc gtt gat cca aca gcc cac gat tcg ggc aac aag gca act gac   163
Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly Asn Lys Ala Thr Asp
                 10                  15                  20

aag ttc aag gca aac cgc gtt tcc tcc gat acc tcc aag gaa cgc gca   211
Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr Ser Lys Glu Arg Ala
             25                  30                  35

aac gcg atc tac gta gat ctg ctc gcg gcg atc gcc cag gtt gct cac   259
Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile Ala Gln Val Ala His
         40                  45                  50

aag cac gaa gtc acc tac gaa gag tac gca gtg ctc aag cag tgg atg   307
Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val Leu Lys Gln Trp Met
```

```
     55                  60                  65

atc gac gtt gga gaa tac ggc gag tgg cca ctg tgg ttg gac gtt ttc   355
Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu Trp Leu Asp Val Phe
 70                  75                  80                  85

gtt gag cat gag atc gaa gag atc aac tac aac cgc cac gac tac acc   403
Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn Arg His Asp Tyr Thr
                90                  95                 100

gga acc aag ggt tcc atc gaa ggc cct tat tac gta gag aac tct ccg   451
Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr Val Glu Asn Ser Pro
            105                 110                 115

aag ctc cct tgg gat gct gaa atg cca atg cgt gac aag gac cgc gca   499
Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg Asp Lys Asp Arg Ala
        120                 125                 130

tgc acc cca ctg atc ttc gag ggg cag gtt act gac ctc gac ggc aac   547
Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr Asp Leu Asp Gly Asn
    135                 140                 145

ggt ctt gat gga gca gaa gtt gag ctc tgg cac gca gat gag gac gga   595
Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His Ala Asp Glu Asp Gly
150                 155                 160                 165

tac tac tcc cag ttc gcg cct gga atc cca gag tgg aac ctg cgt ggc   643
Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu Trp Asn Leu Arg Gly
                170                 175                 180

acc atc gtt acc gat gag gaa ggc cgc tac aag atc aag acc ctg cag   691
Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys Ile Lys Thr Leu Gln
            185                 190                 195

cct gcg cct tac cag atc cct cat gat ggc cca acc ggt tgg ttc att   739
Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro Thr Gly Trp Phe Ile
        200                 205                 210

gag tct tac ggt ggg cac cca                                       760
Glu Ser Tyr Gly Gly His Pro
    215                 220
```

<210> 394
<211> 220
<212> PRT
<213> Corynebacterium glutamicum

<400> 394

```
Met Thr Ser Ala Glu Gln Ile Val Asp Pro Thr Ala His Asp Ser Gly
  1               5                  10                  15

Asn Lys Ala Thr Asp Lys Phe Lys Ala Asn Arg Val Ser Ser Asp Thr
            20                  25                  30

Ser Lys Glu Arg Ala Asn Ala Ile Tyr Val Asp Leu Leu Ala Ala Ile
        35                  40                  45

Ala Gln Val Ala His Lys His Glu Val Thr Tyr Glu Glu Tyr Ala Val
    50                  55                  60
```

```
Leu Lys Gln Trp Met Ile Asp Val Gly Glu Tyr Gly Glu Trp Pro Leu
 65                  70                  75                  80

Trp Leu Asp Val Phe Val Glu His Glu Ile Glu Glu Ile Asn Tyr Asn
                85                  90                  95

Arg His Asp Tyr Thr Gly Thr Lys Gly Ser Ile Glu Gly Pro Tyr Tyr
            100                 105                 110

Val Glu Asn Ser Pro Lys Leu Pro Trp Asp Ala Glu Met Pro Met Arg
        115                 120                 125

Asp Lys Asp Arg Ala Cys Thr Pro Leu Ile Phe Glu Gly Gln Val Thr
    130                 135                 140

Asp Leu Asp Gly Asn Gly Leu Asp Gly Ala Glu Val Glu Leu Trp His
145                 150                 155                 160

Ala Asp Glu Asp Gly Tyr Tyr Ser Gln Phe Ala Pro Gly Ile Pro Glu
                165                 170                 175

Trp Asn Leu Arg Gly Thr Ile Val Thr Asp Glu Glu Gly Arg Tyr Lys
            180                 185                 190

Ile Lys Thr Leu Gln Pro Ala Pro Tyr Gln Ile Pro His Asp Gly Pro
        195                 200                 205

Thr Gly Trp Phe Ile Glu Ser Tyr Gly Gly His Pro
    210                 215                 220
```

<210> 395
<211> 1584
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1561)
<223> RXN01653

<400> 395
ttcattcagg gtgaatgctc tccttgtttc agatgttcaa cgctccataa agtagaccgc 60

```
aatctagaca aagatgtcta ttttaattaa ggagcagaac atg gcc acg gcc gag   115
                                            Met Ala Thr Ala Glu
                                              1               5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg   163
Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
                 10                  15                  20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat   211
Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
             25                  30                  35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag   259
Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
         40                  45                  50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt   307
```

```
Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
     55                  60                  65

gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt   355
Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70                  75                  80                  85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg   403
Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
                 90                  95                 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc   451
Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
            105                 110                 115

tat gag cac ccg tat cct ttt gcg cgg cgt ctg gcc aca ctt gat cac   499
Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu Ala Thr Leu Asp His
        120                 125                 130

ctg act aat ggg cgt gtg ggg tgg aat gtg gtt act ggc tat ctt ccc   547
Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val Thr Gly Tyr Leu Pro
    135                 140                 145

tct gct gct caa aac atg ggt gac acc gat cag ctg cca cat gat gag   595
Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln Leu Pro His Asp Glu
150                 155                 160                 165

cgc tat gac aaa gca gat gaa tac ctg gaa gtg atc tac aag ctt ctc   643
Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val Ile Tyr Lys Leu Leu
                170                 175                 180

gag ggc tcc tgg gaa gac gat gct gtt caa aac aat acg gag acg agt   691
Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn Asn Thr Glu Thr Ser
            185                 190                 195

gtc ttt acg gac tcc tcc aaa gtg cac gcc att aat cat cat ggc aag   739
Val Phe Thr Asp Ser Ser Lys Val His Ala Ile Asn His His Gly Lys
        200                 205                 210

tac ttt gat gtg ccg ggc att gcc atc act gag ccg agt gtg cag cgt   787
Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu Pro Ser Val Gln Arg
    215                 220                 225

acg ccg gtg atc tac cag gcg ggt gca tcg ccg cgc gga ttg aaa ttc   835
Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro Arg Gly Leu Lys Phe
230                 235                 240                 245

gct ggt gag aat gca gaa gca gtg ttt atc aat tcc agc acc gtg gag   883
Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn Ser Ser Thr Val Glu
                250                 255                 260

gca atc acc aag act gtc gca aaa att cgc gct gct gcg gtc gct gcg   931
Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala Ala Ala Val Ala Ala
            265                 270                 275

gga cgt gat cca cat gcg gtg aag atc ttt gcg atg caa acc atc atc   979
Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala Met Gln Thr Ile Ile
        280                 285                 290

act ggt gaa aca gaa gca gat gcg cag gca aag ctg gag gaa tac agt   1027
Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys Leu Glu Glu Tyr Ser
```

```
    295                 300                 305

cgc tat atc gat cct gtc ggt ggt ctg acc ttg atg tct gga tgg acc   1075
Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu Met Ser Gly Trp Thr
310                 315                 320                 325

ggc gcg gat ctg tcg cag tat gac ctg gat gaa ccg atc acc aat att   1123
Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu Pro Ile Thr Asn Ile
                330                 335                 340

gag tca aac gct att cag tcc act gca gcc acc att agc aac ggc acc   1171
Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr Ile Ser Asn Gly Thr
            345                 350                 355

ggt gaa ggt gcg tgg acg gta cgc aaa ctg ggt gag gca acc ggc atc   1219
Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly Glu Ala Thr Gly Ile
        360                 365                 370

ggc ggc ttc gga cca gtg ctt gtg gga tct ggc gct aac gtt gcc gcg   1267
Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly Ala Asn Val Ala Ala
    375                 380                 385

gaa ctt gca cgc atc cag gat ctc agc gat gtt gat ggt ttc aac ctt   1315
Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val Asp Gly Phe Asn Leu
390                 395                 400                 405

gct tat gcc atc acc cca gga act ttt gaa gat gtc gtg gac ttt gtg   1363
Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp Val Val Asp Phe Val
                410                 415                 420

gtg cct gag ctg caa aaa ctt agc cgc tac aag acg gaa tac gcg ccg   1411
Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys Thr Glu Tyr Ala Pro
            425                 430                 435

ggt tcc ttg cgc aac aaa ttg ctc ggt aaa ggt gat cgc ctg gac gat   1459
Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly Asp Arg Leu Asp Asp
        440                 445                 450

acc cac cgc ggc gca agc tac cgc cta ggc gct cgg aac tcc acc gcc   1507
Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala Arg Asn Ser Thr Ala
    455                 460                 465

act att gat ctc agt tcc ata tcc gcc caa cta gtt tcc cag gga gcc   1555
Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu Val Ser Gln Gly Ala
470                 475                 480                 485

cac tca tgatctcacc gcaaacaatc atc                                 1584
His Ser
```

<210> 396
<211> 487
<212> PRT
<213> Corynebacterium glutamicum

<400> 396

```
Met Ala Thr Ala Glu Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe
  1               5                  10                  15

Asn Ala Phe Asp Met Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp
```

```
            20                  25                  30

Thr His Pro Lys Asp Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp
         35                  40                  45

Val His Leu Ala Lys Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe
     50                  55                  60

Ile Ala Asp Val Leu Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu
 65                  70                  75                  80

Ala Ala Leu Ser Ser Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu
                 85                  90                  95

Leu Val Ser Ala Met Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile
            100                 105                 110

Thr Ala Gly Thr Ala Tyr Glu His Pro Tyr Pro Phe Ala Arg Arg Leu
        115                 120                 125

Ala Thr Leu Asp His Leu Thr Asn Gly Arg Val Gly Trp Asn Val Val
    130                 135                 140

Thr Gly Tyr Leu Pro Ser Ala Ala Gln Asn Met Gly Asp Thr Asp Gln
145                 150                 155                 160

Leu Pro His Asp Glu Arg Tyr Asp Lys Ala Asp Glu Tyr Leu Glu Val
                165                 170                 175

Ile Tyr Lys Leu Leu Glu Gly Ser Trp Glu Asp Asp Ala Val Gln Asn
            180                 185                 190

Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His Ala Ile
        195                 200                 205

Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile Thr Glu
    210                 215                 220

Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala Ser Pro
225                 230                 235                 240

Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe Ile Asn
                245                 250                 255

Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile Arg Ala
            260                 265                 270

Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile Phe Ala
        275                 280                 285

Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln Ala Lys
    290                 295                 300

Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu Thr Leu
305                 310                 315                 320

Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu Asp Glu
                325                 330                 335

Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala Ala Thr
            340                 345                 350
```

```
Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys Leu Gly
        355                 360                 365

Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly Ser Gly
    370                 375                 380

Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser Asp Val
385                 390                 395                 400

Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe Glu Asp
                405                 410                 415

Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg Tyr Lys
            420                 425                 430

Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly Lys Gly
        435                 440                 445

Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu Gly Ala
    450                 455                 460

Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala Gln Leu
465                 470                 475                 480

Val Ser Gln Gly Ala His Ser
                485
```

Sequence Listing

<210> 397
<211> 460
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(460)
<223> FRXA00797

<400> 397
ttcattcagg gtgaatgctc tccttgtttc agatgttcaa cgctccataa agtagaccgc 60

aatctagaca aagatgtcta ttttaattaa ggagcagaac atg gcc acg gcc gag 115
                                        Met Ala Thr Ala Glu
                                          1   5

aac aca aca cag gag aat cgg aaa atc ctg ttc aac gca ttt gat atg 163
Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe Asn Ala Phe Asp Met
                10   15   20

aac tgc gtt gcg cat cag tcc cca gga ctg tgg aca cac ccg aag gat 211
Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp Thr His Pro Lys Asp
            25   30   35

aag gcg cga gac tac aac act ctt gat tac tgg gtg cac ctt gcc aag 259
Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp Val His Leu Ala Lys
        40   45   50

act ttg gag aag ggc ctt ttc gac ggc ctt ttc atc gca gat gtg ctt 307
Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe Ile Ala Asp Val Leu
    55   60   65
```
```

```
gga act tac gat gtt tat ggt tct agt aat gaa gcg gcg ttg agc agt   355
Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu Ala Ala Leu Ser Ser
 70                  75                  80                  85

ggt gcg cag gtg cct gtc aat gat ccg atc ctt ctt gtt tct gcg atg   403
Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu Leu Val Ser Ala Met
                 90                  95                 100

gcc tat gcc aca aag aac ctc ggg ttt ggc att act gca ggt act gcc   451
Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile Thr Ala Gly Thr Ala
            105                 110                 115

tat gag cac                                                      460
Tyr Glu His
        120
```

<210> 398
<211> 120
<212> PRT
<213> Corynebacterium glutamicum

<400> 398

```
Met Ala Thr Ala Glu Asn Thr Thr Gln Glu Asn Arg Lys Ile Leu Phe
  1               5                  10                  15

Asn Ala Phe Asp Met Asn Cys Val Ala His Gln Ser Pro Gly Leu Trp
             20                  25                  30

Thr His Pro Lys Asp Lys Ala Arg Asp Tyr Asn Thr Leu Asp Tyr Trp
         35                  40                  45

Val His Leu Ala Lys Thr Leu Glu Lys Gly Leu Phe Asp Gly Leu Phe
     50                  55                  60

Ile Ala Asp Val Leu Gly Thr Tyr Asp Val Tyr Gly Ser Ser Asn Glu
 65                  70                  75                  80

Ala Ala Leu Ser Ser Gly Ala Gln Val Pro Val Asn Asp Pro Ile Leu
                 85                  90                  95

Leu Val Ser Ala Met Ala Tyr Ala Thr Lys Asn Leu Gly Phe Gly Ile
            100                 105                 110

Thr Ala Gly Thr Ala Tyr Glu His
        115                 120
```

<210> 399
<211> 962
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(939)
<223> FRXA01653

<400> 399

```
gga agt gat cta caa gct tct cga ggg ctc ctg gaa gac gat gct gtt   48
```

```
Gly Ser Asp Leu Gln Ala Ser Arg Gly Leu Leu Glu Asp Asp Ala Val
  1               5                  10                  15

caa aac aat acg gag acg agt gtc ttt acg gac tcc tcc aaa gtg cac   96
Gln Asn Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His
            20                  25                  30

gcc att aat cat cat ggc aag tac ttt gat gtg ccg ggc att gcc atc   144
Ala Ile Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile
        35                  40                  45

act gag ccg agt gtg cag cgt acg ccg gtg atc tac cag gcg ggt gca   192
Thr Glu Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala
    50                  55                  60

tcg ccg cgc gga ttg aaa ttc gct ggt gag aat gca gaa gca gtg ttt   240
Ser Pro Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe
65                  70                  75                  80

atc aat tcc agc acc gtg gag gca atc acc aag act gtc gca aaa att   288
Ile Asn Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile
                85                  90                  95

cgc gct gct gcg gtc gct gcg gga cgt gat cca cat gcg gtg aag atc   336
Arg Ala Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile
            100                 105                 110

ttt gcg atg caa acc atc atc act ggt gaa aca gaa gca gat gcg cag   384
Phe Ala Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln
        115                 120                 125

gca aag ctg gag gaa tac agt cgc tat atc gat cct gtc ggt ggt ctg   432
Ala Lys Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu
    130                 135                 140

acc ttg atg tct gga tgg acc ggc gcg gat ctg tcg cag tat gac ctg   480
Thr Leu Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu
145                 150                 155                 160

gat gaa ccg atc acc aat att gag tca aac gct att cag tcc act gca   528
Asp Glu Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala
                165                 170                 175

gcc acc att agc aac ggc acc ggt gaa ggt gcg tgg acg gta cgc aaa   576
Ala Thr Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys
            180                 185                 190

ctg ggt gag gca acc ggc atc ggc ggc ttc gga cca gtg ctt gtg gga   624
Leu Gly Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly
        195                 200                 205

tct ggc gct aac gtt gcc gcg gaa ctt gca cgc atc cag gat ctc agc   672
Ser Gly Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser
    210                 215                 220

gat gtt gat ggt ttc aac ctt gct tat gcc atc acc cca gga act ttt   720
Asp Val Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe
225                 230                 235                 240

gaa gat gtc gtg gac ttt gtg gtg cct gag ctg caa aaa ctt agc cgc   768
Glu Asp Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg
```

```
                245                 250                 255

tac aag acg gaa tac gcg ccg ggt tcc ttg cgc aac aaa ttg ctc ggt   816
Tyr Lys Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly
            260                 265                 270

aaa ggt gat cgc ctg gac gat acc cac cgc ggc gca agc tac cgc cta   864
Lys Gly Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu
        275                 280                 285

ggc gct cgg aac tcc acc gcc act att gat ctc agt tcc ata tcc gcc   912
Gly Ala Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala
    290                 295                 300

caa cta gtt tcc cag gga gcc cac tca tgatctcacc gcaaacaatc         959
Gln Leu Val Ser Gln Gly Ala His Ser
305                 310

atc                                                              962


<210> 400
<211> 313
<212> PRT
<213> Corynebacterium glutamicum

<400> 400
Gly Ser Asp Leu Gln Ala Ser Arg Gly Leu Leu Glu Asp Asp Ala Val
  1               5                  10                  15

Gln Asn Asn Thr Glu Thr Ser Val Phe Thr Asp Ser Ser Lys Val His
            20                  25                  30

Ala Ile Asn His His Gly Lys Tyr Phe Asp Val Pro Gly Ile Ala Ile
        35                  40                  45

Thr Glu Pro Ser Val Gln Arg Thr Pro Val Ile Tyr Gln Ala Gly Ala
    50                  55                  60

Ser Pro Arg Gly Leu Lys Phe Ala Gly Glu Asn Ala Glu Ala Val Phe
65                  70                  75                  80

Ile Asn Ser Ser Thr Val Glu Ala Ile Thr Lys Thr Val Ala Lys Ile
                85                  90                  95

Arg Ala Ala Ala Val Ala Ala Gly Arg Asp Pro His Ala Val Lys Ile
            100                 105                 110

Phe Ala Met Gln Thr Ile Ile Thr Gly Glu Thr Glu Ala Asp Ala Gln
        115                 120                 125

Ala Lys Leu Glu Glu Tyr Ser Arg Tyr Ile Asp Pro Val Gly Gly Leu
    130                 135                 140

Thr Leu Met Ser Gly Trp Thr Gly Ala Asp Leu Ser Gln Tyr Asp Leu
145                 150                 155                 160

Asp Glu Pro Ile Thr Asn Ile Glu Ser Asn Ala Ile Gln Ser Thr Ala
                165                 170                 175

Ala Thr Ile Ser Asn Gly Thr Gly Glu Gly Ala Trp Thr Val Arg Lys
```

```
            180                 185                 190

Leu Gly Glu Ala Thr Gly Ile Gly Gly Phe Gly Pro Val Leu Val Gly
        195                 200                 205

Ser Gly Ala Asn Val Ala Ala Glu Leu Ala Arg Ile Gln Asp Leu Ser
    210                 215                 220

Asp Val Asp Gly Phe Asn Leu Ala Tyr Ala Ile Thr Pro Gly Thr Phe
225                 230                 235                 240

Glu Asp Val Val Asp Phe Val Val Pro Glu Leu Gln Lys Leu Ser Arg
                245                 250                 255

Tyr Lys Thr Glu Tyr Ala Pro Gly Ser Leu Arg Asn Lys Leu Leu Gly
            260                 265                 270

Lys Gly Asp Arg Leu Asp Asp Thr His Arg Gly Ala Ser Tyr Arg Leu
        275                 280                 285

Gly Ala Arg Asn Ser Thr Ala Thr Ile Asp Leu Ser Ser Ile Ser Ala
    290                 295                 300

Gln Leu Val Ser Gln Gly Ala His Ser
305                 310


<210> 401
<211> 780
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(757)
<223> RXN02530

<400> 401
gaggctgagc tttccgtcaa acaacatctt cccaatgtgg atgaaatgac tgtgaccatc 60

acccttcca aaccttgagt cccgtgatac aattgttgat atg tca aca aat tat   115
                                        Met Ser Thr Asn Tyr
                                          1               5

gaa gca atc atc att gga gca ggt cag gct gga ctc gcg gcg gcg cat   163
Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly Leu Ala Ala Ala His
                  10                  15                  20

gaa ctt tcc cgc cgc ggt ttc act ccc gga aaa gat ttt ctc gtc ctc   211
Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys Asp Phe Leu Val Leu
              25                  30                  35

gat tcc aac gac ggg ccc ggt ggc gcc tgg cgg cat agg tgg gat tca   259
Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg His Arg Trp Asp Ser
          40                  45                  50

ctc aca tta ggt aaa gcc cac gga atc gcc gat ctc cca ggg ctt ccc   307
Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp Leu Pro Gly Leu Pro
      55                  60                  65

atg aat cgc ccc gat ccg aaa act ccg gct tcc aca ttg gtt gct ggt   355
```

```
Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser Thr Leu Val Ala Gly
 70                  75                  80                  85

tat tac ggc gct tac gag aac gag ttc tcc ttc gca gtt gtg cgc cca   403
Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
                 90                  95                 100

gtc aaa gtc tca cga gtt gag ccc act tcc gag gat cct tcg agc cca   451
Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
            105                 110                 115

ttg cgc gtg agc agc gac gat ggt cga gag tgg att acc cgc atg gtt   499
Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
        120                 125                 130

ctt aat gca aca ggt acg tgg aca aac cct tat gtt ccg tac att cct   547
Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
    135                 140                 145

ggc atc gat aaa ttc cag ggc aag cag ctc cac acc gtt aat tac cgc   595
Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
150                 155                 160                 165

aag gcc gag gat ttc aaa ggt aag aaa gtc ctg gtc gtc ggc ggt ggt   643
Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
                170                 175                 180

ttg agt gct gtg caa ttt ctg ctg gag ttg gaa ggc ttg gcg gaa acc   691
Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
            185                 190                 195

acc tgg gcg acg cgt cgt ccg cga act tac gca gcg cga gtt cga cgc   739
Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
        200                 205                 210

cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac gca                780
Arg Leu Gly His Cys Gly
    215
```

SEQUENCE LISTING

<210> 402
<211> 219
<212> PRT
<213> Corynebacterium glutamicum

<400> 402

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Met Ser Thr Asn Tyr Glu Ala Ile Ile Ile Gly Ala Gly Gln Ala Gly
  1               5                  10                  15

Leu Ala Ala Ala His Glu Leu Ser Arg Arg Gly Phe Thr Pro Gly Lys
            20                  25                  30

Asp Phe Leu Val Leu Asp Ser Asn Asp Gly Pro Gly Gly Ala Trp Arg
        35                  40                  45

His Arg Trp Asp Ser Leu Thr Leu Gly Lys Ala His Gly Ile Ala Asp
    50                  55                  60

Leu Pro Gly Leu Pro Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Ser
65                  70                  75                  80
```

```
Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
                 85                  90                  95

Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
            100                 105                 110

Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
        115                 120                 125

Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
    130                 135                 140

Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
145                 150                 155                 160

Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
                165                 170                 175

Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
            180                 185                 190

Gly Leu Ala Glu Thr Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala
        195                 200                 205

Ala Arg Val Arg Arg Arg Leu Gly His Cys Gly
    210                 215


<210> 403
<211> 492
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (20)..(469)
<223> FRXA02530

<400> 403
cgatctccca gggcttcccatg aat cgc ccc gat ccg aaa act cca gct ggc   52
                       Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Gly
                         1               5                  10

aca ttg gtt gct ggt tat tac ggc gct tac gag aac gag ttc tcc ttc   100
Thr Leu Val Ala Gly Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe
             15                  20                  25

gca gtt gtg cgc cca gtc aaa gtc tca cga gtt gag ccc act tcc gag   148
Ala Val Val Arg Pro Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu
         30                  35                  40

gat cct tcg agc cca ttg cgc gtg agc agc gac gat ggt cga gag tgg   196
Asp Pro Ser Ser Pro Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp
     45                  50                  55

att acc cgc atg gtt ctt aat gca aca ggt acg tgg aca aac cct tat   244
Ile Thr Arg Met Val Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr
 60                  65                  70                  75

gtt ccg tac att cct ggc atc gat aaa ttc cag ggc aag cag ctc cac   292
Val Pro Tyr Ile Pro Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His
```

```
                80                  85                  90

acc gtt aat tac cgc aag gcc gag gat ttc aaa ggt aag aaa gtc ctg   340
Thr Val Asn Tyr Arg Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu
            95                  100                 105

gtc gtc ggc ggt ggt ttg agt gct gtg caa ttt ctg ctg gag ttg gaa   388
Val Val Gly Gly Gly Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu
        110                 115                 120

ggc ttg gcg gaa acc acc tgg gcg acg cgt cgt ccg cga act tac gca   436
Gly Leu Ala Glu Thr Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala
    125                 130                 135

gcg cga gtt cga cgc cgg ctg ggg cat tgc ggt tgagcgcgcc gtccgcgaac 489
Ala Arg Val Arg Arg Arg Leu Gly His Cys Gly
140                 145                 150

gca                                                               492


<210> 404
<211> 150
<212> PRT
<213> Corynebacterium glutamicum

<400> 404
Met Asn Arg Pro Asp Pro Lys Thr Pro Ala Gly Thr Leu Val Ala Gly
  1               5                  10                  15

Tyr Tyr Gly Ala Tyr Glu Asn Glu Phe Ser Phe Ala Val Val Arg Pro
            20                  25                  30

Val Lys Val Ser Arg Val Glu Pro Thr Ser Glu Asp Pro Ser Ser Pro
        35                  40                  45

Leu Arg Val Ser Ser Asp Asp Gly Arg Glu Trp Ile Thr Arg Met Val
    50                  55                  60

Leu Asn Ala Thr Gly Thr Trp Thr Asn Pro Tyr Val Pro Tyr Ile Pro
65                  70                  75                  80

Gly Ile Asp Lys Phe Gln Gly Lys Gln Leu His Thr Val Asn Tyr Arg
                85                  90                  95

Lys Ala Glu Asp Phe Lys Gly Lys Lys Val Leu Val Val Gly Gly Gly
            100                 105                 110

Leu Ser Ala Val Gln Phe Leu Leu Glu Leu Glu Gly Leu Ala Glu Thr
        115                 120                 125

Thr Trp Ala Thr Arg Arg Pro Arg Thr Tyr Ala Ala Arg Val Arg Arg
    130                 135                 140

Arg Leu Gly His Cys Gly
145                 150


<210> 405
<211> 1533
<212> DNA
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<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1510)
<223> RXA02083

<400> 405
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tttttgtaca tggtctgtgg cacgcattgt ttcgtttgcc ctgccatgtt ggtgttttaa 60

gtgaaggccg ccttttgcgg aatgggtata ggaggcattc atg gag atg gtt atg   115
                                              Met Glu Met Val Met
                                                1               5

aag aat aag cgc gtt gcg att att ggt gca ggt ccg agt ggt atc gct   163
Lys Asn Lys Arg Val Ala Ile Ile Gly Ala Gly Pro Ser Gly Ile Ala
                  10                  15                  20

cag ttg agg gcg ttt gag tct gct gaa aag cag ggg cat gag atc cct   211
Gln Leu Arg Ala Phe Glu Ser Ala Glu Lys Gln Gly His Glu Ile Pro
              25                  30                  35

gag ctg gtg tgt ttt gaa aag cag gat acc tgg ggt ggg cag tgg aat   259
Glu Leu Val Cys Phe Glu Lys Gln Asp Thr Trp Gly Gly Gln Trp Asn
          40                  45                  50

tac tct tgg cgc acg gga aca gac tct tat ggt gag cct gtg cac tca   307
Tyr Ser Trp Arg Thr Gly Thr Asp Ser Tyr Gly Glu Pro Val His Ser
      55                  60                  65

agt atg tac cga aac ctg tgg tca aac ggt ccg aag gaa gtt ctc gaa   355
Ser Met Tyr Arg Asn Leu Trp Ser Asn Gly Pro Lys Glu Val Leu Glu
  70                  75                  80                  85

ttt gct gag tac agc ttc gat gag cac ttc gga aag cca att tct tct   403
Phe Ala Glu Tyr Ser Phe Asp Glu His Phe Gly Lys Pro Ile Ser Ser
                  90                  95                 100

tac cct cca cgt gaa gtg ttg tgg gat tac att gca ggt cgt gca aag   451
Tyr Pro Pro Arg Glu Val Leu Trp Asp Tyr Ile Ala Gly Arg Ala Lys
             105                 110                 115

aag tcg aac gtt gag aag tac atc aag ttc gcg cat gtt gtt cgc tgg   499
Lys Ser Asn Val Glu Lys Tyr Ile Lys Phe Ala His Val Val Arg Trp
         120                 125                 130

gtg agt ttt gat gag gcc acc aag ctg ttc acc gtg acg gtg gag aac   547
Val Ser Phe Asp Glu Ala Thr Lys Leu Phe Thr Val Thr Val Glu Asn
     135                 140                 145

ctc cgc acc ggt gag acc agc agt gat act tat gac aac gtg att gtt   595
Leu Arg Thr Gly Glu Thr Ser Ser Asp Thr Tyr Asp Asn Val Ile Val
150                 155                 160                 165

ggc gct gga cac ttc agc ttc ccg aac gtc cct cac ttt gat ggt gtg   643
Gly Ala Gly His Phe Ser Phe Pro Asn Val Pro His Phe Asp Gly Val
                 170                 175                 180

gag act ttc cca ggt cag atc atg cat gct cac gag ttc cgt ggt gca   691
Glu Thr Phe Pro Gly Gln Ile Met His Ala His Glu Phe Arg Gly Ala
             185                 190                 195
```

```
gag gct gtt gct gac aag gat att ttg ctg att ggt gca agt tat tct   739
Glu Ala Val Ala Asp Lys Asp Ile Leu Leu Ile Gly Ala Ser Tyr Ser
        200                 205                 210

gcg gaa gat atc ggt acc cag gcg tac aag atg ggt gct cgt tcg gtg   787
Ala Glu Asp Ile Gly Thr Gln Ala Tyr Lys Met Gly Ala Arg Ser Val
    215                 220                 225

act ttc tct tac cgc tca aac cca atg ggg tat gag tgg cct gaa gag   835
Thr Phe Ser Tyr Arg Ser Asn Pro Met Gly Tyr Glu Trp Pro Glu Glu
230                 235                 240                 245

atg act gag ctt cct ttg gtt gag cgt ttc gac ggc tcc gag gtt cac   883
Met Thr Glu Leu Pro Leu Val Glu Arg Phe Asp Gly Ser Glu Val His
                250                 255                 260

ttt gtc aat ggt gaa aag cgc aag gtc gac atc gtg gtg ttc tgt act   931
Phe Val Asn Gly Glu Lys Arg Lys Val Asp Ile Val Val Phe Cys Thr
            265                 270                 275

ggt tac tta cac cat tac cca ttt atg ccg tct gag ctg act tta agc   979
Gly Tyr Leu His His Tyr Pro Phe Met Pro Ser Glu Leu Thr Leu Ser
        280                 285                 290

tca cca aac aac ctg tac ccg gat acg ctt tat cgt ggc gtg gtg tcc  1027
Ser Pro Asn Asn Leu Tyr Pro Asp Thr Leu Tyr Arg Gly Val Val Ser
    295                 300                 305

gag gct aat aac cag ctg ttc tgg ttg ggt gct cag gat cag tgg ctg  1075
Glu Ala Asn Asn Gln Leu Phe Trp Leu Gly Ala Gln Asp Gln Trp Leu
310                 315                 320                 325

acg ttc aac atg ttt gat gct cag gct tgg tat gtt cgc gat gtc att  1123
Thr Phe Asn Met Phe Asp Ala Gln Ala Trp Tyr Val Arg Asp Val Ile
                330                 335                 340

ttg ggc cgc gtg gct ctt cct tcc aag gaa gcg cag cgc aat cat atg  1171
Leu Gly Arg Val Ala Leu Pro Ser Lys Glu Ala Gln Arg Asn His Met
            345                 350                 355

gat aag tgg ctg tca cgt ttc gaa ggc ttg aag tct gag aat gat cag  1219
Asp Lys Trp Leu Ser Arg Phe Glu Gly Leu Lys Ser Glu Asn Asp Gln
        360                 365                 370

att gat ttc cag tgc gat tac gtc gag gat ctt atc gat cag acc gat  1267
Ile Asp Phe Gln Cys Asp Tyr Val Glu Asp Leu Ile Asp Gln Thr Asp
    375                 380                 385

tat cct tcg ttt gat ctg aag gaa gtc gcg aat atc ttg aag ggc tgg  1315
Tyr Pro Ser Phe Asp Leu Lys Glu Val Ala Asn Ile Leu Lys Gly Trp
390                 395                 400                 405

gtg aag tcg aag gag gag gat atc ctc aac tac cgt gat tac acc tat  1363
Val Lys Ser Lys Glu Glu Asp Ile Leu Asn Tyr Arg Asp Tyr Thr Tyr
                410                 415                 420

act tcc gtg atg acg ggc acc acc tct gtt gaa cac cac act ccg tgg  1411
Thr Ser Val Met Thr Gly Thr Thr Ser Val Glu His His Thr Pro Trp
            425                 430                 435
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atg att gag ttg gat gat tct ttg gag cgt tac ctc agt gag cca cag   1459
Met Ile Glu Leu Asp Asp Ser Leu Glu Arg Tyr Leu Ser Glu Pro Gln
        440                 445                 450

gaa gat gaa gct cgt cag gtt tac cgt ggc aag aaa gtc cgc gat aaa   1507
Glu Asp Glu Ala Arg Gln Val Tyr Arg Gly Lys Lys Val Arg Asp Lys
    455                 460                 465

gcc taaggaaaag gcctaagcag ccc                                    1533
Ala
470
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<210> 406
<211> 470
<212> PRT
<213> Corynebacterium glutamicum

<400> 406

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Met Glu Met Val Met Lys Asn Lys Arg Val Ala Ile Ile Gly Ala Gly
  1               5                  10                  15

Pro Ser Gly Ile Ala Gln Leu Arg Ala Phe Glu Ser Ala Glu Lys Gln
             20                  25                  30

Gly His Glu Ile Pro Glu Leu Val Cys Phe Glu Lys Gln Asp Thr Trp
         35                  40                  45

Gly Gly Gln Trp Asn Tyr Ser Trp Arg Thr Gly Thr Asp Ser Tyr Gly
     50                  55                  60

Glu Pro Val His Ser Ser Met Tyr Arg Asn Leu Trp Ser Asn Gly Pro
 65                  70                  75                  80

Lys Glu Val Leu Glu Phe Ala Glu Tyr Ser Phe Asp Glu His Phe Gly
                 85                  90                  95

Lys Pro Ile Ser Ser Tyr Pro Pro Arg Glu Val Leu Trp Asp Tyr Ile
            100                 105                 110

Ala Gly Arg Ala Lys Lys Ser Asn Val Glu Lys Tyr Ile Lys Phe Ala
        115                 120                 125

His Val Val Arg Trp Val Ser Phe Asp Glu Ala Thr Lys Leu Phe Thr
    130                 135                 140

Val Thr Val Glu Asn Leu Arg Thr Gly Glu Thr Ser Ser Asp Thr Tyr
145                 150                 155                 160

Asp Asn Val Ile Val Gly Ala Gly His Phe Ser Phe Pro Asn Val Pro
                165                 170                 175

His Phe Asp Gly Val Glu Thr Phe Pro Gly Gln Ile Met His Ala His
            180                 185                 190

Glu Phe Arg Gly Ala Glu Ala Val Ala Asp Lys Asp Ile Leu Leu Ile
        195                 200                 205

Gly Ala Ser Tyr Ser Ala Glu Asp Ile Gly Thr Gln Ala Tyr Lys Met
    210                 215                 220
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Gly Ala Arg Ser Val Thr Phe Ser Tyr Arg Ser Asn Pro Met Gly Tyr
225 230 235 240

Glu Trp Pro Glu Glu Met Thr Glu Leu Pro Leu Val Glu Arg Phe Asp
245 250 255

Gly Ser Glu Val His Phe Val Asn Gly Glu Lys Arg Lys Val Asp Ile
260 265 270

Val Val Phe Cys Thr Gly Tyr Leu His His Tyr Pro Phe Met Pro Ser
275 280 285

Glu Leu Thr Leu Ser Ser Pro Asn Asn Leu Tyr Pro Asp Thr Leu Tyr
290 295 300

Arg Gly Val Val Ser Glu Ala Asn Asn Gln Leu Phe Trp Leu Gly Ala
305 310 315 320

Gln Asp Gln Trp Leu Thr Phe Asn Met Phe Asp Ala Gln Ala Trp Tyr
325 330 335

Val Arg Asp Val Ile Leu Gly Arg Val Ala Leu Pro Ser Lys Glu Ala
340 345 350

Gln Arg Asn His Met Asp Lys Trp Leu Ser Arg Phe Glu Gly Leu Lys
355 360 365

Ser Glu Asn Asp Gln Ile Asp Phe Gln Cys Asp Tyr Val Glu Asp Leu
370 375 380

Ile Asp Gln Thr Asp Tyr Pro Ser Phe Asp Leu Lys Glu Val Ala Asn
385 390 395 400

Ile Leu Lys Gly Trp Val Lys Ser Lys Glu Glu Asp Ile Leu Asn Tyr
405 410 415

Arg Asp Tyr Thr Tyr Thr Ser Val Met Thr Gly Thr Thr Ser Val Glu
420 425 430

His His Thr Pro Trp Met Ile Glu Leu Asp Asp Ser Leu Glu Arg Tyr
435 440 445

Leu Ser Glu Pro Gln Glu Asp Glu Ala Arg Gln Val Tyr Arg Gly Lys
450 455 460

Lys Val Arg Asp Lys Ala
465 470

<210> 407
<211> 1017
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(994)
<223> RXA00892

<400> 407
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acagtcatag tgaccgatac tagttgctag agttttcatc atg tct gcc acc tct   115
                                            Met Ser Ala Thr Ser
                                              1               5

tcc gtc acc gtt gaa tgc ccg gcg gga acc atc acc ggc gag ccc cat   163
Ser Val Thr Val Glu Cys Pro Ala Gly Thr Ile Thr Gly Glu Pro His
                 10                  15                  20

tat ttc cgc tcg att ccc tac gca aag gcg cgc ccg ttt gct gat gcc   211
Tyr Phe Arg Ser Ile Pro Tyr Ala Lys Ala Arg Pro Phe Ala Asp Ala
             25                  30                  35

gaa aag cta gaa ccc ctg cgc att gat gcg acc ggc aag cac gag ggt   259
Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr Gly Lys His Glu Gly
         40                  45                  50

ctc tat tta acg ttg gca acc ccg gag gca cgg ttc ggc gcg gat gcc   307
Leu Tyr Leu Thr Leu Ala Thr Pro Glu Ala Arg Phe Gly Ala Asp Ala
     55                  60                  65

ccg gtg atc gtt tat atc cac ggc gga gga tat gac ggt ggc acg cgt   355
Pro Val Ile Val Tyr Ile His Gly Gly Gly Tyr Asp Gly Gly Thr Arg
 70                  75                  80                  85

ttc gat gcc cgc acc gag ccc act ttc ttc cgt gag cag ggc ttt gtg   403
Phe Asp Ala Arg Thr Glu Pro Thr Phe Phe Arg Glu Gln Gly Phe Val
                 90                  95                 100

gtg gtc tcc atc gat tac cgc gtc ggc ctg gag ggc ttt gcg cgc ttc   451
Val Val Ser Ile Asp Tyr Arg Val Gly Leu Glu Gly Phe Ala Arg Phe
             105                 110                 115

cac gac gac gag gcc aat cgt tac cgc ggc atc gat gat tgc gtg ctc   499
His Asp Asp Glu Ala Asn Arg Tyr Arg Gly Ile Asp Asp Cys Val Leu
         120                 125                 130

gcg ctg gag tgg gtg cag aaa aac atc gag cat ttc ggc ggc gat ccc   547
Ala Leu Glu Trp Val Gln Lys Asn Ile Glu His Phe Gly Gly Asp Pro
     135                 140                 145

acc aac gtc acc ctc atc ggg cag tcc gcg ggc gcc ggc atc gcg ctc   595
Thr Asn Val Thr Leu Ile Gly Gln Ser Ala Gly Ala Gly Ile Ala Leu
150                 155                 160                 165

tgg ctc acg cgc cta gac cac tat aaa ggt gct ttt cga cgc ctg gtt   643
Trp Leu Thr Arg Leu Asp His Tyr Lys Gly Ala Phe Arg Arg Leu Val
                170                 175                 180

gcg ctc tcc ccc agc ttc ccg cgc cag cca ttc gct gcc cga aaa ggt   691
Ala Leu Ser Pro Ser Phe Pro Arg Gln Pro Phe Ala Ala Arg Lys Gly
            185                 190                 195

gct tta cga cgc gcc ctg ggc aaa ccc gtc acc cgc gcc tcg ctg gcg   739
Ala Leu Arg Arg Ala Leu Gly Lys Pro Val Thr Arg Ala Ser Leu Ala
        200                 205                 210

ggc atc aag ccc gca cgc ttg gac aaa ggc tac cgt cgc ttt gct cgc   787
Gly Ile Lys Pro Ala Arg Leu Asp Lys Gly Tyr Arg Arg Phe Ala Arg
    215                 220                 225
```

PCT/US2004/009950

```
cgc tac ttc acc gac ctg gca ctc ggc cct acc cca tac gac ccg aat   835
Arg Tyr Phe Thr Asp Leu Ala Leu Gly Pro Thr Pro Tyr Asp Pro Asn
230                 235                 240                 245

gag ctg gcc gac atc gat ttg atc atc tcc tcc acc cgc gat gaa atg   883
Glu Leu Ala Asp Ile Asp Leu Ile Ile Ser Ser Thr Arg Asp Glu Met
                250                 255                 260

tac gga cac cgc gca ggc tta tgg ttc gac cag cgt ggc ttc ggc gca   931
Tyr Gly His Arg Ala Gly Leu Trp Phe Asp Gln Arg Gly Phe Gly Ala
            265                 270                 275

aaa ctg gcc gcg cga ctt ttt ggc ctg gag aat tcg gat acc aat att   979
Lys Leu Ala Ala Arg Leu Phe Gly Leu Glu Asn Ser Asp Thr Asn Ile
        280                 285                 290

aag gaa gcc cca aga tgacaaccgc gttgtaggcc gca                    1017
Lys Glu Ala Pro Arg
    295
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<210> 408
<211> 298
<212> PRT
<213> Corynebacterium glutamicum

<400> 408

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Met Ser Ala Thr Ser Ser Val Thr Val Glu Cys Pro Ala Gly Thr Ile
  1               5                  10                  15

Thr Gly Glu Pro His Tyr Phe Arg Ser Ile Pro Tyr Ala Lys Ala Arg
            20                  25                  30

Pro Phe Ala Asp Ala Glu Lys Leu Glu Pro Leu Arg Ile Asp Ala Thr
        35                  40                  45

Gly Lys His Glu Gly Leu Tyr Leu Thr Leu Ala Thr Pro Glu Ala Arg
    50                  55                  60

Phe Gly Ala Asp Ala Pro Val Ile Val Tyr Ile His Gly Gly Gly Tyr
65                  70                  75                  80

Asp Gly Gly Thr Arg Phe Asp Ala Arg Thr Glu Pro Thr Phe Phe Arg
                85                  90                  95

Glu Gln Gly Phe Val Val Val Ser Ile Asp Tyr Arg Val Gly Leu Glu
            100                 105                 110

Gly Phe Ala Arg Phe His Asp Asp Glu Ala Asn Arg Tyr Arg Gly Ile
        115                 120                 125

Asp Asp Cys Val Leu Ala Leu Glu Trp Val Gln Lys Asn Ile Glu His
    130                 135                 140

Phe Gly Gly Asp Pro Thr Asn Val Thr Leu Ile Gly Gln Ser Ala Gly
145                 150                 155                 160

Ala Gly Ile Ala Leu Trp Leu Thr Arg Leu Asp His Tyr Lys Gly Ala
                165                 170                 175

Phe Arg Arg Leu Val Ala Leu Ser Pro Ser Phe Pro Arg Gln Pro Phe
```

```
            180                 185                 190

Ala Ala Arg Lys Gly Ala Leu Arg Arg Ala Leu Gly Lys Pro Val Thr
        195                 200                 205

Arg Ala Ser Leu Ala Gly Ile Lys Pro Ala Arg Leu Asp Lys Gly Tyr
    210                 215                 220

Arg Arg Phe Ala Arg Arg Tyr Phe Thr Asp Leu Ala Leu Gly Pro Thr
225                 230                 235                 240

Pro Tyr Asp Pro Asn Glu Leu Ala Asp Ile Asp Leu Ile Ile Ser Ser
                245                 250                 255

Thr Arg Asp Glu Met Tyr Gly His Arg Ala Gly Leu Trp Phe Asp Gln
            260                 265                 270

Arg Gly Phe Gly Ala Lys Leu Ala Ala Arg Leu Phe Gly Leu Glu Asn
        275                 280                 285

Ser Asp Thr Asn Ile Lys Glu Ala Pro Arg
    290                 295
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SEQUENCE LISTING

<210> 409
<211> 1761
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1738)
<223> RXA02092

<400> 409

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catgaatagt tcgacgtgga cacctcggta ctcaccgcat atg gct aac agt gca   115
                                            Met Ala Asn Ser Ala
                                              1               5

gcg ggt tcg gtg ttg gcg gat gag atg gtg gtt ccc acc tca aca ggg   163
Ala Gly Ser Val Leu Ala Asp Glu Met Val Val Pro Thr Ser Thr Gly
                  10                  15                  20

ttt gtt aaa ggc gtc aaa gga cca ggg ctt aaa acc tgg agg gga att   211
Phe Val Lys Gly Val Lys Gly Pro Gly Leu Lys Thr Trp Arg Gly Ile
              25                  30                  35

ccc tac ggc cga aac act ggc gga aaa tat cgc ttc cgg gca ccc cgg   259
Pro Tyr Gly Arg Asn Thr Gly Gly Lys Tyr Arg Phe Arg Ala Pro Arg
          40                  45                  50

ccc gcc aag aaa tgg gac ggc gtg cgc gat tgc tca atg ttc ggt gaa   307
Pro Ala Lys Lys Trp Asp Gly Val Arg Asp Cys Ser Met Phe Gly Glu
      55                  60                  65

gta gct tct cag cca acg tac tcc tgg aca gat aag att cgc ggt tca   355
Val Ala Ser Gln Pro Thr Tyr Ser Trp Thr Asp Lys Ile Arg Gly Ser
  70                  75                  80                  85
```

```
gaa gac tgc ctt aac ctc gat gtc gtg cgg cct gat tcc gaa gaa aag   403
Glu Asp Cys Leu Asn Leu Asp Val Val Arg Pro Asp Ser Glu Glu Lys
                 90                  95                 100

ctt cct gtt gtg gtg tat ctc cac ggc ggt tcc ttc atc atg ggc tca   451
Leu Pro Val Val Val Tyr Leu His Gly Gly Ser Phe Ile Met Gly Ser
            105                 110                 115

tca agc gaa aaa gcg ctg cgc gga tat aac ctc gtc aca aac atg aat   499
Ser Ser Glu Lys Ala Leu Arg Gly Tyr Asn Leu Val Thr Asn Met Asn
        120                 125                 130

gtg gtc tac gtg tcc gtt aat ttc cgc ctc ggc gct ttg ggc tat cta   547
Val Val Tyr Val Ser Val Asn Phe Arg Leu Gly Ala Leu Gly Tyr Leu
    135                 140                 145

gat ctg cgt tcc gtg ggg gag gat tgc gta gcc aac ccc gcg ctc cac   595
Asp Leu Arg Ser Val Gly Glu Asp Cys Val Ala Asn Pro Ala Leu His
150                 155                 160                 165

gat cag ctc ctg gcc ctg cag tgg gtc agc cgt aat atc aaa gca ttc   643
Asp Gln Leu Leu Ala Leu Gln Trp Val Ser Arg Asn Ile Lys Ala Phe
                170                 175                 180

ggt ggg gat cct gac aac gtc acc ctc atg ggc gaa tcc gcg ggc gct   691
Gly Gly Asp Pro Asp Asn Val Thr Leu Met Gly Glu Ser Ala Gly Ala
            185                 190                 195

gca gca gtg gtt gca ctc atg tgt gtg ccc gct gca gga gga cta ttc   739
Ala Ala Val Val Ala Leu Met Cys Val Pro Ala Ala Gly Gly Leu Phe
        200                 205                 210

cac cgc gcc atc gcc caa tcc gcg ccg gtc atc tct gtg cac tca tct   787
His Arg Ala Ile Ala Gln Ser Ala Pro Val Ile Ser Val His Ser Ser
    215                 220                 225

acc caa gca aaa ttc tgg gca cgt gaa ctg atc tac cgc atg gca ttg   835
Thr Gln Ala Lys Phe Trp Ala Arg Glu Leu Ile Tyr Arg Met Ala Leu
230                 235                 240                 245

ccc agg gaa acc acc ttg gat gaa ctg cgc caa gaa tcc gcc gat gat   883
Pro Arg Glu Thr Thr Leu Asp Glu Leu Arg Gln Glu Ser Ala Asp Asp
                250                 255                 260

cta gtg cgc gcc ggg cag tcg atg atg tgg cgc tcc ggc gaa ctg ctc   931
Leu Val Arg Ala Gly Gln Ser Met Met Trp Arg Ser Gly Glu Leu Leu
            265                 270                 275

caa ctc aac tct tgt tac ggg ccc acg gtg gat ggt tcc ttg cta cct   979
Gln Leu Asn Ser Cys Tyr Gly Pro Thr Val Asp Gly Ser Leu Leu Pro
        280                 285                 290

gag cac ccg ctc acc atg ttt gaa cag gga aga caa cac cgc att ccc   1027
Glu His Pro Leu Thr Met Phe Glu Gln Gly Arg Gln His Arg Ile Pro
    295                 300                 305

ttc atg atc ggt act aat aac gga gaa act tct ttc tcc aaa gcc ttt   1075
Phe Met Ile Gly Thr Asn Asn Gly Glu Thr Ser Phe Ser Lys Ala Phe
310                 315                 320                 325

tat tta aga agc tct gcc cga cgt cgc tct gcc tta cgc atg ctg tct   1123
```

```
Tyr Leu Arg Ser Ser Ala Arg Arg Arg Ser Ala Leu Arg Met Leu Ser
                330                 335                 340

gtg tat gat ccc cac aat gca gaa cgc gtg gtt agc gcc tat ggc gga   1171
Val Tyr Asp Pro His Asn Ala Glu Arg Val Val Ser Ala Tyr Gly Gly
            345                 350                 355

ggc gag gca cgc aca gac ttt tct gaa cta ctc gct gac gcg ctg ttc   1219
Gly Glu Ala Arg Thr Asp Phe Ser Glu Leu Leu Ala Asp Ala Leu Phe
        360                 365                 370

tgg gca ccg tcg gtt aga ttg gcg cag tcg cac gcc tcc caa gat gaa   1267
Trp Ala Pro Ser Val Arg Leu Ala Gln Ser His Ala Ser Gln Asp Glu
    375                 380                 385

gat acc tgg atg tac cgc ttc gat tac gcc cca caa tcc atg cgg aaa   1315
Asp Thr Trp Met Tyr Arg Phe Asp Tyr Ala Pro Gln Ser Met Arg Lys
390                 395                 400                 405

ctt ggc ctc ggc gcg att cac tct ttc gaa ctc aac gct gtc ttt ggc   1363
Leu Gly Leu Gly Ala Ile His Ser Phe Glu Leu Asn Ala Val Phe Gly
                410                 415                 420

gat cat gaa tct tct cgc tcc atg aac ctt gcg aaa att gcc ggc ggc   1411
Asp His Glu Ser Ser Arg Ser Met Asn Leu Ala Lys Ile Ala Gly Gly
            425                 430                 435

atg gat cat ttg gat aaa gtc acc gaa ctt gtc caa gag cat tgg aag   1459
Met Asp His Leu Asp Lys Val Thr Glu Leu Val Gln Glu His Trp Lys
        440                 445                 450

caa ttc atc tac ttc ggc agg ccc ggt gaa gag tgg aag gct tac cgc   1507
Gln Phe Ile Tyr Phe Gly Arg Pro Gly Glu Glu Trp Lys Ala Tyr Arg
    455                 460                 465

ggc cgc agc gat acc gaa ccg ggc cgt gct aca ttt gtc atc gat atc   1555
Gly Arg Ser Asp Thr Glu Pro Gly Arg Ala Thr Phe Val Ile Asp Ile
470                 475                 480                 485

aac tcc cga atc gcg tgg gat cca cgc cag gac aaa cgc acg gcg tgg   1603
Asn Ser Arg Ile Ala Trp Asp Pro Arg Gln Asp Lys Arg Thr Ala Trp
                490                 495                 500

gaa aat tac gac atg ctc gaa tgg ggc aca ggc cgc cca gat cta gcc   1651
Glu Asn Tyr Asp Met Leu Glu Trp Gly Thr Gly Arg Pro Asp Leu Ala
            505                 510                 515

aac gaa ctt gat ttc atc gag ccg gaa gag aca gaa gaa gag cag caa   1699
Asn Glu Leu Asp Phe Ile Glu Pro Glu Glu Thr Glu Glu Glu Gln Gln
        520                 525                 530

ttg aag tgg ctt agc ctt atg cag ttt ttt gga agt aga taaatgagca   1748
Leu Lys Trp Leu Ser Leu Met Gln Phe Phe Gly Ser Arg
    535                 540                 545

tctggaaacg tct                                                  1761


<210> 410
<211> 546
<212> PRT
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<213> Corynebacterium glutamicum

<400> 410

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Met Ala Asn Ser Ala Ala Gly Ser Val Leu Ala Asp Glu Met Val Val
 1               5                  10                  15

Pro Thr Ser Thr Gly Phe Val Lys Gly Val Lys Gly Pro Gly Leu Lys
            20                  25                  30

Thr Trp Arg Gly Ile Pro Tyr Gly Arg Asn Thr Gly Gly Lys Tyr Arg
        35                  40                  45

Phe Arg Ala Pro Arg Pro Ala Lys Lys Trp Asp Gly Val Arg Asp Cys
    50                  55                  60

Ser Met Phe Gly Glu Val Ala Ser Gln Pro Thr Tyr Ser Trp Thr Asp
65                  70                  75                  80

Lys Ile Arg Gly Ser Glu Asp Cys Leu Asn Leu Asp Val Val Arg Pro
                85                  90                  95

Asp Ser Glu Glu Lys Leu Pro Val Val Val Tyr Leu His Gly Gly Ser
            100                 105                 110

Phe Ile Met Gly Ser Ser Ser Glu Lys Ala Leu Arg Gly Tyr Asn Leu
        115                 120                 125

Val Thr Asn Met Asn Val Val Tyr Val Ser Val Asn Phe Arg Leu Gly
    130                 135                 140

Ala Leu Gly Tyr Leu Asp Leu Arg Ser Val Gly Glu Asp Cys Val Ala
145                 150                 155                 160

Asn Pro Ala Leu His Asp Gln Leu Leu Ala Leu Gln Trp Val Ser Arg
                165                 170                 175

Asn Ile Lys Ala Phe Gly Gly Asp Pro Asp Asn Val Thr Leu Met Gly
            180                 185                 190

Glu Ser Ala Gly Ala Ala Ala Val Val Ala Leu Met Cys Val Pro Ala
        195                 200                 205

Ala Gly Gly Leu Phe His Arg Ala Ile Ala Gln Ser Ala Pro Val Ile
    210                 215                 220

Ser Val His Ser Ser Thr Gln Ala Lys Phe Trp Ala Arg Glu Leu Ile
225                 230                 235                 240

Tyr Arg Met Ala Leu Pro Arg Glu Thr Thr Leu Asp Glu Leu Arg Gln
                245                 250                 255

Glu Ser Ala Asp Asp Leu Val Arg Ala Gly Gln Ser Met Met Trp Arg
            260                 265                 270

Ser Gly Glu Leu Leu Gln Leu Asn Ser Cys Tyr Gly Pro Thr Val Asp
        275                 280                 285

Gly Ser Leu Leu Pro Glu His Pro Leu Thr Met Phe Glu Gln Gly Arg
    290                 295                 300

Gln His Arg Ile Pro Phe Met Ile Gly Thr Asn Asn Gly Glu Thr Ser
```

305 310 315 320

Phe Ser Lys Ala Phe Tyr Leu Arg Ser Ser Ala Arg Arg Arg Ser Ala
325 330 335

Leu Arg Met Leu Ser Val Tyr Asp Pro His Asn Ala Glu Arg Val Val
340 345 350

Ser Ala Tyr Gly Gly Gly Glu Ala Arg Thr Asp Phe Ser Glu Leu Leu
355 360 365

Ala Asp Ala Leu Phe Trp Ala Pro Ser Val Arg Leu Ala Gln Ser His
370 375 380

Ala Ser Gln Asp Glu Asp Thr Trp Met Tyr Arg Phe Asp Tyr Ala Pro
385 390 395 400

Gln Ser Met Arg Lys Leu Gly Leu Gly Ala Ile His Ser Phe Glu Leu
405 410 415

Asn Ala Val Phe Gly Asp His Glu Ser Ser Arg Ser Met Asn Leu Ala
420 425 430

Lys Ile Ala Gly Gly Met Asp His Leu Asp Lys Val Thr Glu Leu Val
435 440 445

Gln Glu His Trp Lys Gln Phe Ile Tyr Phe Gly Arg Pro Gly Glu Glu
450 455 460

Trp Lys Ala Tyr Arg Gly Arg Ser Asp Thr Glu Pro Gly Arg Ala Thr
465 470 475 480

Phe Val Ile Asp Ile Asn Ser Arg Ile Ala Trp Asp Pro Arg Gln Asp
485 490 495

Lys Arg Thr Ala Trp Glu Asn Tyr Asp Met Leu Glu Trp Gly Thr Gly
500 505 510

Arg Pro Asp Leu Ala Asn Glu Leu Asp Phe Ile Glu Pro Glu Glu Thr
515 520 525

Glu Glu Glu Gln Gln Leu Lys Trp Leu Ser Leu Met Gln Phe Phe Gly
530 535 540

Ser Arg
545

<210> 411
<211> 816
<212> DNA
<213> Corynebacterium glutamicum

<220>
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<222> (101)..(793)
<223> RXN00658

<400> 411
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acaacgtctg gctggaagct cagccacgtg ctttctggtc gtg cgc cac gac gag   115
                                              Val Arg His Asp Glu
                                                1               5

cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc   163
His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
                  10                  15                  20

acc ctc atc gcc cct cag ctg gaa gat cca gag gcg gag gag ttc acc   211
Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr
             25                  30                  35

gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg   259
Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met
         40                  45                  50

gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag   307
Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys
     55                  60                  65

tcc gat att gct tta cga cgc tgc gat gcg gtg acc acc cac atc ggc   355
Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly
 70                  75                  80                  85

cac gaa cac tcc gcc gat ggt cac tgg agg atc tac gta ttc gct ggc   403
His Glu His Ser Ala Asp Gly His Trp Arg Ile Tyr Val Phe Ala Gly
                 90                  95                 100

caa gcc acc cca caa gat tcc gag tct gca ctg aac aag tgg gcg cag   451
Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu Asn Lys Trp Ala Gln
            105                 110                 115

tgg atg gag gaa agc gaa gac tca cca ctc aac cgc ttc acc cca gaa   499
Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn Arg Phe Thr Pro Glu
        120                 125                 130

gcc ggc gac cgc aac gca gtc ttc gat atc aag gct acc tac cag cag   547
Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys Ala Thr Tyr Gln Gln
    135                 140                 145

cat tac cac tcc ttc gac ctg ttc gat gcg cca gag gtc ttc ttc cca   595
His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro Glu Val Phe Phe Pro
150                 155                 160                 165

cga gtt gga cca tac aag ctg caa aac ctc gaa aac gtt tgg acc gca   643
Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu Asn Val Trp Thr Ala
                170                 175                 180

ctg gat tcc caa gac atc ttt gag tcc cgt ggc atc agt cgc gat ggc   691
Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly Ile Ser Arg Asp Gly
            185                 190                 195

gca att gtt gtc gtt cgc cca gac cag tac gtc gca gca gtc ctc cca   739
Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val Ala Ala Val Leu Pro
        200                 205                 210

ctc gaa gac acc gca gca ctg gct gag ttc ttc aat ggc aat ctg ctt   787
Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe Asn Gly Asn Leu Leu
    215                 220                 225

gag cca taaaccctaa attctaggaa cga                                816
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Glu Pro
230

<210> 412
<211> 231
<212> PRT
<213> Corynebacterium glutamicum

<400> 412
Val Arg His Asp Glu His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe
1 5 10 15

Asp Lys Gly Trp Ser Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu
20 25 30

Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu
35 40 45

Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
50 55 60

Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val
65 70 75 80

Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile
85 90 95

Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln Asp Ser Glu Ser Ala Leu
100 105 110

Asn Lys Trp Ala Gln Trp Met Glu Glu Ser Glu Asp Ser Pro Leu Asn
115 120 125

Arg Phe Thr Pro Glu Ala Gly Asp Arg Asn Ala Val Phe Asp Ile Lys
130 135 140

Ala Thr Tyr Gln Gln His Tyr His Ser Phe Asp Leu Phe Asp Ala Pro
145 150 155 160

Glu Val Phe Phe Pro Arg Val Gly Pro Tyr Lys Leu Gln Asn Leu Glu
165 170 175

Asn Val Trp Thr Ala Leu Asp Ser Gln Asp Ile Phe Glu Ser Arg Gly
180 185 190

Ile Ser Arg Asp Gly Ala Ile Val Val Val Arg Pro Asp Gln Tyr Val
195 200 205

Ala Ala Val Leu Pro Leu Glu Asp Thr Ala Ala Leu Ala Glu Phe Phe
210 215 220

Asn Gly Asn Leu Leu Glu Pro
225 230

<210> 413
<211> 418
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(418)
<223> FRXA00658

<400> 413
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acaacgtctg gctggaagct cagccacgtg ctttctggtc gtg cgc cac gac gag 115
Val Arg His Asp Glu
1 5

cac tac cca gct gcg gca aac ctc att gct ttc gat aag gga tgg tcc 163
His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe Asp Lys Gly Trp Ser
10 15 20

acc ctc atc gcc cct cag ctg gaa gat cca gag gcg gag gag ttc acc 211
Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu Ala Glu Glu Phe Thr
25 30 35

gcc gga ttc ctc acc gaa tac cag gac aat ctg atc act gcg ggc atg 259
Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu Ile Thr Ala Gly Met
40 45 50

gag cac cag gcg ctc gcg agc ggc ttc ccg gtg ggg cgt cgc ttc aag 307
Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val Gly Arg Arg Phe Lys
55 60 65

tcc gat att gct tta cga cgc tgc gat gcg gtg acc acc cac atc ggc 355
Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val Thr Thr His Ile Gly
70 75 80 85

cac gaa cac tcc gcc gat ggt cac tgg agg atc tac gta ttc gct ggc 403
His Glu His Ser Ala Asp Gly His Trp Arg Ile Tyr Val Phe Ala Gly
90 95 100

caa gcc acc cca caa 418
Gln Ala Thr Pro Gln
105

<210> 414
<211> 106
<212> PRT
<213> Corynebacterium glutamicum

<400> 414
Val Arg His Asp Glu His Tyr Pro Ala Ala Ala Asn Leu Ile Ala Phe
1 5 10 15

Asp Lys Gly Trp Ser Thr Leu Ile Ala Pro Gln Leu Glu Asp Pro Glu
20 25 30

Ala Glu Glu Phe Thr Ala Gly Phe Leu Thr Glu Tyr Gln Asp Asn Leu
35 40 45

Ile Thr Ala Gly Met Glu His Gln Ala Leu Ala Ser Gly Phe Pro Val
50 55 60

Gly Arg Arg Phe Lys Ser Asp Ile Ala Leu Arg Arg Cys Asp Ala Val
65 70 75 80

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Thr Thr His Ile Gly His Glu His Ser Ala Asp Gly His Trp Arg Ile
                 85                  90                  95

Tyr Val Phe Ala Gly Gln Ala Thr Pro Gln
            100                 105


<210> 415
<211> 2004
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1981)
<223> RXA01385

<400> 415
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tccgtgaatg agataggaaa tcccctcgaa aggaccagac atg cag ttt cat tat   115
                                              Met Gln Phe His Tyr
                                                1               5

gaa gga tac gca acc ggt gac cca atg gag atg cgc gcg gaa ggt agc   163
Glu Gly Tyr Ala Thr Gly Asp Pro Met Glu Met Arg Ala Glu Gly Ser
                10                  15                  20

gga atc aac cgc ccg gac gat ctc ccc gag gtc atg gat gtt ctc atc   211
Gly Ile Asn Arg Pro Asp Asp Leu Pro Glu Val Met Asp Val Leu Ile
            25                  30                  35

gtt ggt gca ggt ccg gct ggc acc atc gca gcg gct cag ctt tcc cga   259
Val Gly Ala Gly Pro Ala Gly Thr Ile Ala Ala Ala Gln Leu Ser Arg
        40                  45                  50

ttc ccc aat gtg acc acc cgc ctc gta gag aga agc gac cgt cgc ctc   307
Phe Pro Asn Val Thr Thr Arg Leu Val Glu Arg Ser Asp Arg Arg Leu
    55                  60                  65

gaa cta gcc aat gca gat ggc gtg cac tcc cga acc att gaa act ttc   355
Glu Leu Ala Asn Ala Asp Gly Val His Ser Arg Thr Ile Glu Thr Phe
70                  75                  80                  85

cag gca ttt ggt ttc gcc cac gag atc ctc gcc gaa gct cat gaa atc   403
Gln Ala Phe Gly Phe Ala His Glu Ile Leu Ala Glu Ala His Glu Ile
                90                  95                 100

acc gac atg gcg ttc tgg aag ccg gac ccg caa aac cct cgt gag atc   451
Thr Asp Met Ala Phe Trp Lys Pro Asp Pro Gln Asn Pro Arg Glu Ile
            105                 110                 115

att cgc gac aac agc acc cgc gag ctg cca cag cac atc agt gaa ttt   499
Ile Arg Asp Asn Ser Thr Arg Glu Leu Pro Gln His Ile Ser Glu Phe
        120                 125                 130

ccg atg gcg ttg ctc acc cag acc cgc atc atc gac cac ttc aac cgg   547
Pro Met Ala Leu Leu Thr Gln Thr Arg Ile Ile Asp His Phe Asn Arg
    135                 140                 145
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ttc atg aag aac tcc cca acc agg atg aag cct gac tat gga tac gag   595
Phe Met Lys Asn Ser Pro Thr Arg Met Lys Pro Asp Tyr Gly Tyr Glu
150                 155                 160                 165

ttc gtg gac ttt gaa gta gaa gaa gac gca gaa tat ccg gta att gtc   643
Phe Val Asp Phe Glu Val Glu Glu Asp Ala Glu Tyr Pro Val Ile Val
                170                 175                 180

acc ctc cgc cgc acc agt ggc gag caa act ggc gaa ttg gtc acc gtc   691
Thr Leu Arg Arg Thr Ser Gly Glu Gln Thr Gly Glu Leu Val Thr Val
            185                 190                 195

cga acc aag tac ctg gtc ggt gcc gat ggt gca cga agc caa gtg cgc   739
Arg Thr Lys Tyr Leu Val Gly Ala Asp Gly Ala Arg Ser Gln Val Arg
        200                 205                 210

aaa tca ctg gga tac cga ctc caa ggt aag cag gct aac cac gct tgg   787
Lys Ser Leu Gly Tyr Arg Leu Gln Gly Lys Gln Ala Asn His Ala Trp
    215                 220                 225

ggt gtg atg gat att cac gcg aac acc gag ttc ccc gac gtg cgc aag   835
Gly Val Met Asp Ile His Ala Asn Thr Glu Phe Pro Asp Val Arg Lys
230                 235                 240                 245

aag tgc acc atc aaa tct gat tcg ggt cgc acc atc ttg ctc atc cca   883
Lys Cys Thr Ile Lys Ser Asp Ser Gly Arg Thr Ile Leu Leu Ile Pro
                250                 255                 260

cgt gag ggt ggc ttc ctc ttc cgt ctc tac gtt gac ctg ggc gaa gta   931
Arg Glu Gly Gly Phe Leu Phe Arg Leu Tyr Val Asp Leu Gly Glu Val
            265                 270                 275

cct gat gat ggc agc aag gct gtt cgt gat acc cca ctc cag gat gtc   979
Pro Asp Asp Gly Ser Lys Ala Val Arg Asp Thr Pro Leu Gln Asp Val
        280                 285                 290

atc gac acc gcg aac cag atc atg gct cca ttc acc ctc gac gtg aaa   1027
Ile Asp Thr Ala Asn Gln Ile Met Ala Pro Phe Thr Leu Asp Val Lys
    295                 300                 305

aac gtt gtg tgg aac tcc atc tac gag gta ggc cac cgc gtc gca gac   1075
Asn Val Val Trp Asn Ser Ile Tyr Glu Val Gly His Arg Val Ala Asp
310                 315                 320                 325

cat ttc gat gac cgt gtt tca gaa aaa acc tcg agc gaa cac cca cgc   1123
His Phe Asp Asp Arg Val Ser Glu Lys Thr Ser Ser Glu His Pro Arg
                330                 335                 340

att ttc att gct ggc gac gcc tgc cac acc cac agc gct aag gct ggc   1171
Ile Phe Ile Ala Gly Asp Ala Cys His Thr His Ser Ala Lys Ala Gly
            345                 350                 355

cag ggc atg aac gtg tcc atg cag gac gga ttc aac ctt ggc tgg aag   1219
Gln Gly Met Asn Val Ser Met Gln Asp Gly Phe Asn Leu Gly Trp Lys
        360                 365                 370

ctt gga cat gtg gcc agc gga aat agc cca cgc gaa cta ctt cag acc   1267
Leu Gly His Val Ala Ser Gly Asn Ser Pro Arg Glu Leu Leu Gln Thr
    375                 380                 385

tac gct gaa gag cgc gaa gac att gcc tac aag ctc atc gag tac gac   1315
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Tyr Ala Glu Glu Arg Glu Asp Ile Ala Tyr Lys Leu Ile Glu Tyr Asp
390                 395                 400                 405

aag aac tgg tca aca ctc atg gca aag cca agc agc gaa atg ggc agt   1363
Lys Asn Trp Ser Thr Leu Met Ala Lys Pro Ser Ser Glu Met Gly Ser
                410                 415                 420

gcc caa gac ctt gag gat ttc tac cgc gcg aac tct gag ttc aat gcc   1411
Ala Gln Asp Leu Glu Asp Phe Tyr Arg Ala Asn Ser Glu Phe Asn Ala
            425                 430                 435

ggc tac atg acc cac tat cct cct tct tcc atc aca atg gat ggc agc   1459
Gly Tyr Met Thr His Tyr Pro Pro Ser Ser Ile Thr Met Asp Gly Ser
        440                 445                 450

aac caa gat ctg gca aag ggc tac cca att ggc cga cgc ttc aag tca   1507
Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly Arg Arg Phe Lys Ser
    455                 460                 465

gcg atg gtt ggt cga gtc tgc gac ttc acc gaa aca cac ctc ggt cac   1555
Ala Met Val Gly Arg Val Cys Asp Phe Thr Glu Thr His Leu Gly His
470                 475                 480                 485

caa gca aca gcc gac gga cgc atg cgc gca tac gtc ttc gca gga tcc   1603
Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr Val Phe Ala Gly Ser
                490                 495                 500

gat gca ctt aac ggc gag ggt tct gag cta gac cgc tgg gca gaa tgg   1651
Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp Arg Trp Ala Glu Trp
            505                 510                 515

gca gag gcg aac ctt gac ccc acg ctt gtc gac gcc aag gtg att tac   1699
Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp Ala Lys Val Ile Tyr
        520                 525                 530

caa agc cct tat acc gag ctc gac acc cgc cag gtt cca tcc gtg ttc   1747
Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln Val Pro Ser Val Phe
    535                 540                 545

aaa cct gca gtc ggg atc ttc gaa ctg acc aat gtg gaa aac tcc ttc   1795
Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn Val Glu Asn Ser Phe
550                 555                 560                 565

ggt atc acc acg gac tcc gac atc ttt gat agt cgc gag atc tcc cgc   1843
Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser Arg Glu Ile Ser Arg
                570                 575                 580

gat ggt gtc gtg gtg gta gtc cga cca gac caa tac gtt tcc gga atc   1891
Asp Gly Val Val Val Val Val Arg Pro Asp Gln Tyr Val Ser Gly Ile
            585                 590                 595

ttc cca ctc act gat acc caa ggg ctt ggc gaa ttc ctc acc gga tac   1939
Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu Phe Leu Thr Gly Tyr
        600                 605                 610

ttc ccc aaa atg aaa ggc gca cat cag cta atc aac gcg aac            1981
Phe Pro Lys Met Lys Gly Ala His Gln Leu Ile Asn Ala Asn
    615                 620                 625

taaggcacag ctgttaaaac agt                                         2004
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<210> 416
<211> 627
<212> PRT
<213> Corynebacterium glutamicum

<400> 416
Met Gln Phe His Tyr Glu Gly Tyr Ala Thr Gly Asp Pro Met Glu Met
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Arg Ala Glu Gly Ser Gly Ile Asn Arg Pro Asp Asp Leu Pro Glu Val
20 25 30

Met Asp Val Leu Ile Val Gly Ala Gly Pro Ala Gly Thr Ile Ala Ala
35 40 45

Ala Gln Leu Ser Arg Phe Pro Asn Val Thr Thr Arg Leu Val Glu Arg
50 55 60

Ser Asp Arg Arg Leu Glu Leu Ala Asn Ala Asp Gly Val His Ser Arg
65 70 75 80

Thr Ile Glu Thr Phe Gln Ala Phe Gly Phe Ala His Glu Ile Leu Ala
85 90 95

Glu Ala His Glu Ile Thr Asp Met Ala Phe Trp Lys Pro Asp Pro Gln
100 105 110

Asn Pro Arg Glu Ile Ile Arg Asp Asn Ser Thr Arg Glu Leu Pro Gln
115 120 125

His Ile Ser Glu Phe Pro Met Ala Leu Leu Thr Gln Thr Arg Ile Ile
130 135 140

Asp His Phe Asn Arg Phe Met Lys Asn Ser Pro Thr Arg Met Lys Pro
145 150 155 160

Asp Tyr Gly Tyr Glu Phe Val Asp Phe Glu Val Glu Glu Asp Ala Glu
165 170 175

Tyr Pro Val Ile Val Thr Leu Arg Arg Thr Ser Gly Glu Gln Thr Gly
180 185 190

Glu Leu Val Thr Val Arg Thr Lys Tyr Leu Val Gly Ala Asp Gly Ala
195 200 205

Arg Ser Gln Val Arg Lys Ser Leu Gly Tyr Arg Leu Gln Gly Lys Gln
210 215 220

Ala Asn His Ala Trp Gly Val Met Asp Ile His Ala Asn Thr Glu Phe
225 230 235 240

Pro Asp Val Arg Lys Lys Cys Thr Ile Lys Ser Asp Ser Gly Arg Thr
245 250 255

Ile Leu Leu Ile Pro Arg Glu Gly Gly Phe Leu Phe Arg Leu Tyr Val
260 265 270

Asp Leu Gly Glu Val Pro Asp Asp Gly Ser Lys Ala Val Arg Asp Thr
275 280 285

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Pro Leu Gln Asp Val Ile Asp Thr Ala Asn Gln Ile Met Ala Pro Phe
    290                 295                 300

Thr Leu Asp Val Lys Asn Val Val Trp Asn Ser Ile Tyr Glu Val Gly
305                 310                 315                 320

His Arg Val Ala Asp His Phe Asp Asp Arg Val Ser Glu Lys Thr Ser
                325                 330                 335

Ser Glu His Pro Arg Ile Phe Ile Ala Gly Asp Ala Cys His Thr His
            340                 345                 350

Ser Ala Lys Ala Gly Gln Gly Met Asn Val Ser Met Gln Asp Gly Phe
        355                 360                 365

Asn Leu Gly Trp Lys Leu Gly His Val Ala Ser Gly Asn Ser Pro Arg
    370                 375                 380

Glu Leu Leu Gln Thr Tyr Ala Glu Glu Arg Glu Asp Ile Ala Tyr Lys
385                 390                 395                 400

Leu Ile Glu Tyr Asp Lys Asn Trp Ser Thr Leu Met Ala Lys Pro Ser
                405                 410                 415

Ser Glu Met Gly Ser Ala Gln Asp Leu Glu Asp Phe Tyr Arg Ala Asn
            420                 425                 430

Ser Glu Phe Asn Ala Gly Tyr Met Thr His Tyr Pro Pro Ser Ser Ile
        435                 440                 445

Thr Met Asp Gly Ser Asn Gln Asp Leu Ala Lys Gly Tyr Pro Ile Gly
    450                 455                 460

Arg Arg Phe Lys Ser Ala Met Val Gly Arg Val Cys Asp Phe Thr Glu
465                 470                 475                 480

Thr His Leu Gly His Gln Ala Thr Ala Asp Gly Arg Met Arg Ala Tyr
                485                 490                 495

Val Phe Ala Gly Ser Asp Ala Leu Asn Gly Glu Gly Ser Glu Leu Asp
            500                 505                 510

Arg Trp Ala Glu Trp Ala Glu Ala Asn Leu Asp Pro Thr Leu Val Asp
        515                 520                 525

Ala Lys Val Ile Tyr Gln Ser Pro Tyr Thr Glu Leu Asp Thr Arg Gln
    530                 535                 540

Val Pro Ser Val Phe Lys Pro Ala Val Gly Ile Phe Glu Leu Thr Asn
545                 550                 555                 560

Val Glu Asn Ser Phe Gly Ile Thr Thr Asp Ser Asp Ile Phe Asp Ser
                565                 570                 575

Arg Glu Ile Ser Arg Asp Gly Val Val Val Val Arg Pro Asp Gln
            580                 585                 590

Tyr Val Ser Gly Ile Phe Pro Leu Thr Asp Thr Gln Gly Leu Gly Glu
        595                 600                 605

Phe Leu Thr Gly Tyr Phe Pro Lys Met Lys Gly Ala His Gln Leu Ile
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610 615 620

Asn Ala Asn
625

<210> 417
<211> 735
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(712)
<223> RXN01461

<400> 417
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gtggccgcaa cgccacccca tttgagtaaa gggttttgca atg att gat aca ggg 115
Met Ile Asp Thr Gly
1 5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
10 15 20

gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
25 30 35

cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
40 45 50

tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307
Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
55 60 65

gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
70 75 80 85

ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
90 95 100

gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
105 110 115

gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
120 125 130

cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
135 140 145

tac act cgc gca tac ctg cca gac gcc gat ttg agc acc gac cca gtt 595
Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu Ser Thr Asp Pro Val

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150                 155                 160                 165

ttg gct gtg gtc cca gct gat cga cgt gac ctc ctg gtg gct caa aag   643
Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu Leu Val Ala Gln Lys
                170                 175                 180

acc gat gat gga ttc cgc ttc gac atc act gtc cag gct gaa gac aat   691
Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val Gln Ala Glu Asp Asn
            185                 190                 195

gaa acc cca ttt ttt gga ctc taaattgacc cgatctttat act             735
Glu Thr Pro Phe Phe Gly Leu
        200


<210> 418
<211> 204
<212> PRT
<213> Corynebacterium glutamicum

<400> 418
Met Ile Asp Thr Gly Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn
  1               5                  10                  15

Ile Ile Asp Gln Asn Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr
             20                  25                  30

Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
         35                  40                  45

Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
     50                  55                  60

Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65                  70                  75                  80

Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
                 85                  90                  95

Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
            100                 105                 110

Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
        115                 120                 125

Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly
    130                 135                 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala Tyr Leu Pro Asp Ala Asp Leu
145                 150                 155                 160

Ser Thr Asp Pro Val Leu Ala Val Val Pro Ala Asp Arg Arg Asp Leu
                165                 170                 175

Leu Val Ala Gln Lys Thr Asp Asp Gly Phe Arg Phe Asp Ile Thr Val
            180                 185                 190

Gln Ala Glu Asp Asn Glu Thr Pro Phe Phe Gly Leu
        195                 200
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<210> 419
<211> 559
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(559)
<223> FRXA01461

<400> 419
tcgactatga cgagacccgt gaaaacttcg cgcttggtta caagttcgac atcgtccttc 60

gtggccgcaa cgccacccca tttgagtaaa gggttttgca atg att gat aca ggg 115
Met Ile Asp Thr Gly
1 5

aag aac ggc gag ttc cgc tac gag cag tcg aat atc atc gat cag aac 163
Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn Ile Ile Asp Gln Asn
10 15 20

gaa gcc gag ttc ggc atc act cct tca cag acc gtg ggc cct tac gtc 211
Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr Val Gly Pro Tyr Val
25 30 35

cac atc ggt ttg acc ctt gaa ggt gcg gag cat ctc gtg gag cca ggt 259
His Ile Gly Leu Thr Leu Glu Gly Ala Glu His Leu Val Glu Pro Gly
40 45 50

tcg gaa ggc gcg gtg tcc ttt act gtt tcc gca act gat ggc aac ggc 307
Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala Thr Asp Gly Asn Gly
55 60 65

gac ccc atc gcg gat gcc atg ttt gaa ctg tgg cag gcc gat cca gag 355
Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp Gln Ala Asp Pro Glu
70 75 80 85

ggc atc cac aac tct gat ttg gat cca aac cgc aca gca cca gca acc 403
Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg Thr Ala Pro Ala Thr
90 95 100

gca gat ggc ttc cgc ggg ctt ggt cgc gcg atg gca aac gcg cag ggt 451
Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met Ala Asn Ala Gln Gly
105 110 115

gag gca acg ttc acc act ttg gtt ccg gga gca ttc gca gat gag gca 499
Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala Phe Ala Asp Glu Ala
120 125 130

cca cac ttc aag gtt ggt gtg ttc gcc cgt ggc atg ctg gag cgt ctg 547
Pro His Phe Lys Val Gly Val Phe Ala Arg Gly Met Leu Glu Arg Leu
135 140 145

tac act cgc gca 559
Tyr Thr Arg Ala
150

<210> 420
<211> 153
<212> PRT

<213> Corynebacterium glutamicum

<400> 420

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Met Ile Asp Thr Gly Lys Asn Gly Glu Phe Arg Tyr Glu Gln Ser Asn
  1               5                  10                  15

Ile Ile Asp Gln Asn Glu Ala Glu Phe Gly Ile Thr Pro Ser Gln Thr
             20                  25                  30

Val Gly Pro Tyr Val His Ile Gly Leu Thr Leu Glu Gly Ala Glu His
         35                  40                  45

Leu Val Glu Pro Gly Ser Glu Gly Ala Val Ser Phe Thr Val Ser Ala
     50                  55                  60

Thr Asp Gly Asn Gly Asp Pro Ile Ala Asp Ala Met Phe Glu Leu Trp
 65                  70                  75                  80

Gln Ala Asp Pro Glu Gly Ile His Asn Ser Asp Leu Asp Pro Asn Arg
                 85                  90                  95

Thr Ala Pro Ala Thr Ala Asp Gly Phe Arg Gly Leu Gly Arg Ala Met
            100                 105                 110

Ala Asn Ala Gln Gly Glu Ala Thr Phe Thr Thr Leu Val Pro Gly Ala
        115                 120                 125

Phe Ala Asp Glu Ala Pro His Phe Lys Val Gly Val Phe Ala Arg Gly
    130                 135                 140

Met Leu Glu Arg Leu Tyr Thr Arg Ala
145                 150
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<210> 421
<211> 813
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(790)
<223> RXA01462

<400> 421

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ttcgcgcgcg atctgacatg ttcgccccgc gaactacttg tcaacggcct caatcatccc 60

tactttgaga tctatatcac tagacgcaga aaggtctcgc atg gac atc cca cac   115
                                              Met Asp Ile Pro His
                                                1               5

ttc gcc ccg acg gga ggc gaa tac tcc cca ctg cac ttc ccg gag tac   163
Phe Ala Pro Thr Gly Gly Glu Tyr Ser Pro Leu His Phe Pro Glu Tyr
            10                  15                  20

cgg acc acc atc aag cgc aac cca agc aac gat ctc atc atg gtt cct   211
Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp Leu Ile Met Val Pro
        25                  30                  35

agt cgc ctc ggc gag tcc acg gga cct gtc ttc ggc gac cgc gac ttg   259
Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe Gly Asp Arg Asp Leu
```

```
         40                  45                  50

gga gac atc gac aac gac atg acc aag gtg aac ggt ggc gag gct atc   307
Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn Gly Gly Glu Ala Ile
     55                  60                  65

ggc cag cgc atc ttc gtt cac ggc cgt gtc ctc ggt ttc gat ggc aag   355
Gly Gln Arg Ile Phe Val His Gly Arg Val Leu Gly Phe Asp Gly Lys
 70                  75                  80                  85

cca gtt ccg cac acc ttg gtc gag gcg tgg cag gca aac gcc gca ggc   403
Pro Val Pro His Thr Leu Val Glu Ala Trp Gln Ala Asn Ala Ala Gly
                 90                  95                 100

cgt tac cgc cac aag aat gac tcc tgg cca gcg cca ctg gat cca cac   451
Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala Pro Leu Asp Pro His
            105                 110                 115

ttc aac ggt gtt gca cgt act ctc acc gac aag gac ggc cag tac cac   499
Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys Asp Gly Gln Tyr His
        120                 125                 130

ttc tgg acc gtt atg cca ggt aat tac cct tgg ggt aac cac cac aac   547
Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp Gly Asn His His Asn
    135                 140                 145

gca tgg cgc ccg gcg cac att cac ttc tcg ctc tat ggt cgt cag ttt   595
Ala Trp Arg Pro Ala His Ile His Phe Ser Leu Tyr Gly Arg Gln Phe
150                 155                 160                 165

acg gag cgt ctg gtc acc cag atg tac ttc ccg aac gat cca ttg ttc   643
Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro Asn Asp Pro Leu Phe
                170                 175                 180

ttc cag gat ccg atc tac aac gcg gtg cca aag ggt gca cgt gag cgc   691
Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys Gly Ala Arg Glu Arg
            185                 190                 195

atg atc gca acg ttc gac tat gac gag acc cgt gaa aac ttc gcg ctt   739
Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg Glu Asn Phe Ala Leu
        200                 205                 210

ggt tac aag ttc gac atc gtc ctt cgt ggc cgc aac gcc acc cca ttt   787
Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg Asn Ala Thr Pro Phe
    215                 220                 225

gag taaagggttt tgcaatgatt gat                                    813
Glu
230
```

<210> 422
<211> 230
<212> PRT
<213> Corynebacterium glutamicum

<400> 422

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Met Asp Ile Pro His Phe Ala Pro Thr Gly Gly Glu Tyr Ser Pro Leu
  1               5                  10                  15

His Phe Pro Glu Tyr Arg Thr Thr Ile Lys Arg Asn Pro Ser Asn Asp
```

```
            20                  25                  30

Leu Ile Met Val Pro Ser Arg Leu Gly Glu Ser Thr Gly Pro Val Phe
        35                  40                  45

Gly Asp Arg Asp Leu Gly Asp Ile Asp Asn Asp Met Thr Lys Val Asn
    50                  55                  60

Gly Gly Glu Ala Ile Gly Gln Arg Ile Phe Val His Gly Arg Val Leu
65                  70                  75                  80

Gly Phe Asp Gly Lys Pro Val Pro His Thr Leu Val Glu Ala Trp Gln
                85                  90                  95

Ala Asn Ala Ala Gly Arg Tyr Arg His Lys Asn Asp Ser Trp Pro Ala
            100                 105                 110

Pro Leu Asp Pro His Phe Asn Gly Val Ala Arg Thr Leu Thr Asp Lys
        115                 120                 125

Asp Gly Gln Tyr His Phe Trp Thr Val Met Pro Gly Asn Tyr Pro Trp
    130                 135                 140

Gly Asn His His Asn Ala Trp Arg Pro Ala His Ile His Phe Ser Leu
145                 150                 155                 160

Tyr Gly Arg Gln Phe Thr Glu Arg Leu Val Thr Gln Met Tyr Phe Pro
                165                 170                 175

Asn Asp Pro Leu Phe Phe Gln Asp Pro Ile Tyr Asn Ala Val Pro Lys
            180                 185                 190

Gly Ala Arg Glu Arg Met Ile Ala Thr Phe Asp Tyr Asp Glu Thr Arg
        195                 200                 205

Glu Asn Phe Ala Leu Gly Tyr Lys Phe Asp Ile Val Leu Arg Gly Arg
    210                 215                 220

Asn Ala Thr Pro Phe Glu
225                 230


<210> 423
<211> 1614
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1591)
<223> RXN00641

<400> 423
tgcggaattg ctcgcaaatg tcacacaccg cttcaaagca aaaacgaaaa cgacatcgcg 60

gtggcaatac caacttcttt tcactctctt ggaggttcac atg tcc aca cca gtt   115
                                                Met Ser Thr Pro Val
                                                  1               5

tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac   163
Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
```

```
                  10                  15                  20

cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac   211
Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
            25                  30                  35

cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg   259
Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
        40                  45                  50

atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc   307
Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
    55                  60                  65

acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc aag gaa   355
Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser Lys Glu
70                  75                  80                  85

ggc aca ctc aac ggc ctg atc aac gcg tgt tct cac cgt ggc gcc atg   403
Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser His Arg Gly Ala Met
                90                  95                  100

ctc tgc cgt ggc aag agt gac aac cgc acc tcc ttg acc tgc cca ttc   451
Leu Cys Arg Gly Lys Ser Asp Asn Arg Thr Ser Leu Thr Cys Pro Phe
            105                 110                 115

cac ggc tgg cca ttc tgc aac ggc ggc gca ctg ctc aag gtc aag ggc   499
His Gly Trp Pro Phe Cys Asn Gly Gly Ala Leu Leu Lys Val Lys Gly
        120                 125                 130

gaa aaa gaa ggc gcc tac cca gag aat ttc cgc acc gac ggc tcc cac   547
Glu Lys Glu Gly Ala Tyr Pro Glu Asn Phe Arg Thr Asp Gly Ser His
    135                 140                 145

gat gtg cgt cgc gtt cct aag tta gag tcc tac cgt ggc ttc ctc ttc   595
Asp Val Arg Arg Val Pro Lys Leu Glu Ser Tyr Arg Gly Phe Leu Phe
150                 155                 160                 165

ggc tcc ctc aac gat gat gtc gtt tct ttg gaa gag cac ctc ggc gac   643
Gly Ser Leu Asn Asp Asp Val Val Ser Leu Glu Glu His Leu Gly Asp
                170                 175                 180

acc cgt acc gtc att gac atg ctg gtt gac caa tcc cca gaa ggc ctc   691
Thr Arg Thr Val Ile Asp Met Leu Val Asp Gln Ser Pro Glu Gly Leu
            185                 190                 195

gaa gta ctg cgc gga tcc tcc acc tac acc tac gac ggc aac tgg aag   739
Glu Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys
        200                 205                 210

ctc cag acc gaa aac ggt gca gac ggc tac cac gtt tcc tcc acc cac   787
Leu Gln Thr Glu Asn Gly Ala Asp Gly Tyr His Val Ser Ser Thr His
    215                 220                 225

tgg aac tac gct gca acc acc tcc cgc cgt ggc act ggt gaa tcc gcg   835
Trp Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala
230                 235                 240                 245

aac gaa acc aag gca atg gac gct ggt acc tgg ggc aag cag ggt ggc   883
Asn Glu Thr Lys Ala Met Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly
                250                 255                 260
```

```
gga tac ttc tcc tac cct tac ggc cac atg ctg ctg tgg atg tgg tgg   931
Gly Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu Leu Trp Met Trp Trp
            265                 270                 275

ggc aac cca gaa gac cgc cca ctg ttc gag cgc cgc gac gag ttc aag   979
Gly Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys
        280                 285                 290

aag gaa ttc ggc gaa gaa aag ggc gag ttc atg gtt ggt gct tcc cgc   1027
Lys Glu Phe Gly Glu Glu Lys Gly Glu Phe Met Val Gly Ala Ser Arg
    295                 300                 305

aat ctg tgc ctc tac ccc aat gtt tac ctg atg gat cag ttc tcc tca   1075
Asn Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met Asp Gln Phe Ser Ser
310                 315                 320                 325

cag atc cgc cac atc cgc cca atc tca gtt gat cag acc gaa gtc acc   1123
Gln Ile Arg His Ile Arg Pro Ile Ser Val Asp Gln Thr Glu Val Thr
                330                 335                 340

atc tac tgc atc gca cct aag ggc gag tcc gcg gaa gca cgt gca aac   1171
Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn
            345                 350                 355

cgc atc cgc cag tac gaa gac ttc ttc aac gca acg ggc atg gca acc   1219
Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr
        360                 365                 370

cca gat gac ctg gag gaa ttc cgc tcc tgc cag aag acc tac cag gca   1267
Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala
    375                 380                 385

tct gcc ttc cca tgg aat gac atg acc cgc ggt ttg ggc cac cag gta   1315
Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val
390                 395                 400                 405

cag gga cca aac gag gtt gcc aag ggc cta ggc atg aac gaa gtt ctt   1363
Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu
                410                 415                 420

tcc tcc gga gca cgc acc gaa gat gaa ggc ctc tac cca atc cag cac   1411
Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His
            425                 430                 435

ggc ttc tgg cat gaa ctc atg cag gag gct gtg aat aag cag agc atc   1459
Gly Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile
        440                 445                 450

aag gaa aag gaa ttg gct gac gat acc gct tct tcc ctt gcc acc gta   1507
Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val
    455                 460                 465

gct gca gcc aaa atc cgt gag gaa gca aag gca gcc gcg aag tcc gac   1555
Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp
470                 475                 480                 485

gct gga gag cct cgc cgc cgt cgt cgc acc cgc ggt tagtcgtcga        1601
Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg Gly
                490                 495
```

aaagcaaaaa atc 1614

<210> 424
<211> 497
<212> PRT
<213> Corynebacterium glutamicum

<400> 424

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Met Ser Thr Pro Val Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp
  1               5                  10                  15

His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg
             20                  25                  30

Asn Ile Phe Thr Asp Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile
         35                  40                  45

Phe Glu Gly Ile Trp Met Asp Met Ala His Glu Ser Gln Ile Pro Asn
     50                  55                  60

Gly Gly Asp Tyr Phe Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile
 65                  70                  75                  80

Thr Arg Ser Lys Glu Gly Thr Leu Asn Gly Leu Ile Asn Ala Cys Ser
                 85                  90                  95

His Arg Gly Ala Met Leu Cys Arg Gly Lys Ser Asp Asn Arg Thr Ser
            100                 105                 110

Leu Thr Cys Pro Phe His Gly Trp Pro Phe Cys Asn Gly Gly Ala Leu
        115                 120                 125

Leu Lys Val Lys Gly Glu Lys Glu Gly Ala Tyr Pro Glu Asn Phe Arg
    130                 135                 140

Thr Asp Gly Ser His Asp Val Arg Arg Val Pro Lys Leu Glu Ser Tyr
145                 150                 155                 160

Arg Gly Phe Leu Phe Gly Ser Leu Asn Asp Asp Val Val Ser Leu Glu
                165                 170                 175

Glu His Leu Gly Asp Thr Arg Thr Val Ile Asp Met Leu Val Asp Gln
            180                 185                 190

Ser Pro Glu Gly Leu Glu Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr
        195                 200                 205

Asp Gly Asn Trp Lys Leu Gln Thr Glu Asn Gly Ala Asp Gly Tyr His
    210                 215                 220

Val Ser Ser Thr His Trp Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly
225                 230                 235                 240

Thr Gly Glu Ser Ala Asn Glu Thr Lys Ala Met Asp Ala Gly Thr Trp
                245                 250                 255

Gly Lys Gln Gly Gly Gly Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu
            260                 265                 270

Leu Trp Met Trp Trp Gly Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg
```

275 280 285

Arg Asp Glu Phe Lys Lys Glu Phe Gly Glu Glu Lys Gly Glu Phe Met
290 295 300

Val Gly Ala Ser Arg Asn Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met
305 310 315 320

Asp Gln Phe Ser Ser Gln Ile Arg His Ile Arg Pro Ile Ser Val Asp
325 330 335

Gln Thr Glu Val Thr Ile Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala
340 345 350

Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala
355 360 365

Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln
370 375 380

Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn Asp Met Thr Arg Gly
385 390 395 400

Leu Gly His Gln Val Gln Gly Pro Asn Glu Val Ala Lys Gly Leu Gly
405 410 415

Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu
420 425 430

Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu Met Gln Glu Ala Val
435 440 445

Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser
450 455 460

Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala
465 470 475 480

Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg
485 490 495

Gly

<210> 425
<211> 372
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(349)
<223> FRXA00640

<400> 425
tgcggaattg ctcgcaaatg tcacacaccg cttcaaagca aaaacgaaaa cgacatcgcg 60

gtggcaatac caacttcttt tcactctctt ggaggttcac atg tcc aca cca gtt 115
Met Ser Thr Pro Val
1 5

```
tca aat ttg gca agc gtt cag aaa act ctg gac cat gcg ctt gag gac   163
Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp His Ala Leu Glu Asp
                10                  15                  20

cgc cct gaa gag gga atc gtc cgc gtc aac cgc aac atc ttc act gac   211
Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg Asn Ile Phe Thr Asp
            25                  30                  35

cct gag atc ttc gag ctg gag atg cgc cac atc ttc gaa ggc atc tgg   259
Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile Phe Glu Gly Ile Trp
        40                  45                  50

atg gac atg gct cac gag tcc cag atc cct aac ggt gga gac tac ttc   307
Met Asp Met Ala His Glu Ser Gln Ile Pro Asn Gly Gly Asp Tyr Phe
    55                  60                  65

acc acc tac att ggc tgc cag cgg atc atg atc acc cgt tcc           349
Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile Thr Arg Ser
70                  75                  80

naggnnggca cactnaangg cct                                        372
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20050244850

<210> 426
<211> 83
<212> PRT
<213> Corynebacterium glutamicum

<400> 426

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Met Ser Thr Pro Val Ser Asn Leu Ala Ser Val Gln Lys Thr Leu Asp
  1               5                  10                  15

His Ala Leu Glu Asp Arg Pro Glu Glu Gly Ile Val Arg Val Asn Arg
            20                  25                  30

Asn Ile Phe Thr Asp Pro Glu Ile Phe Glu Leu Glu Met Arg His Ile
        35                  40                  45

Phe Glu Gly Ile Trp Met Asp Met Ala His Glu Ser Gln Ile Pro Asn
    50                  55                  60

Gly Gly Asp Tyr Phe Thr Thr Tyr Ile Gly Cys Gln Arg Ile Met Ile
65                  70                  75                  80

Thr Arg Ser
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<210> 427
<211> 1164
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1141)
<223> FRXA00641

<400> 427

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ccacggttga nnantcngca aggncggnnc actgctcaag gtcaaggatg aaaaagaagg 60
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cncctaccca gagtatttcc gcaccgangg ntcccangat gtg cgt cgc gtt cct   115
                                             Val Arg Arg Val Pro
                                               1               5

aag tta gag tcc tac cgt ggc ttc ctc ttc ggc tcc ctc aac gat gat   163
Lys Leu Glu Ser Tyr Arg Gly Phe Leu Phe Gly Ser Leu Asn Asp Asp
                 10                  15                  20

gtc gtt tct ttg gaa gag cac ctc ggc gac acc cgt acc gtc att gac   211
Val Val Ser Leu Glu Glu His Leu Gly Asp Thr Arg Thr Val Ile Asp
             25                  30                  35

atg ctg gtt gac caa tcc cca gaa ggc ctc gaa gta ctg cgc gga tcc   259
Met Leu Val Asp Gln Ser Pro Glu Gly Leu Glu Val Leu Arg Gly Ser
         40                  45                  50

tcc acc tac acc tac gac ggc aac tgg aag ctc cag acc gaa aac ggt   307
Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys Leu Gln Thr Glu Asn Gly
     55                  60                  65

gca gac ggc tac cac gtt tcc tcc acc cac tgg aac tac gct gca acc   355
Ala Asp Gly Tyr His Val Ser Ser Thr His Trp Asn Tyr Ala Ala Thr
 70                  75                  80                  85

acc tcc cgc cgt ggc act ggt gaa tcc gcg aac gaa acc aag gca atg   403
Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala Asn Glu Thr Lys Ala Met
                 90                  95                 100

gac gct ggt acc tgg ggc aag cag ggt ggc gga tac ttc tcc tac cct   451
Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly Gly Tyr Phe Ser Tyr Pro
             105                 110                 115

tac ggc cac atg ctg ctg tgg atg tgg tgg ggc aac cca gaa gac cgc   499
Tyr Gly His Met Leu Leu Trp Met Trp Trp Gly Asn Pro Glu Asp Arg
         120                 125                 130

cca ctg ttc gag cgc cgc gac gag ttc aag aag gaa ttc ggc gaa gaa   547
Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys Lys Glu Phe Gly Glu Glu
     135                 140                 145

aag ggc gag ttc atg gtt ggt gct tcc cgc aat ctg tgc ctc tac ccc   595
Lys Gly Glu Phe Met Val Gly Ala Ser Arg Asn Leu Cys Leu Tyr Pro
150                 155                 160                 165

aat gtt tac ctg atg gat cag ttc tcc tca cag atc cgc cac atc cgc   643
Asn Val Tyr Leu Met Asp Gln Phe Ser Ser Gln Ile Arg His Ile Arg
                 170                 175                 180

cca atc tca gtt gat cag acc gaa gtc acc atc tac tgc atc gca cct   691
Pro Ile Ser Val Asp Gln Thr Glu Val Thr Ile Tyr Cys Ile Ala Pro
             185                 190                 195

aag ggc gag tcc gcg gaa gca cgt gca aac cgc atc cgc cag tac gaa   739
Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn Arg Ile Arg Gln Tyr Glu
         200                 205                 210

gac ttc ttc aac gca acg ggc atg gca acc cca gat gac ctg gag gaa   787
Asp Phe Phe Asn Ala Thr Gly Met Ala Thr Pro Asp Asp Leu Glu Glu
     215                 220                 225
```

```
ttc cgc tcc tgc cag aag acc tac cag gca tct gcc ttc cca tgg aat   835
Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala Ser Ala Phe Pro Trp Asn
230                 235                 240                 245

gac atg acc cgc ggt ttg ggc cac cag gta cag gga cca aac gag gtt   883
Asp Met Thr Arg Gly Leu Gly His Gln Val Gln Gly Pro Asn Glu Val
                250                 255                 260

gcc aag ggc cta ggc atg aac gaa gtt ctt tcc tcc gga gca cgc acc   931
Ala Lys Gly Leu Gly Met Asn Glu Val Leu Ser Ser Gly Ala Arg Thr
            265                 270                 275

gaa gat gaa ggc ctc tac cca atc cag cac ggc ttc tgg cat gaa ctc   979
Glu Asp Glu Gly Leu Tyr Pro Ile Gln His Gly Phe Trp His Glu Leu
        280                 285                 290

atg cag gag gct gtg aat aag cag agc atc aag gaa aag gaa ttg gct   1027
Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys Glu Lys Glu Leu Ala
    295                 300                 305

gac gat acc gct tct tcc ctt gcc acc gta gct gca gcc aaa atc cgt   1075
Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala Ala Ala Lys Ile Arg
310                 315                 320                 325

gag gaa gca aag gca gcc gcg aag tcc gac gct gga gag cct cgc cgc   1123
Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala Gly Glu Pro Arg Arg
                330                 335                 340

cgt cgt cgc acc cgc ggt tagtcgtcga aaagcaaaaa atc                1164
Arg Arg Arg Thr Arg Gly
            345
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SEQUENCE LISTING

<210> 428
<211> 347
<212> PRT
<213> Corynebacterium glutamicum

<400> 428

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Val Arg Arg Val Pro Lys Leu Glu Ser Tyr Arg Gly Phe Leu Phe Gly
  1               5                  10                  15

Ser Leu Asn Asp Asp Val Val Ser Leu Glu Glu His Leu Gly Asp Thr
             20                  25                  30

Arg Thr Val Ile Asp Met Leu Val Asp Gln Ser Pro Glu Gly Leu Glu
         35                  40                  45

Val Leu Arg Gly Ser Ser Thr Tyr Thr Tyr Asp Gly Asn Trp Lys Leu
     50                  55                  60

Gln Thr Glu Asn Gly Ala Asp Gly Tyr His Val Ser Ser Thr His Trp
 65                  70                  75                  80

Asn Tyr Ala Ala Thr Thr Ser Arg Arg Gly Thr Gly Glu Ser Ala Asn
                 85                  90                  95

Glu Thr Lys Ala Met Asp Ala Gly Thr Trp Gly Lys Gln Gly Gly Gly
            100                 105                 110

Tyr Phe Ser Tyr Pro Tyr Gly His Met Leu Leu Trp Met Trp Trp Gly
```

```
        115                 120                 125

Asn Pro Glu Asp Arg Pro Leu Phe Glu Arg Arg Asp Glu Phe Lys Lys
    130                 135                 140

Glu Phe Gly Glu Glu Lys Gly Glu Phe Met Val Gly Ala Ser Arg Asn
145                 150                 155                 160

Leu Cys Leu Tyr Pro Asn Val Tyr Leu Met Asp Gln Phe Ser Ser Gln
                165                 170                 175

Ile Arg His Ile Arg Pro Ile Ser Val Asp Gln Thr Glu Val Thr Ile
            180                 185                 190

Tyr Cys Ile Ala Pro Lys Gly Glu Ser Ala Glu Ala Arg Ala Asn Arg
        195                 200                 205

Ile Arg Gln Tyr Glu Asp Phe Phe Asn Ala Thr Gly Met Ala Thr Pro
    210                 215                 220

Asp Asp Leu Glu Glu Phe Arg Ser Cys Gln Lys Thr Tyr Gln Ala Ser
225                 230                 235                 240

Ala Phe Pro Trp Asn Asp Met Thr Arg Gly Leu Gly His Gln Val Gln
                245                 250                 255

Gly Pro Asn Glu Val Ala Lys Gly Leu Gly Met Asn Glu Val Leu Ser
            260                 265                 270

Ser Gly Ala Arg Thr Glu Asp Glu Gly Leu Tyr Pro Ile Gln His Gly
        275                 280                 285

Phe Trp His Glu Leu Met Gln Glu Ala Val Asn Lys Gln Ser Ile Lys
    290                 295                 300

Glu Lys Glu Leu Ala Asp Asp Thr Ala Ser Ser Leu Ala Thr Val Ala
305                 310                 315                 320

Ala Ala Lys Ile Arg Glu Glu Ala Lys Ala Ala Ala Lys Ser Asp Ala
                325                 330                 335

Gly Glu Pro Arg Arg Arg Arg Arg Thr Arg Gly
            340                 345
```

<210> 429
<211> 615
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(592)
<223> RXA00642

<400> 429
aaaggcagcc gcgaagtccg acgctggaga gcctcgccgc cgtcgtcgca cccgcggtta 60

gtcgtcgaaa agcaaaaaat cttttaagga gaacacctaa atg tct gaa atc acc 115
                                                Met Ser Glu Ile Thr
                                                  1   5

```
cgc tct gag atc gaa gct ttc ctc tac tac gag gct cgc ctg ctc gat   163
Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu Ala Arg Leu Leu Asp
                 10                  15                  20

gac cgt aaa ttt gaa gaa tgg ctc gaa tgc tac cgc gag gac gcc gag   211
Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr Arg Glu Asp Ala Glu
             25                  30                  35

ttt tgg atg cca gcc tgg gac gac aac ggt gaa ctg act gaa gat cca   259
Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu Leu Thr Glu Asp Pro
         40                  45                  50

cag tct gaa att tcc ctc atc tac tac cca aac cgt ggt gga ctt gag   307
Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn Arg Gly Gly Leu Glu
     55                  60                  65

gac cgc gtc ttc cgc atc cgc acc gaa cgc tcc tct gca act tcc cta   355
Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser Ser Ala Thr Ser Leu
 70                  75                  80                  85

cct gaa cca cgc acc ggc cac agc acc acc aac gtg gaa atc ctg gag   403
Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn Val Glu Ile Leu Glu
                 90                  95                 100

cgc cgc gac ggc gaa gta gat atc cgc ttc aac tgg atc acc ttc tac   451
Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn Trp Ile Thr Phe Tyr
             105                 110                 115

tac cgt tac aac acc acc gac acc tac ttc ggc acc acg ttt atc acc   499
Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly Thr Thr Phe Ile Thr
         120                 125                 130

ctt gat gtc agt ggt gaa acc ccg aag atc gtc aag aag aag gtc gtt   547
Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val Lys Lys Lys Val Val
     135                 140                 145

ttg aag aac gac tac atc cac cac atc gtc gat att tac cac gtc       592
Leu Lys Asn Asp Tyr Ile His His Ile Val Asp Ile Tyr His Val
150                 155                 160

taggaggcac tcacatgact cac                                        615


<210> 430
<211> 164
<212> PRT
<213> Corynebacterium glutamicum

<400> 430
Met Ser Glu Ile Thr Arg Ser Glu Ile Glu Ala Phe Leu Tyr Tyr Glu
  1               5                  10                  15

Ala Arg Leu Leu Asp Asp Arg Lys Phe Glu Glu Trp Leu Glu Cys Tyr
             20                  25                  30

Arg Glu Asp Ala Glu Phe Trp Met Pro Ala Trp Asp Asp Asn Gly Glu
         35                  40                  45

Leu Thr Glu Asp Pro Gln Ser Glu Ile Ser Leu Ile Tyr Tyr Pro Asn
     50                  55                  60
```

```
Arg Gly Gly Leu Glu Asp Arg Val Phe Arg Ile Arg Thr Glu Arg Ser
 65                  70                  75                  80

Ser Ala Thr Ser Leu Pro Glu Pro Arg Thr Gly His Ser Thr Thr Asn
                 85                  90                  95

Val Glu Ile Leu Glu Arg Arg Asp Gly Glu Val Asp Ile Arg Phe Asn
            100                 105                 110

Trp Ile Thr Phe Tyr Tyr Arg Tyr Asn Thr Thr Asp Thr Tyr Phe Gly
        115                 120                 125

Thr Thr Phe Ile Thr Leu Asp Val Ser Gly Glu Thr Pro Lys Ile Val
    130                 135                 140

Lys Lys Lys Val Val Leu Lys Asn Asp Tyr Ile His His Ile Val Asp
145                 150                 155                 160

Ile Tyr His Val
```

Sequence Listing

<210> 431
<211> 1659
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1636)
<223> RXA00643

<400> 431
tcagtggtga aaccccgaag atcgtcaaga agaaggtcgt tttgaagaac gactacatcc 60

accacatcgt cgatatttac cacgtctagg aggcactcac atg act cac caa gtt 115
                                              Met Thr His Gln Val
                                                1   5

gca ctt gcc ttt gaa gac ggc atc acc cga ttc atc gac tgc gaa gat 163
Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe Ile Asp Cys Glu Asp
               10   15   20

gac caa act gtt gca gat gcc gcc tac cag gca cgc atc aac att cct 211
Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala Arg Ile Asn Ile Pro
           25   30   35

ttc gac tgc cgc gac ggc gcc tgc gga acc tgc aaa gcg ttc tgc gaa 259
Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys Lys Ala Phe Cys Glu
       40   45   50

tcc ggc gac ttt gac gaa ggc gac tac atc gac gac gcc ctg tcc gaa 307
Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp Asp Ala Leu Ser Glu
   55   60   65

gat gaa gca gcc gac ggc tac tgc ctg cct tgc cag atg acc cca aag 355
Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys Gln Met Thr Pro Lys
 70   75   80   85

acc gac ctc atc ttg cag atc gcc acc acc tcc gtg ctg gca aag acc 403
```
```

```
Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser Val Leu Ala Lys Thr
                 90                  95                 100

ggc gca tcc act ttc gat ggc gag ttg aag gag atc aat cac ttc tct   451
Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu Ile Asn His Phe Ser
            105                 110                 115

gat tcc acc atc ggc att gag atc gaa ctg gaa aac cgc caa gat ttg   499
Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu Asn Arg Gln Asp Leu
        120                 125                 130

gcg ttc ctc cct ggt caa tac atg aac atc cag gtt cca ggc agc gac   547
Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln Val Pro Gly Ser Asp
    135                 140                 145

cag act cgt tcc tac tct ttc tcc tgc gct caa gat tcc ggc aac gtg   595
Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln Asp Ser Gly Asn Val
150                 155                 160                 165

cag ttc ctg atc aag gta acc cca ggt gga ctc atg acc acc tat ctc   643
Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu Met Thr Thr Tyr Leu
                170                 175                 180

acc gat cac gcg aag gtc ggc gac aag ctc acc ttg acc ggc ccg atg   691
Thr Asp His Ala Lys Val Gly Asp Lys Leu Thr Leu Thr Gly Pro Met
            185                 190                 195

ggt tcc ttc ttc ctg cgt gaa cct gtc cgc ccg atc ctg ctg ctc gcc   739
Gly Ser Phe Phe Leu Arg Glu Pro Val Arg Pro Ile Leu Leu Leu Ala
        200                 205                 210

ggc gga act gga ctt gca ccg atc ttg gct att ttg gaa aag ctt tcc   787
Gly Gly Thr Gly Leu Ala Pro Ile Leu Ala Ile Leu Glu Lys Leu Ser
    215                 220                 225

cgc gat gag ctt ctc gac gtc cca atc cgc ctg gtt tac ggc gcg aac   835
Arg Asp Glu Leu Leu Asp Val Pro Ile Arg Leu Val Tyr Gly Ala Asn
230                 235                 240                 245

ttc acc cac gat ctg gtg gaa ttg gat cga ctt gat gcc ttc aag gac   883
Phe Thr His Asp Leu Val Glu Leu Asp Arg Leu Asp Ala Phe Lys Asp
                250                 255                 260

aag ttc gac ttc gat tac atc acc gtg ctt tcc gac aag gac acc gag   931
Lys Phe Asp Phe Asp Tyr Ile Thr Val Leu Ser Asp Lys Asp Thr Glu
            265                 270                 275

cat cca cgc aag ggc tac gtc cca gca cac ctg acc ggc gaa tat gag   979
His Pro Arg Lys Gly Tyr Val Pro Ala His Leu Thr Gly Glu Tyr Glu
        280                 285                 290

cca gat gag gac act gat gtg tac ctc tgc ggc cct cct cca atg gtc   1027
Pro Asp Glu Asp Thr Asp Val Tyr Leu Cys Gly Pro Pro Pro Met Val
    295                 300                 305

gag gcc gtg cgc caa ttc ctg ggc acc ctg gag cat cct ccg ctg gac   1075
Glu Ala Val Arg Gln Phe Leu Gly Thr Leu Glu His Pro Pro Leu Asp
310                 315                 320                 325

ttt tat tac gag aag ttc act tcc gcc gct gcc cct gct gct ggt aag   1123
Phe Tyr Tyr Glu Lys Phe Thr Ser Ala Ala Ala Pro Ala Ala Gly Lys
```

```
                330                 335                 340

cca gag atc acc gtg gag acc agc gaa gtt gca gag gat ttc aac ctg   1171
Pro Glu Ile Thr Val Glu Thr Ser Glu Val Ala Glu Asp Phe Asn Leu
            345                 350                 355

gtc gag gtg tcc act cca ggc atg tct tcc ggc gag gtg cac tct tct   1219
Val Glu Val Ser Thr Pro Gly Met Ser Ser Gly Glu Val His Ser Ser
        360                 365                 370

gca acc cag ctg cag gcc cgc atg gct ctg gag ctc ggc gcg ctg gag   1267
Ala Thr Gln Leu Gln Ala Arg Met Ala Leu Glu Leu Gly Ala Leu Glu
    375                 380                 385

ctt gcg atc aac aaa ctc ggc gag cgc gac atc gag cga ttc cgc aac   1315
Leu Ala Ile Asn Lys Leu Gly Glu Arg Asp Ile Glu Arg Phe Arg Asn
390                 395                 400                 405

ttg gcc gac atc gcg aac tcc ttc atc gac ggc gat aag ttt atc gac   1363
Leu Ala Asp Ile Ala Asn Ser Phe Ile Asp Gly Asp Lys Phe Ile Asp
                410                 415                 420

gcg gtg aag ttc acc gag gcc aac gcc gat ttc cac gag ttc ctc ttc   1411
Ala Val Lys Phe Thr Glu Ala Asn Ala Asp Phe His Glu Phe Leu Phe
            425                 430                 435

cgc cgc gca aac aac gag gcg ctg ctt gcg gcg tac cag aac ctc cag   1459
Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala Tyr Gln Asn Leu Gln
        440                 445                 450

gtt gtt caa gaa atg aac gca acc ctt cca ggc gcc gag tgg att gat   1507
Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly Ala Glu Trp Ile Asp
    455                 460                 465

ccg gca att gcc acc gag cac ttg gcg ctt gtc gac gcc gtc tcc cag   1555
Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val Asp Ala Val Ser Gln
470                 475                 480                 485

aat gat ctc gag acc gcg aga aca atc att cgt gaa cac gcg gag cac   1603
Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg Glu His Ala Glu His
                490                 495                 500

ggc att gac act atg gtt aag gcc ctc gag aaa tgagcgcgcc agtaggacaa 1656
Gly Ile Asp Thr Met Val Lys Ala Leu Glu Lys
            505                 510

ggc                                                               1659


<210> 432
<211> 512
<212> PRT
<213> Corynebacterium glutamicum

<400> 432
Met Thr His Gln Val Ala Leu Ala Phe Glu Asp Gly Ile Thr Arg Phe
  1               5                  10                  15

Ile Asp Cys Glu Asp Asp Gln Thr Val Ala Asp Ala Ala Tyr Gln Ala
             20                  25                  30
```

```
Arg Ile Asn Ile Pro Phe Asp Cys Arg Asp Gly Ala Cys Gly Thr Cys
         35                  40                  45

Lys Ala Phe Cys Glu Ser Gly Asp Phe Asp Glu Gly Asp Tyr Ile Asp
     50                  55                  60

Asp Ala Leu Ser Glu Asp Glu Ala Ala Asp Gly Tyr Cys Leu Pro Cys
 65                  70                  75                  80

Gln Met Thr Pro Lys Thr Asp Leu Ile Leu Gln Ile Ala Thr Thr Ser
                 85                  90                  95

Val Leu Ala Lys Thr Gly Ala Ser Thr Phe Asp Gly Glu Leu Lys Glu
            100                 105                 110

Ile Asn His Phe Ser Asp Ser Thr Ile Gly Ile Glu Ile Glu Leu Glu
        115                 120                 125

Asn Arg Gln Asp Leu Ala Phe Leu Pro Gly Gln Tyr Met Asn Ile Gln
    130                 135                 140

Val Pro Gly Ser Asp Gln Thr Arg Ser Tyr Ser Phe Ser Cys Ala Gln
145                 150                 155                 160

Asp Ser Gly Asn Val Gln Phe Leu Ile Lys Val Thr Pro Gly Gly Leu
                165                 170                 175

Met Thr Thr Tyr Leu Thr Asp His Ala Lys Val Gly Asp Lys Leu Thr
            180                 185                 190

Leu Thr Gly Pro Met Gly Ser Phe Phe Leu Arg Glu Pro Val Arg Pro
        195                 200                 205

Ile Leu Leu Leu Ala Gly Gly Thr Gly Leu Ala Pro Ile Leu Ala Ile
    210                 215                 220

Leu Glu Lys Leu Ser Arg Asp Glu Leu Leu Asp Val Pro Ile Arg Leu
225                 230                 235                 240

Val Tyr Gly Ala Asn Phe Thr His Asp Leu Val Glu Leu Asp Arg Leu
                245                 250                 255

Asp Ala Phe Lys Asp Lys Phe Asp Phe Asp Tyr Ile Thr Val Leu Ser
            260                 265                 270

Asp Lys Asp Thr Glu His Pro Arg Lys Gly Tyr Val Pro Ala His Leu
        275                 280                 285

Thr Gly Glu Tyr Glu Pro Asp Glu Asp Thr Asp Val Tyr Leu Cys Gly
    290                 295                 300

Pro Pro Pro Met Val Glu Ala Val Arg Gln Phe Leu Gly Thr Leu Glu
305                 310                 315                 320

His Pro Pro Leu Asp Phe Tyr Tyr Glu Lys Phe Thr Ser Ala Ala Ala
                325                 330                 335

Pro Ala Ala Gly Lys Pro Glu Ile Thr Val Glu Thr Ser Glu Val Ala
            340                 345                 350

Glu Asp Phe Asn Leu Val Glu Val Ser Thr Pro Gly Met Ser Ser Gly
```

Confidential - Pending

```
        355                 360                 365

Glu Val His Ser Ser Ala Thr Gln Leu Gln Ala Arg Met Ala Leu Glu
    370                 375                 380

Leu Gly Ala Leu Glu Leu Ala Ile Asn Lys Leu Gly Glu Arg Asp Ile
385                 390                 395                 400

Glu Arg Phe Arg Asn Leu Ala Asp Ile Ala Asn Ser Phe Ile Asp Gly
                405                 410                 415

Asp Lys Phe Ile Asp Ala Val Lys Phe Thr Glu Ala Asn Ala Asp Phe
            420                 425                 430

His Glu Phe Leu Phe Arg Arg Ala Asn Asn Glu Ala Leu Leu Ala Ala
        435                 440                 445

Tyr Gln Asn Leu Gln Val Val Gln Glu Met Asn Ala Thr Leu Pro Gly
    450                 455                 460

Ala Glu Trp Ile Asp Pro Ala Ile Ala Thr Glu His Leu Ala Leu Val
465                 470                 475                 480

Asp Ala Val Ser Gln Asn Asp Leu Glu Thr Ala Arg Thr Ile Ile Arg
                485                 490                 495

Glu His Ala Glu His Gly Ile Asp Thr Met Val Lys Ala Leu Glu Lys
            500                 505                 510
```

<210> 433
<211> 1166
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (16)..(1143)
<223> RXN01993

<400> 433

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ctttaggagt tcaccatg aca ctg tcc gaa cgc aag ctc acc acc acc gcc   51
                Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala
                  1               5                  10

aag att ctt ccc cac cca ctc aac gcc tgg tac gtc gcc gct tgg gat   99
Lys Ile Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp
         15                  20                  25

tat gaa gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa   147
Tyr Glu Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys
     30                  35                  40

cca ctc gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca   195
Pro Leu Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala
 45                  50                  55                  60

gac gcc tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg   243
```

```
Asp Ala Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val
                 65                  70                  75

ggc aca gac gga atc caa tgc cct tat cac ggc ttg gag tac aac tcc   291
Gly Thr Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser
             80                  85                  90

gcg ggc cgc tgc atg aaa atg ccc gcg cag gaa acc ctc aac ccg tca   339
Ala Gly Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser
         95                 100                 105

gca gcc gtc aac tcc tac ccc gtg gtg gaa gcc cac cgc ttt gtg tgg   387
Ala Ala Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp
    110                 115                 120

gtg tgg ctg ggc gat ccc aca ttg gca gat ccc acc caa gta ccc gat   435
Val Trp Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp
125                 130                 135                 140

atg cac cag atg agc cac ccc gaa tgg gca ggc gat gga cgc acc atc   483
Met His Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile
                145                 150                 155

tcc gct gac tgc aac tac caa tta gtg ctg gac aac ttg atg gac ctc   531
Ser Ala Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu
            160                 165                 170

acc cac gaa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt   579
Thr His Glu Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu
        175                 180                 185

agt gaa tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc   627
Ser Glu Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val
    190                 195                 200

acc cgc tgg atg cat gac ata gat gca cca ccg ttt tgg caa aag aac   675
Thr Arg Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn
205                 210                 215                 220

atg aat gat aag ttc cca gga ttt gaa ggc aag gtg gat cgt tgg cag   723
Met Asn Asp Lys Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln
                225                 230                 235

atc atc cac tac tac tac cct tcc acc atc tgc att gat gtt ggt gta   771
Ile Ile His Tyr Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val
            240                 245                 250

gca aag gct gga act ggc gcg cag gaa ggc gac cgc agc cag ggc gtt   819
Ala Lys Ala Gly Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val
        255                 260                 265

aat ggg tat gtc atg aac acc att acc cca gat tca gat cgt tcc tct   867
Asn Gly Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser
    270                 275                 280

cat tac ttc tgg gca ttc atg cgc aac tac cgc ctg gaa agc caa acc   915
His Tyr Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr
285                 290                 295                 300

atc acc acc cag ctg cgc gac ggt gta tcc ggt gta ttc aaa gaa gac   963
Ile Thr Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp
```

```
                305                 310                 315

gaa gac atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac   1011
Glu Asp Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp
            320                 325                 330

tac gag ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc   1059
Tyr Glu Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg
        335                 340                 345

cga atc ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc   1107
Arg Ile Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro
    350                 355                 360

acc aca ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga        1153
Thr Thr Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
365                 370                 375

actcgcaatg gca                                                   1166
```

<210> 434
<211> 376
<212> PRT
<213> Corynebacterium glutamicum

<400> 434

```
Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile Leu Pro
  1               5                  10                  15

His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu Val Thr
             20                  25                  30

Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu Ala Leu
         35                  40                  45

Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala Cys Trp
     50                  55                  60

His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr Asp Gly
 65                  70                  75                  80

Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly Arg Cys
                 85                  90                  95

Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala Val Asn
            100                 105                 110

Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp Leu Gly
        115                 120                 125

Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His Gln Met
    130                 135                 140

Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala Asp Cys
145                 150                 155                 160

Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His Glu Glu
                165                 170                 175

Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu Ser Glu
```

```
            180                 185                 190

Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg Trp Met
        195                 200                 205

His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met Asn Asp Lys
    210                 215                 220

Phe Pro Gly Phe Glu Gly Lys Val Asp Arg Trp Gln Ile Ile His Tyr
225                 230                 235                 240

Tyr Tyr Pro Ser Thr Ile Cys Ile Asp Val Gly Val Ala Lys Ala Gly
                245                 250                 255

Thr Gly Ala Gln Glu Gly Asp Arg Ser Gln Gly Val Asn Gly Tyr Val
            260                 265                 270

Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Ser Ser His Tyr Phe Trp
        275                 280                 285

Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr Thr Gln
    290                 295                 300

Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp Met Leu
305                 310                 315                 320

Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu Phe Tyr
                325                 330                 335

Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile Leu Glu
            340                 345                 350

Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr Phe Pro
        355                 360                 365

Arg Ala Thr Pro Lys Pro Glu Ala
    370                 375
```

Substitute Sheet (Rule 26)

<210> 435
<211> 389
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(366)
<223> FRXA01993

<400> 435

```
gct gga act ggc gcg cag gat ggc gac cgc agc cag ggc gtt aat ggg   48
Ala Gly Thr Gly Ala Gln Asp Gly Asp Arg Ser Gln Gly Val Asn Gly
  1               5                  10                  15

tat gtc atg aac acc att acc cca gat tca gat cgt ttt tct cat tac   96
Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Phe Ser His Tyr
             20                  25                  30

ttc tgg gca ttc atg cgc aac tac cgc ctg gaa agc caa acc atc acc   144
Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr
         35                  40                  45
```

```
acc cag ctg cgc gac ggt gta tcc ggt gta ttc aaa gaa gac gaa gac   192
Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp
     50                  55                  60

atg ctg acc gct cag caa gat gcc atc gac gcc aac acc gac tac gag   240
Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu
 65                  70                  75                  80

ttt tac agc ctc aac att gat gcc ggt ggc atg tgg gtg cgc cga atc   288
Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile
                 85                  90                  95

ctc gag gaa gca ctc tcc aag gaa ggc cga ctg gat atc ccc acc aca   336
Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr
            100                 105                 110

ttc ccc cgc gca aca ccg aag ccg gag gca taaaccatga actcgcaatg     386
Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
        115                 120

gca                                                               389
```

09605135.1

<210> 436
<211> 122
<212> PRT
<213> Corynebacterium glutamicum

<400> 436

```
Ala Gly Thr Gly Ala Gln Asp Gly Asp Arg Ser Gln Gly Val Asn Gly
  1               5                  10                  15

Tyr Val Met Asn Thr Ile Thr Pro Asp Ser Asp Arg Phe Ser His Tyr
             20                  25                  30

Phe Trp Ala Phe Met Arg Asn Tyr Arg Leu Glu Ser Gln Thr Ile Thr
         35                  40                  45

Thr Gln Leu Arg Asp Gly Val Ser Gly Val Phe Lys Glu Asp Glu Asp
     50                  55                  60

Met Leu Thr Ala Gln Gln Asp Ala Ile Asp Ala Asn Thr Asp Tyr Glu
 65                  70                  75                  80

Phe Tyr Ser Leu Asn Ile Asp Ala Gly Gly Met Trp Val Arg Arg Ile
                 85                  90                  95

Leu Glu Glu Ala Leu Ser Lys Glu Gly Arg Leu Asp Ile Pro Thr Thr
            100                 105                 110

Phe Pro Arg Ala Thr Pro Lys Pro Glu Ala
        115                 120
```

<210> 437
<211> 669
<212> DNA
<213> Corynebacterium glutamicum

<220>

<221> CDS
<222> (1)..(669)
<223> FRXA02012

<400> 437

```
ttc acc atg aca ctg tcc gaa cgc aag ctc acc acc acc gcc aag att   48
Phe Thr Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile
  1               5                  10                  15

ctt ccc cac cca ctc aac gcc tgg tac gtc gcc gct tgg gat tat gaa   96
Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu
             20                  25                  30

gtc aca tct aaa aag ccc atg gcc agg aca atc gcc aac aaa cca ctc   144
Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
         35                  40                  45

gct ttg tac cgc acc aaa gat ggc cga gcc gtt gcc ctt gca gac gcc   192
Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
     50                  55                  60

tgc tgg cac cgc ctc gca ccg cta tcc aag gga aaa ctc gtg ggc aca   240
Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr
 65                  70                  75                  80

gac gga atc caa tgc cct tat cac ggc ttg gag tac aac tcc gcg ggc   288
Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly
                 85                  90                  95

cgc tgc atg aaa atg ccc gcg cag gaa acc ctc aac ccg tca gca gcc   336
Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala
            100                 105                 110

gtc aac tcc tac ccc gtg gtg gaa gcc cac cgc ttt gtg tgg gtg tgg   384
Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp
        115                 120                 125

ctg ggc gat ccc aca ttg gca gat ccc acc caa gta ccc gat atg cac   432
Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His
    130                 135                 140

cag atg agc cac ccc gaa tgg gca ggc gat gga cgc acc atc tcc gct   480
Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala
145                 150                 155                 160

gac tgc aac tac caa tta gtg ctg gac aac ttg atg gac ctc acc cac   528
Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His
                165                 170                 175

caa gag ttc gtg cac tcc tcc agc atc gga caa gac gaa ctt agt gaa   576
Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu
            180                 185                 190

tca gag ttc gtg gtc acc cac act gaa gat tcc gtg acg gtc acc cgc   624
Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg
        195                 200                 205

tgg atg cat gac ata gat gca cca ccg ttt tgg caa aag aac atg       669
Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met
    210                 215                 220
```

<210> 438
<211> 223
<212> PRT
<213> Corynebacterium glutamicum

<400> 438
Phe Thr Met Thr Leu Ser Glu Arg Lys Leu Thr Thr Thr Ala Lys Ile
1 5 10 15

Leu Pro His Pro Leu Asn Ala Trp Tyr Val Ala Ala Trp Asp Tyr Glu
20 25 30

Val Thr Ser Lys Lys Pro Met Ala Arg Thr Ile Ala Asn Lys Pro Leu
35 40 45

Ala Leu Tyr Arg Thr Lys Asp Gly Arg Ala Val Ala Leu Ala Asp Ala
50 55 60

Cys Trp His Arg Leu Ala Pro Leu Ser Lys Gly Lys Leu Val Gly Thr
65 70 75 80

Asp Gly Ile Gln Cys Pro Tyr His Gly Leu Glu Tyr Asn Ser Ala Gly
85 90 95

Arg Cys Met Lys Met Pro Ala Gln Glu Thr Leu Asn Pro Ser Ala Ala
100 105 110

Val Asn Ser Tyr Pro Val Val Glu Ala His Arg Phe Val Trp Val Trp
115 120 125

Leu Gly Asp Pro Thr Leu Ala Asp Pro Thr Gln Val Pro Asp Met His
130 135 140

Gln Met Ser His Pro Glu Trp Ala Gly Asp Gly Arg Thr Ile Ser Ala
145 150 155 160

Asp Cys Asn Tyr Gln Leu Val Leu Asp Asn Leu Met Asp Leu Thr His
165 170 175

Gln Glu Phe Val His Ser Ser Ser Ile Gly Gln Asp Glu Leu Ser Glu
180 185 190

Ser Glu Phe Val Val Thr His Thr Glu Asp Ser Val Thr Val Thr Arg
195 200 205

Trp Met His Asp Ile Asp Ala Pro Pro Phe Trp Gln Lys Asn Met
210 215 220

<210> 439
<211> 1098
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1075)
<223> RXA01994

<400> 439

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gtgggtgcgc cgaatcctcg aggaagcact ctccaaggaa ggccgactgg atatccccac 60

cacattcccc cgcgcaacac cgaagccgga ggcataaacc atg aac tcg caa tgg   115
                                            Met Asn Ser Gln Trp
                                              1               5

caa gat gca cat gtt gtt tcc agc gaa atc atc gct gca gac att cgg   163
Gln Asp Ala His Val Val Ser Ser Glu Ile Ile Ala Ala Asp Ile Arg
                 10                  15                  20

cga ata gaa cta tcc ccg aaa ttt gcg att cca gta aaa ccc ggc gaa   211
Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro Val Lys Pro Gly Glu
             25                  30                  35

cat ctc aag atc atg gtg ccc cta aaa act gga cag gaa aag aga tcg   259
His Leu Lys Ile Met Val Pro Leu Lys Thr Gly Gln Glu Lys Arg Ser
         40                  45                  50

tac tcc atc gtt gac gct cgt cac gac ggt tcg act ctc gcc ctg agc   307
Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser Thr Leu Ala Leu Ser
     55                  60                  65

gta ctc aaa acc aga aac tcc cgt gga gga tct gag ttc atg cat acg   355
Val Leu Lys Thr Arg Asn Ser Arg Gly Gly Ser Glu Phe Met His Thr
 70                  75                  80                  85

ctt cga gct gga gac aca gtt act gtc tcc agg ccg tct cag gat ttt   403
Leu Arg Ala Gly Asp Thr Val Thr Val Ser Arg Pro Ser Gln Asp Phe
                 90                  95                 100

cct ctc cgc gtg ggt gcg cct gag tat gta ctt gtt gcc ggc gga att   451
Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu Val Ala Gly Gly Ile
            105                 110                 115

gga atc aca gcg atc cgt tca atg gca tct tta tta aag aaa ttg gga   499
Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu Leu Lys Lys Leu Gly
        120                 125                 130

gcg aac tac cgc atc cat ttc gca gca cgc agc ctt gat gcc atg gct   547
Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser Leu Asp Ala Met Ala
    135                 140                 145

tac aaa gat gag ctc gtg gca gaa cac ggc gac aag ctg cac ctg cat   595
Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp Lys Leu His Leu His
150                 155                 160                 165

cta gat tct gaa ggc acc acc atc gat gtc cca gca ttg atc gaa acc   643
Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro Ala Leu Ile Glu Thr
                170                 175                 180

tta aac ccc cac act gag ctt tat atg tgc ggc ccc atc cgc ttg atg   691
Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly Pro Ile Arg Leu Met
            185                 190                 195

gat gcc atc cgg cgc gca tgg aac acc cgc gga ctt gac ccc acc aat   739
Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly Leu Asp Pro Thr Asn
        200                 205                 210

ctg cgt ttc gaa acg ttt gga aac agt gga tgg ttc tcc cca gag gtt   787
Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp Phe Ser Pro Glu Val
    215                 220                 225
```

```
ttc cac atc caa gta cca gag ctg ggg ctt cac gcc aca gtc aac aag   835
Phe His Ile Gln Val Pro Glu Leu Gly Leu His Ala Thr Val Asn Lys
230                 235                 240                 245

gat gaa agc atg ctg gag gct ttg caa aag gct ggg gcg aat atg atg   883
Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala Gly Ala Asn Met Met
                250                 255                 260

ttt gat tgt cga aaa ggc gaa tgt ggt ttg tgc cag gtt cgc gtt cta   931
Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys Gln Val Arg Val Leu
            265                 270                 275

gaa gtc gat ggc cag gtt gat cac cgc gat gtg ttc ttc tct gat cgt   979
Glu Val Asp Gly Gln Val Asp His Arg Asp Val Phe Phe Ser Asp Arg
        280                 285                 290

caa aaa gaa tcc gac gca aag gca tgc gcc tgc gtg tct cga gta gtc   1027
Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys Val Ser Arg Val Val
    295                 300                 305

tcc tcc cct tcc tcg tcc cca acc tcg acc att acg gtc gcc ctc tcc   1075
Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile Thr Val Ala Leu Ser
310                 315                 320                 325

taaaggagcc tggcatggat atc                                        1098
```

<210> 440
<211> 325
<212> PRT
<213> Corynebacterium glutamicum

<400> 440

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Met Asn Ser Gln Trp Gln Asp Ala His Val Val Ser Ser Glu Ile Ile
  1               5                  10                  15

Ala Ala Asp Ile Arg Arg Ile Glu Leu Ser Pro Lys Phe Ala Ile Pro
             20                  25                  30

Val Lys Pro Gly Glu His Leu Lys Ile Met Val Pro Leu Lys Thr Gly
         35                  40                  45

Gln Glu Lys Arg Ser Tyr Ser Ile Val Asp Ala Arg His Asp Gly Ser
     50                  55                  60

Thr Leu Ala Leu Ser Val Leu Lys Thr Arg Asn Ser Arg Gly Gly Ser
 65                  70                  75                  80

Glu Phe Met His Thr Leu Arg Ala Gly Asp Thr Val Thr Val Ser Arg
                 85                  90                  95

Pro Ser Gln Asp Phe Pro Leu Arg Val Gly Ala Pro Glu Tyr Val Leu
            100                 105                 110

Val Ala Gly Gly Ile Gly Ile Thr Ala Ile Arg Ser Met Ala Ser Leu
        115                 120                 125

Leu Lys Lys Leu Gly Ala Asn Tyr Arg Ile His Phe Ala Ala Arg Ser
    130                 135                 140
```

```
Leu Asp Ala Met Ala Tyr Lys Asp Glu Leu Val Ala Glu His Gly Asp
145                 150                 155                 160

Lys Leu His Leu His Leu Asp Ser Glu Gly Thr Thr Ile Asp Val Pro
                165                 170                 175

Ala Leu Ile Glu Thr Leu Asn Pro His Thr Glu Leu Tyr Met Cys Gly
            180                 185                 190

Pro Ile Arg Leu Met Asp Ala Ile Arg Arg Ala Trp Asn Thr Arg Gly
        195                 200                 205

Leu Asp Pro Thr Asn Leu Arg Phe Glu Thr Phe Gly Asn Ser Gly Trp
    210                 215                 220

Phe Ser Pro Glu Val Phe His Ile Gln Val Pro Glu Leu Gly Leu His
225                 230                 235                 240

Ala Thr Val Asn Lys Asp Glu Ser Met Leu Glu Ala Leu Gln Lys Ala
                245                 250                 255

Gly Ala Asn Met Met Phe Asp Cys Arg Lys Gly Glu Cys Gly Leu Cys
            260                 265                 270

Gln Val Arg Val Leu Glu Val Asp Gly Gln Val Asp His Arg Asp Val
        275                 280                 285

Phe Phe Ser Asp Arg Gln Lys Glu Ser Asp Ala Lys Ala Cys Ala Cys
    290                 295                 300

Val Ser Arg Val Val Ser Ser Pro Ser Ser Ser Pro Thr Ser Thr Ile
305                 310                 315                 320

Thr Val Ala Leu Ser
                325
```

Sequence Listing

<210> 441
<211> 1278
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1255)
<223> RXA02535

<400> 441
aggattgggt gaggagggag gcgtcgaaaa gcaagaaacg cctgacacgc gtagccgtgg 60

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ctgcgcacct tttaccttga ttaggtgcac aatagggagt gtg aca cct cgc cct   115
                                              Val Thr Pro Arg Pro
                                                1               5

gtt tct tct gtt gcg cga ctc gtt gag gat aac gcg caa gat ttt ctt   163
Val Ser Ser Val Ala Arg Leu Val Glu Asp Asn Ala Gln Asp Phe Leu
                  10                  15                  20

cgc gcc gtt cag gcg aaa ctt tta acg ctc gcg cca cag gct cgt ggg   211
Arg Ala Val Gln Ala Lys Leu Leu Thr Leu Ala Pro Gln Ala Arg Gly
              25                  30                  35
```

```
cat ttt ccc act gcg gat gat gcg act cat atc agc atc gcc gaa atg   259
His Phe Pro Thr Ala Asp Asp Ala Thr His Ile Ser Ile Ala Glu Met
         40                  45                  50

gtg agt gcg ctg ttg gaa ggc act ggt gag gaa ggg aaa gta gac gac   307
Val Ser Ala Leu Leu Glu Gly Thr Gly Glu Glu Gly Lys Val Asp Asp
     55                  60                  65

aaa aca ctg gag ttc ttt aaa gaa gcg gcg tta gat gcg cgt cga ttt   355
Lys Thr Leu Glu Phe Phe Lys Glu Ala Ala Leu Asp Ala Arg Arg Phe
 70                  75                  80                  85

ggc ctg acc cca gaa atg cac agc gct ttg ggt gag gcc gtg cgc agc   403
Gly Leu Thr Pro Glu Met His Ser Ala Leu Gly Glu Ala Val Arg Ser
                90                  95                 100

gaa cta ttg tca tta tgc gag gat ctt ccc ttt gaa aat gtg ctg ttt   451
Glu Leu Leu Ser Leu Cys Glu Asp Leu Pro Phe Glu Asn Val Leu Phe
            105                 110                 115

gcc gag cgt gcg att gct gca acc acg gct gtt tcc gtc gag gcg gtt   499
Ala Glu Arg Ala Ile Ala Ala Thr Thr Ala Val Ser Val Glu Ala Val
        120                 125                 130

cgt gaa gct gat gag gca cac att cct gcc tca tat cag gca gaa att   547
Arg Glu Ala Asp Glu Ala His Ile Pro Ala Ser Tyr Gln Ala Glu Ile
    135                 140                 145

gta gaa gtt gaa aag cgc agc cgt agg ttc acc gtc gtg cgc atg caa   595
Val Glu Val Glu Lys Arg Ser Arg Arg Phe Thr Val Val Arg Met Gln
150                 155                 160                 165

gct gaa acg caa ctg ccc tac cta ccg gga caa tat ctt gca gca act   643
Ala Glu Thr Gln Leu Pro Tyr Leu Pro Gly Gln Tyr Leu Ala Ala Thr
                170                 175                 180

gcg gat ttt ctg ccc aac aca tgg cgc tac ctg tgc cct tcg atc ccc   691
Ala Asp Phe Leu Pro Asn Thr Trp Arg Tyr Leu Cys Pro Ser Ile Pro
            185                 190                 195

act aac gaa tgg ggg cag gtg gag ttt cac atc caa tca gac gca gat   739
Thr Asn Glu Trp Gly Gln Val Glu Phe His Ile Gln Ser Asp Ala Asp
        200                 205                 210

gat atc gct gga ctt tta gcc acc aca cgc ctt ggc gat aaa tgg cga   787
Asp Ile Ala Gly Leu Leu Ala Thr Thr Arg Leu Gly Asp Lys Trp Arg
    215                 220                 225

ctt ggc ccc ggt cgt gga gat ttc gga caa agc aaa att agt tcc ggc   835
Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser Lys Ile Ser Ser Gly
230                 235                 240                 245

aat gat ttg tta ttt att gca cat gga acg ggc cta gct cct ctt cgc   883
Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly Leu Ala Pro Leu Arg
                250                 255                 260

gct tac atg ttt gag ctg atg aac caa gca gca cct cca cgt ttg cac   931
Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala Pro Pro Arg Leu His
            265                 270                 275
```

```
ttt ttc gtc ggt gcc gac tac ccc ggt gag ctg tat gaa ctc acc ggc   979
Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu Tyr Glu Leu Thr Gly
        280                 285                 290

atg tgg aat ttt gct gca gcc agc cca tgg ctt tct gtc gta ccg gtg   1027
Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu Ser Val Val Pro Val
    295                 300                 305

tca acg cat gac aag gat gcg tgg tgg gtt caa gcc acc gaa gca tcg   1075
Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln Ala Thr Glu Ala Ser
310                 315                 320                 325

cag cca ccg agg ggt ttg cat ttg cat caa acg ggt tcg atg gcg aag   1123
Gln Pro Pro Arg Gly Leu His Leu His Gln Thr Gly Ser Met Ala Lys
                330                 335                 340

atc gtc acc gaa gca ggt gct tgg gcc gac cgc gac gtg tta att gct   1171
Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg Asp Val Leu Ile Ala
            345                 350                 355

ggc cct gaa tcg tgg gct cgg gat gtt cgg cgc gcg atg att agg cgt   1219
Gly Pro Glu Ser Trp Ala Arg Asp Val Arg Arg Ala Met Ile Arg Arg
        360                 365                 370

gga act ccg gcc cag cag att gag att tta ggg ttc taggttgcct       1265
Gly Thr Pro Ala Gln Gln Ile Glu Ile Leu Gly Phe
    375                 380                 385

caccgggctg acc                                                  1278
```

<210> 442
<211> 385
<212> PRT
<213> Corynebacterium glutamicum

<400> 442

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Val Thr Pro Arg Pro Val Ser Ser Val Ala Arg Leu Val Glu Asp Asn
  1               5                  10                  15

Ala Gln Asp Phe Leu Arg Ala Val Gln Ala Lys Leu Leu Thr Leu Ala
             20                  25                  30

Pro Gln Ala Arg Gly His Phe Pro Thr Ala Asp Asp Ala Thr His Ile
         35                  40                  45

Ser Ile Ala Glu Met Val Ser Ala Leu Leu Glu Gly Thr Gly Glu Glu
     50                  55                  60

Gly Lys Val Asp Asp Lys Thr Leu Glu Phe Phe Lys Glu Ala Ala Leu
 65                  70                  75                  80

Asp Ala Arg Arg Phe Gly Leu Thr Pro Glu Met His Ser Ala Leu Gly
                 85                  90                  95

Glu Ala Val Arg Ser Glu Leu Leu Ser Leu Cys Glu Asp Leu Pro Phe
            100                 105                 110

Glu Asn Val Leu Phe Ala Glu Arg Ala Ile Ala Ala Thr Thr Ala Val
        115                 120                 125
```

```
Ser Val Glu Ala Val Arg Glu Ala Asp Glu Ala His Ile Pro Ala Ser
    130                 135                 140

Tyr Gln Ala Glu Ile Val Glu Val Glu Lys Arg Ser Arg Arg Phe Thr
145                 150                 155                 160

Val Val Arg Met Gln Ala Glu Thr Gln Leu Pro Tyr Leu Pro Gly Gln
                165                 170                 175

Tyr Leu Ala Ala Thr Ala Asp Phe Leu Pro Asn Thr Trp Arg Tyr Leu
            180                 185                 190

Cys Pro Ser Ile Pro Thr Asn Glu Trp Gly Gln Val Glu Phe His Ile
        195                 200                 205

Gln Ser Asp Ala Asp Asp Ile Ala Gly Leu Leu Ala Thr Thr Arg Leu
    210                 215                 220

Gly Asp Lys Trp Arg Leu Gly Pro Gly Arg Gly Asp Phe Gly Gln Ser
225                 230                 235                 240

Lys Ile Ser Ser Gly Asn Asp Leu Leu Phe Ile Ala His Gly Thr Gly
                245                 250                 255

Leu Ala Pro Leu Arg Ala Tyr Met Phe Glu Leu Met Asn Gln Ala Ala
            260                 265                 270

Pro Pro Arg Leu His Phe Phe Val Gly Ala Asp Tyr Pro Gly Glu Leu
        275                 280                 285

Tyr Glu Leu Thr Gly Met Trp Asn Phe Ala Ala Ala Ser Pro Trp Leu
    290                 295                 300

Ser Val Val Pro Val Ser Thr His Asp Lys Asp Ala Trp Trp Val Gln
305                 310                 315                 320

Ala Thr Glu Ala Ser Gln Pro Pro Arg Gly Leu His Leu His Gln Thr
                325                 330                 335

Gly Ser Met Ala Lys Ile Val Thr Glu Ala Gly Ala Trp Ala Asp Arg
            340                 345                 350

Asp Val Leu Ile Ala Gly Pro Glu Ser Trp Ala Arg Asp Val Arg Arg
        355                 360                 365

Ala Met Ile Arg Arg Gly Thr Pro Ala Gln Gln Ile Glu Ile Leu Gly
    370                 375                 380

Phe
385
```

<210> 443
<211> 1248
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1225)
<223> RXA00964

<400> 443

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ttcaagggct agacgtatgc aggtgttggg gattgcttat ctcaagggca atcacaccct 60

tcatacgcat ctacaacatc cgtaaaggag gactccaaca atg ggc gcc cca ggt   115
                                            Met Gly Ala Pro Gly
                                              1               5

aaa aac gat tac gca act gaa cac gtc aag caa gaa gtc cca ccc gca   163
Lys Asn Asp Tyr Ala Thr Glu His Val Lys Gln Glu Val Pro Pro Ala
                 10                  15                  20

act cca gaa gag cag gca gag ctg gac acc atg tat aaa cgc atg gat   211
Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met Tyr Lys Arg Met Asp
             25                  30                  35

gac ctg cat cta aag ccc ctg tgg act caa atc ggt ggg ttg atg cca   259
Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile Gly Gly Leu Met Pro
         40                  45                  50

aac cac ccg gaa cca cga gct gtg gca cac aag tgg gat tgg gcg gaa   307
Asn His Pro Glu Pro Arg Ala Val Ala His Lys Trp Asp Trp Ala Glu
     55                  60                  65

ctc ctg aag ctc gcg cag cgc tcc ggt gaa ctc gtt cca gtt ggg cgc   355
Leu Leu Lys Leu Ala Gln Arg Ser Gly Glu Leu Val Pro Val Gly Arg
 70                  75                  80                  85

ggt ggc gaa cgc cgt gcc att ggc ctg gca aac cca ggt tta gac ggc   403
Gly Gly Glu Arg Arg Ala Ile Gly Leu Ala Asn Pro Gly Leu Asp Gly
                 90                  95                 100

aat acc tac atc tcc cct acc ctg tgg gca gca att cag tac ctc gct   451
Asn Thr Tyr Ile Ser Pro Thr Leu Trp Ala Ala Ile Gln Tyr Leu Ala
            105                 110                 115

ccg ggt gag aac gct cca gag cac cgc cac tca caa aac gca ttc cgc   499
Pro Gly Glu Asn Ala Pro Glu His Arg His Ser Gln Asn Ala Phe Arg
        120                 125                 130

ttt gtt atc gaa ggc gaa ggc gtg tgg act gtc gtt aac ggc gat cca   547
Phe Val Ile Glu Gly Glu Gly Val Trp Thr Val Val Asn Gly Asp Pro
    135                 140                 145

gta cca atg cga cgc ggc gac ttc ctg ctc acc cca ggc tgg aac tac   595
Val Pro Met Arg Arg Gly Asp Phe Leu Leu Thr Pro Gly Trp Asn Tyr
150                 155                 160                 165

cac ggc cac cac aac atc gcg acc gag cca atg gcc tgg cta gac ggg   643
His Gly His His Asn Ile Ala Thr Glu Pro Met Ala Trp Leu Asp Gly
                170                 175                 180

ctc gat atc cca ttt gcc tac caa atg gac acc gga ttc ttt gag tac   691
Leu Asp Ile Pro Phe Ala Tyr Gln Met Asp Thr Gly Phe Phe Glu Tyr
            185                 190                 195

ggc acc gaa aaa ctc act gac gaa tcc acc cca gac ctc tcc cgt tca   739
Gly Thr Glu Lys Leu Thr Asp Glu Ser Thr Pro Asp Leu Ser Arg Ser
        200                 205                 210

gaa cgc ctg tgg gcc cac cca gga ctt cgc cca gtc tcc ttc cca gga   787
```

```
Glu Arg Leu Trp Ala His Pro Gly Leu Arg Pro Val Ser Phe Pro Gly
    215                 220                 225

aaa act tcc tac tca cca att ggg cgc tac gcc tgg gag cac acc gac   835
Lys Thr Ser Tyr Ser Pro Ile Gly Arg Tyr Ala Trp Glu His Thr Asp
230                 235                 240                 245

gca gca ctc aac gat cag ctg gca ttg gaa gaa gca gga cac cca gga   883
Ala Ala Leu Asn Asp Gln Leu Ala Leu Glu Glu Ala Gly His Pro Gly
                250                 255                 260

aca gtc gcg ccg gga cat gct gcg att cgc ttc tcc aac cca act acc   931
Thr Val Ala Pro Gly His Ala Ala Ile Arg Phe Ser Asn Pro Thr Thr
            265                 270                 275

ggt ggc gat gtc atg acc acc atc cgc gcg gag ttc cac cgc ctg cgc   979
Gly Gly Asp Val Met Thr Thr Ile Arg Ala Glu Phe His Arg Leu Arg
        280                 285                 290

cca ggt gca tcc act gcc ccc att cat gag gta gga aac cgt tgc ttc   1027
Pro Gly Ala Ser Thr Ala Pro Ile His Glu Val Gly Asn Arg Cys Phe
    295                 300                 305

cag gta ttt gag ggt tcc gca aca atc aat gtt gga gat aaa acc ttt   1075
Gln Val Phe Glu Gly Ser Ala Thr Ile Asn Val Gly Asp Lys Thr Phe
310                 315                 320                 325

gaa gct aac cac ggc gat gtg atc aat gta ccg tcg tgg cag aag tgg   1123
Glu Ala Asn His Gly Asp Val Ile Asn Val Pro Ser Trp Gln Lys Trp
                330                 335                 340

aat atc gtc gct ggc tct gac ggc gtc gac ttg ttc tgc ttc tct gat   1171
Asn Ile Val Ala Gly Ser Asp Gly Val Asp Leu Phe Cys Phe Ser Asp
            345                 350                 355

aca cca att ttc gag gcc ctt aac ctc gca cgt act ttt act ccg gaa   1219
Thr Pro Ile Phe Glu Ala Leu Asn Leu Ala Arg Thr Phe Thr Pro Glu
        360                 365                 370

gga atc tagaacttat gcgtcttgca aca                                1248
Gly Ile
    375


<210> 444
<211> 375
<212> PRT
<213> Corynebacterium glutamicum

<400> 444
Met Gly Ala Pro Gly Lys Asn Asp Tyr Ala Thr Glu His Val Lys Gln
  1               5                  10                  15

Glu Val Pro Pro Ala Thr Pro Glu Glu Gln Ala Glu Leu Asp Thr Met
             20                  25                  30

Tyr Lys Arg Met Asp Asp Leu His Leu Lys Pro Leu Trp Thr Gln Ile
         35                  40                  45

Gly Gly Leu Met Pro Asn His Pro Glu Pro Arg Ala Val Ala His Lys
     50                  55                  60
```

```
Trp Asp Trp Ala Glu Leu Leu Lys Leu Ala Gln Arg Ser Gly Glu Leu
 65                  70                  75                  80

Val Pro Val Gly Arg Gly Gly Glu Arg Arg Ala Ile Gly Leu Ala Asn
                 85                  90                  95

Pro Gly Leu Asp Gly Asn Thr Tyr Ile Ser Pro Thr Leu Trp Ala Ala
            100                 105                 110

Ile Gln Tyr Leu Ala Pro Gly Glu Asn Ala Pro Glu His Arg His Ser
        115                 120                 125

Gln Asn Ala Phe Arg Phe Val Ile Glu Gly Glu Gly Val Trp Thr Val
    130                 135                 140

Val Asn Gly Asp Pro Val Pro Met Arg Arg Gly Asp Phe Leu Leu Thr
145                 150                 155                 160

Pro Gly Trp Asn Tyr His Gly His His Asn Ile Ala Thr Glu Pro Met
                165                 170                 175

Ala Trp Leu Asp Gly Leu Asp Ile Pro Phe Ala Tyr Gln Met Asp Thr
            180                 185                 190

Gly Phe Phe Glu Tyr Gly Thr Glu Lys Leu Thr Asp Glu Ser Thr Pro
        195                 200                 205

Asp Leu Ser Arg Ser Glu Arg Leu Trp Ala His Pro Gly Leu Arg Pro
    210                 215                 220

Val Ser Phe Pro Gly Lys Thr Ser Tyr Ser Pro Ile Gly Arg Tyr Ala
225                 230                 235                 240

Trp Glu His Thr Asp Ala Ala Leu Asn Asp Gln Leu Ala Leu Glu Glu
                245                 250                 255

Ala Gly His Pro Gly Thr Val Ala Pro Gly His Ala Ala Ile Arg Phe
            260                 265                 270

Ser Asn Pro Thr Thr Gly Gly Asp Val Met Thr Thr Ile Arg Ala Glu
        275                 280                 285

Phe His Arg Leu Arg Pro Gly Ala Ser Thr Ala Pro Ile His Glu Val
    290                 295                 300

Gly Asn Arg Cys Phe Gln Val Phe Glu Gly Ser Ala Thr Ile Asn Val
305                 310                 315                 320

Gly Asp Lys Thr Phe Glu Ala Asn His Gly Asp Val Ile Asn Val Pro
                325                 330                 335

Ser Trp Gln Lys Trp Asn Ile Val Ala Gly Ser Asp Gly Val Asp Leu
            340                 345                 350

Phe Cys Phe Ser Asp Thr Pro Ile Phe Glu Ala Leu Asn Leu Ala Arg
        355                 360                 365

Thr Phe Thr Pro Glu Gly Ile
    370                 375
```

<210> 445
<211> 1083
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1060)
<223> RXN01466

<400> 445
aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60

cggctcattg cggggaaaag ctcataaagc aaggctaaag atg acg cca aat ggt 115
Met Thr Pro Asn Gly
1 5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt 163
Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
10 15 20

acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac 211
Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
25 30 35

ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg 259
Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr
40 45 50

gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat 307
Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr
55 60 65

tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc 355
Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser
70 75 80 85

gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca 403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro
90 95 100

gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc 451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile
105 110 115

cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc 499
His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu
120 125 130

ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt 547
Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu
135 140 145

cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca 595
Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser
150 155 160 165

tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac 643
Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp
170 175 180

```
aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc   691
Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe
            185                 190                 195

cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc   739
Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val
        200                 205                 210

ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg   787
Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met
    215                 220                 225

atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctc   835
Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu
230                 235                 240                 245

caa gaa cac gac gaa ctc gat gcc gca cca gca ttg gaa ggc ctc aaa   883
Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala Leu Glu Gly Leu Lys
                250                 255                 260

ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca att agc caa   931
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro Ile Ser Gln
            265                 270                 275

gcc gac cgc atc tgc gaa gtc tgg ccc ggc gca cgc ctt caa atc gca   979
Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala Arg Leu Gln Ile Ala
        280                 285                 290

gaa gga gca ggt cat atg ctt ccg ctt gaa gcg cca gga atc ctc aat   1027
Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala Pro Gly Ile Leu Asn
    295                 300                 305

aat gcg atc ggc aac att ttg gac ggg ctg ggc tgaggaacct ggttcgggcg 1080
Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
310                 315                 320

tgg                                                               1083
```

<210> 446
<211> 320
<212> PRT
<213> Corynebacterium glutamicum

<400> 446

```
Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
  1               5                  10                  15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
             20                  25                  30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
         35                  40                  45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
     50                  55                  60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
 65                  70                  75                  80
```

```
Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
                 85                  90                  95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
            100                 105                 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
        115                 120                 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
    130                 135                 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
145                 150                 155                 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
                165                 170                 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
            180                 185                 190

Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
        195                 200                 205

Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
    210                 215                 220

Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly
225                 230                 235                 240

Phe Phe Asp Asp Leu Gln Glu His Asp Glu Leu Asp Ala Ala Pro Ala
                245                 250                 255

Leu Glu Gly Leu Lys Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val
            260                 265                 270

Thr Pro Ile Ser Gln Ala Asp Arg Ile Cys Glu Val Trp Pro Gly Ala
        275                 280                 285

Arg Leu Gln Ile Ala Glu Gly Ala Gly His Met Leu Pro Leu Glu Ala
    290                 295                 300

Pro Gly Ile Leu Asn Asn Ala Ile Gly Asn Ile Leu Asp Gly Leu Gly
305                 310                 315                 320
```

<210> 447
<211> 922
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(922)
<223> FRXA01466

<400> 447
aatccatgat cccaaactac ctcaaagcgc ttgtaggcta agacttatgg atacacaacg 60

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cggctcattg cggggaaaag ctcataaagc aaggctaaag atg acg cca aat ggt   115
                                              Met Thr Pro Asn Gly
                                                1               5

cgc agg caa ctc ctc ctg gag cgt ggc gca gca ttt agc aaa aac cgt   163
Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala Phe Ser Lys Asn Arg
                10                  15                  20

acc ccg ggt cta aaa cac gtc gac cgc cac acc atc gtg gac tcc gac   211
Thr Pro Gly Leu Lys His Val Asp Arg His Thr Ile Val Asp Ser Asp
            25                  30                  35

ggc ctc agc atc cac acg tac atg gtt ggc cat gcc gaa aat gcc acg   259
Gly Leu Ser Ile His Thr Tyr Met Val Gly His Ala Glu Asn Ala Thr
        40                  45                  50

gca acg gtc gtg ttc atc cac ggc ttc acc ctc gcc gcc gaa gtg tat   307
Ala Thr Val Val Phe Ile His Gly Phe Thr Leu Ala Ala Glu Val Tyr
    55                  60                  65

tac atg cag gtc gac tac cta caa acc ttt tac cca aat att aaa agc   355
Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr Pro Asn Ile Lys Ser
70                  75                  80                  85

gtg ctt atc gac gcc cgc ggc cac ggc gcc acc ggc cag atc cgc cca   403
Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr Gly Gln Ile Arg Pro
                90                  95                  100

gag ctc tgc acc atc gaa gga aca gcg aac gat gtt ctc gca gcc atc   451
Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp Val Leu Ala Ala Ile
            105                 110                 115

cac gaa cac gca ccg acc ggc ccg ctc att ttg gtt ggg cat tcc ctc   499
His Glu His Ala Pro Thr Gly Pro Leu Ile Leu Val Gly His Ser Leu
        120                 125                 130

ggc gga ctc acg gca ctt aac ctg gtt aaa cgg gca gat cac tca ctt   547
Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg Ala Asp His Ser Leu
    135                 140                 145

cgg aag agg atc gtc ggc atg gtt cta gtc gcc aca tcg atc gaa tca   595
Arg Lys Arg Ile Val Gly Met Val Leu Val Ala Thr Ser Ile Glu Ser
150                 155                 160                 165

tta tcc acc caa ggt cta cca caa gtc ctg gca tca ccc ctt gcc gac   643
Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala Ser Pro Leu Ala Asp
                170                 175                 180

aac atc aaa aac gcc gtc gaa gca gcc ccc aac gat gcc caa aaa ttc   691
Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn Asp Ala Gln Lys Phe
            185                 190                 195

cgc caa tac gcc acc aca ttt cta gcc ccc acc ctg gcc acc gca gtc   739
Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr Leu Ala Thr Ala Val
        200                 205                 210

ttc caa cga gac aca aac gat gaa gtc atc gat ttc cac gcc gcc atg   787
Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp Phe His Ala Ala Met
    215                 220                 225
```

atc cac gaa acc ccc ttg gat acc ttc gtc ggt ttc ttc gac gac ctt 835
Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly Phe Phe Asp Asp Leu
230 235 240 245

caa gaa cac gac gaa ctc gat gcc gca cca aca ttg gaa ggc ctc aaa 883
Gln Glu His Asp Glu Leu Asp Ala Ala Pro Thr Leu Glu Gly Leu Lys
250 255 260

ggc tac gtc ctt gcc ggc gaa tta gat gat gtc acc cca 922
Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val Thr Pro
265 270

<210> 448
<211> 274
<212> PRT
<213> Corynebacterium glutamicum

<400> 448
Met Thr Pro Asn Gly Arg Arg Gln Leu Leu Leu Glu Arg Gly Ala Ala
1 5 10 15

Phe Ser Lys Asn Arg Thr Pro Gly Leu Lys His Val Asp Arg His Thr
20 25 30

Ile Val Asp Ser Asp Gly Leu Ser Ile His Thr Tyr Met Val Gly His
35 40 45

Ala Glu Asn Ala Thr Ala Thr Val Val Phe Ile His Gly Phe Thr Leu
50 55 60

Ala Ala Glu Val Tyr Tyr Met Gln Val Asp Tyr Leu Gln Thr Phe Tyr
65 70 75 80

Pro Asn Ile Lys Ser Val Leu Ile Asp Ala Arg Gly His Gly Ala Thr
85 90 95

Gly Gln Ile Arg Pro Glu Leu Cys Thr Ile Glu Gly Thr Ala Asn Asp
100 105 110

Val Leu Ala Ala Ile His Glu His Ala Pro Thr Gly Pro Leu Ile Leu
115 120 125

Val Gly His Ser Leu Gly Gly Leu Thr Ala Leu Asn Leu Val Lys Arg
130 135 140

Ala Asp His Ser Leu Arg Lys Arg Ile Val Gly Met Val Leu Val Ala
145 150 155 160

Thr Ser Ile Glu Ser Leu Ser Thr Gln Gly Leu Pro Gln Val Leu Ala
165 170 175

Ser Pro Leu Ala Asp Asn Ile Lys Asn Ala Val Glu Ala Ala Pro Asn
180 185 190

Asp Ala Gln Lys Phe Arg Gln Tyr Ala Thr Thr Phe Leu Ala Pro Thr
195 200 205

Leu Ala Thr Ala Val Phe Gln Arg Asp Thr Asn Asp Glu Val Ile Asp
210 215 220

```
Phe His Ala Ala Met Ile His Glu Thr Pro Leu Asp Thr Phe Val Gly
225                 230                 235                 240

Phe Phe Asp Asp Leu Gln Glu His Asp Glu Leu Asp Ala Ala Pro Thr
                245                 250                 255

Leu Glu Gly Leu Lys Gly Tyr Val Leu Ala Gly Glu Leu Asp Asp Val
            260                 265                 270

Thr Pro
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<210> 449
<211> 766
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> RXN03036

<400> 449

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tagaaaaatc tacccagtaa gcattcagga accattcaga atcttttctt agcatgtctc 60

tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg   115
                                          Met Ala Glu Gln Leu
                                            1               5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa   163
Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
                10                  15                  20

gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag   211
Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
            25                  30                  35

gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct   259
Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala
        40                  45                  50

tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc   307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser
    55                  60                  65

agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag   355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu
70                  75                  80                  85

atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt   403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly
                90                  95                  100

ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag   451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys
            105                 110                 115

tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act   499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr
        120                 125                 130
```

```
atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct   547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala
    135                 140                 145

gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac   595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr
150                 155                 160                 165

gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc   643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr
                170                 175                 180

gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat   691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr
            185                 190                 195

gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac   739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp
        200                 205                 210

agc atc acg gat tcc acg aac aac att                               766
Ser Ile Thr Asp Ser Thr Asn Asn Ile
    215                 220
```

<210> 450
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 450

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Met Ala Glu Gln Leu Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln
  1               5                  10                  15

Ser Glu Asp Leu Glu Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val
             20                  25                  30

Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly
         35                  40                  45

Val Ala Leu Ala Ala Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser
     50                  55                  60

Thr Ser Ser Ala Ser Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala
 65                  70                  75                  80

Glu Thr Leu Thr Glu Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly
                 85                  90                  95

Asp Gly Ser Asn Gly Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg
            100                 105                 110

Gln Asp Ile Thr Lys Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val
        115                 120                 125

Pro Leu Thr Leu Thr Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln
    130                 135                 140

Pro Met Glu Gly Ala Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly
145                 150                 155                 160
```

Arg Tyr Ser Met Tyr Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg
165 170 175

Gly Val Gln Ile Thr Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile
180 185 190

Phe Pro Gly Cys Tyr Ala Gly Arg Trp Val His Ile His Phe Glu Val
195 200 205

Phe Pro Asp Arg Asp Ser Ile Thr Asp Ser Thr Asn Asn Ile
210 215 220

<210> 451
<211> 766
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(766)
<223> FRXA02895

<400> 451
tagaaaaatc tacccagtaa gcattcagga accattcaga atcttttctt agcatgtctc 60

tatcagcgta aacgtccgaa catgaaaggc tagaaaagcc atg gct gag cag ttg 115
Met Ala Glu Gln Leu
1 5

cgt caa ttt gaa ggc agg gtc ctc cct aat caa tcc gag gac ttg gaa 163
Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln Ser Glu Asp Leu Glu
10 15 20

gat cag ggt ttg gga ttt gac ctg gga acc gtt ttc tcc cgc agg aag 211
Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val Phe Ser Arg Arg Lys
25 30 35

gtt ttg gga ttc atc ggt gtt ggt gga gca ggt gtg gca ctt gct gct 259
Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly Val Ala Leu Ala Ala
40 45 50

tgt tca cct tct ggt tct tcc gcg gca tcg agc acc tca agc gcg tcc 307
Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser Thr Ser Ser Ala Ser
55 60 65

agc agc gca gct gca acc acc agt gca gca gca gag act ttg act gag 355
Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala Glu Thr Leu Thr Glu
70 75 80 85

atg aag tcg gag act gct ggt ccg tac ccg ggc gat ggt tcg aat ggt 403
Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly Asp Gly Ser Asn Gly
90 95 100

ccg gat gtg ttg gag gtc tcc ggt gtg gag cgc cag gac atc acc aag 451
Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg Gln Asp Ile Thr Lys
105 110 115

tcg att gat tct gac acc gtg gca gag ggc gta cct ctg acg ttg act 499
Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val Pro Leu Thr Leu Thr

```
        120                 125                 130

atg acc att ttg gac atg aac aac aac aat cag cca atg gag ggt gct   547
Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln Pro Met Glu Gly Ala
    135                 140                 145

gcg gtg tac gtg tgg cac tgt gat gcg ccg ggt cga tat tcg atg tac   595
Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly Arg Tyr Ser Met Tyr
150                 155                 160                 165

gac tct gag ctg gaa gat gag acc tat tta cgc ggt gtg cag att acc   643
Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg Gly Val Gln Ile Thr
                170                 175                 180

gat aag tat ggc cag gtc acg ttc gat acc att ttc cct ggt tgt tat   691
Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile Phe Pro Gly Cys Tyr
            185                 190                 195

gcg ggc cgt tgg gtg cat att cat ttc gag gtg ttc ccg gat cga gac   739
Ala Gly Arg Trp Val His Ile His Phe Glu Val Phe Pro Asp Arg Asp
        200                 205                 210

agc atc acg gat tcc acg aac aac att                               766
Ser Ile Thr Asp Ser Thr Asn Asn Ile
    215                 220


<210> 452
<211> 222
<212> PRT
<213> Corynebacterium glutamicum

<400> 452
Met Ala Glu Gln Leu Arg Gln Phe Glu Gly Arg Val Leu Pro Asn Gln
  1               5                  10                  15

Ser Glu Asp Leu Glu Asp Gln Gly Leu Gly Phe Asp Leu Gly Thr Val
             20                  25                  30

Phe Ser Arg Arg Lys Val Leu Gly Phe Ile Gly Val Gly Gly Ala Gly
         35                  40                  45

Val Ala Leu Ala Ala Cys Ser Pro Ser Gly Ser Ser Ala Ala Ser Ser
     50                  55                  60

Thr Ser Ser Ala Ser Ser Ser Ala Ala Ala Thr Thr Ser Ala Ala Ala
 65                  70                  75                  80

Glu Thr Leu Thr Glu Met Lys Ser Glu Thr Ala Gly Pro Tyr Pro Gly
                 85                  90                  95

Asp Gly Ser Asn Gly Pro Asp Val Leu Glu Val Ser Gly Val Glu Arg
            100                 105                 110

Gln Asp Ile Thr Lys Ser Ile Asp Ser Asp Thr Val Ala Glu Gly Val
        115                 120                 125

Pro Leu Thr Leu Thr Met Thr Ile Leu Asp Met Asn Asn Asn Asn Gln
    130                 135                 140

Pro Met Glu Gly Ala Ala Val Tyr Val Trp His Cys Asp Ala Pro Gly
```

```
145                 150                 155                 160

Arg Tyr Ser Met Tyr Asp Ser Glu Leu Glu Asp Glu Thr Tyr Leu Arg
                165                 170                 175

Gly Val Gln Ile Thr Asp Lys Tyr Gly Gln Val Thr Phe Asp Thr Ile
            180                 185                 190

Phe Pro Gly Cys Tyr Ala Gly Arg Trp Val His Ile His Phe Glu Val
        195                 200                 205

Phe Pro Asp Arg Asp Ser Ile Thr Asp Ser Thr Asn Asn Ile
    210                 215                 220


<210> 453
<211> 1026
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1003)
<223> RXA02449

<400> 453
acctcagcag attgctcgaa gcagcactca acggtgagga tccggcagtt cttagcgcag 60

tactcagtaa ctaacccggc gatttttcaa ggagaaaatc atg aca acc acc acc   115
                                              Met Thr Thr Thr Thr
                                                1               5

gca gac cac aac atc agc gcg cag caa aag gct gtt gaa gaa aat ctg   163
Ala Asp His Asn Ile Ser Ala Gln Gln Lys Ala Val Glu Glu Asn Leu
                  10                  15                  20

gtg aac cgt gtc ctc caa tct ttt gat gcg tgt gaa aac ccg cgc ctc   211
Val Asn Arg Val Leu Gln Ser Phe Asp Ala Cys Glu Asn Pro Arg Leu
              25                  30                  35

aag cag ctg atg gaa tcg ctg gtt gtg cat ctg cac gat ttc atc cgg   259
Lys Gln Leu Met Glu Ser Leu Val Val His Leu His Asp Phe Ile Arg
          40                  45                  50

gat gtg cgc ctc acc gag gat gag tgg aat tac gcc att gat ttc ctc   307
Asp Val Arg Leu Thr Glu Asp Glu Trp Asn Tyr Ala Ile Asp Phe Leu
      55                  60                  65

aca gcg gtt ggc cac att act gat gac aag cgc caa gag ttt gtg ttg   355
Thr Ala Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu
  70                  75                  80                  85

ctt tcc gat acc ttg ggc gcc tcg atg cag acc atc gcg gtg aac aac   403
Leu Ser Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn
                  90                  95                 100

gaa gcg tat gaa aac tca acg gaa gct aca gtc ttt ggt cca ttc ttc   451
Glu Ala Tyr Glu Asn Ser Thr Glu Ala Thr Val Phe Gly Pro Phe Phe
              105                 110                 115

ctc gat gac gct cct gag gtt gag ctg ggt gga gat atc gcc ggc ggc   499
```

```
Leu Asp Asp Ala Pro Glu Val Glu Leu Gly Gly Asp Ile Ala Gly Gly
        120                 125                 130

gcc cag ggg cag gca gcg tgg att gaa gga acc gtc acc gac act gaa   547
Ala Gln Gly Gln Ala Ala Trp Ile Glu Gly Thr Val Thr Asp Thr Glu
    135                 140                 145

ggc aat ccc gtt ccg aat gct cgt atc gag gtg tgg gag tgc gat gaa   595
Gly Asn Pro Val Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu
150                 155                 160                 165

gat gga ctc tac gat gtc caa tat gcc gat gag cgc atg gcg ggt cgc   643
Asp Gly Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Met Ala Gly Arg
                170                 175                 180

gcg tat atg cac acc gac gcc aat ggc gat tac cgc ttc tgg ggt ctg   691
Ala Tyr Met His Thr Asp Ala Asn Gly Asp Tyr Arg Phe Trp Gly Leu
            185                 190                 195

act ccg gtt cct tat cca atc ccc cac gat ggc ccc gtg ggc aac atg   739
Thr Pro Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Asn Met
        200                 205                 210

ctc aag gcg gtt ggt cgt tcg ccg gtg cgc tgc gcc cac ctt cac ttc   787
Leu Lys Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe
    215                 220                 225

atg gtg acc gct cct gaa ttg cgc acc ttg gtc act cac att ttc gtt   835
Met Val Thr Ala Pro Glu Leu Arg Thr Leu Val Thr His Ile Phe Val
230                 235                 240                 245

gag ggt gat ccg cag cta gaa atc ggc gat tcc gtc ttc ggg gtc aag   883
Glu Gly Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys
                250                 255                 260

gac tcg ttg atc aag aag ttt gag gag cag gcg cca ggc act cct acc   931
Asp Ser Leu Ile Lys Lys Phe Glu Glu Gln Ala Pro Gly Thr Pro Thr
            265                 270                 275

cca gat ggt cgg gat ctc ggc gat cag acg tgg gcg cgc acg cgc ttc   979
Pro Asp Gly Arg Asp Leu Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe
        280                 285                 290

gac atc gtg ctc gcg ccg ggc gcg taggatttcg cttttcgacg caa        1026
Asp Ile Val Leu Ala Pro Gly Ala
    295                 300


<210> 454
<211> 301
<212> PRT
<213> Corynebacterium glutamicum

<400> 454
Met Thr Thr Thr Thr Ala Asp His Asn Ile Ser Ala Gln Gln Lys Ala
  1               5                  10                  15

Val Glu Glu Asn Leu Val Asn Arg Val Leu Gln Ser Phe Asp Ala Cys
             20                  25                  30

Glu Asn Pro Arg Leu Lys Gln Leu Met Glu Ser Leu Val Val His Leu
```

```
         35                  40                  45

His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Asp Glu Trp Asn Tyr
     50                  55                  60

Ala Ile Asp Phe Leu Thr Ala Val Gly His Ile Thr Asp Asp Lys Arg
 65                  70                  75                  80

Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala Ser Met Gln Thr
                 85                  90                  95

Ile Ala Val Asn Asn Glu Ala Tyr Glu Asn Ser Thr Glu Ala Thr Val
            100                 105                 110

Phe Gly Pro Phe Phe Leu Asp Asp Ala Pro Glu Val Glu Leu Gly Gly
        115                 120                 125

Asp Ile Ala Gly Gly Ala Gln Gly Gln Ala Ala Trp Ile Glu Gly Thr
    130                 135                 140

Val Thr Asp Thr Glu Gly Asn Pro Val Pro Asn Ala Arg Ile Glu Val
145                 150                 155                 160

Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln Tyr Ala Asp Glu
                165                 170                 175

Arg Met Ala Gly Arg Ala Tyr Met His Thr Asp Ala Asn Gly Asp Tyr
            180                 185                 190

Arg Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile Pro His Asp Gly
        195                 200                 205

Pro Val Gly Asn Met Leu Lys Ala Val Gly Arg Ser Pro Val Arg Cys
    210                 215                 220

Ala His Leu His Phe Met Val Thr Ala Pro Glu Leu Arg Thr Leu Val
225                 230                 235                 240

Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu Ile Gly Asp Ser
                245                 250                 255

Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe Glu Glu Gln Ala
            260                 265                 270

Pro Gly Thr Pro Thr Pro Asp Gly Arg Asp Leu Gly Asp Gln Thr Trp
        275                 280                 285

Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly Ala
    290                 295                 300


<210> 455
<211> 1008
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(985)
<223> RXN00178
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aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca 115
Met Thr Ile Ser Ala
1 5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct 163
Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser
10 15 20

ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg 211
Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu
25 30 35

act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa 259
Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu
40 45 50

gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc 307
Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr
55 60 65

gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca 355
Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala
70 75 80 85

tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc 403
Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr
90 95 100

gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc 451
Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp Asp Ala Pro Leu Val
105 110 115

caa aac gga gat gac att gcc ttt ggc gca gtc ggc cag ccg gca tgg 499
Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val Gly Gln Pro Ala Trp
120 125 130

gtg gag gga acg gtc aaa gac act gaa gga aac ccc att ccc aat gca 547
Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn Pro Ile Pro Asn Ala
135 140 145

cgc att gaa gta tgg gaa tgc gat gaa gat gga ctt tat gat gtg caa 595
Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln
150 155 160 165

tac gcc gat gag cgc agt gct gga cgc gca cac ctg tat tca gat gaa 643
Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu
170 175 180

aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc 691
Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile
185 190 195

cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc 739
Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser
200 205 210

ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag 787
Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys

```
    215                 220                 225

cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag   835
Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu
230                 235                 240                 245

atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc   883
Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe
                250                 255                 260

gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt   931
Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly
            265                 270                 275

gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc   979
Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly
        280                 285                 290

aat gtc taagtagaag cagcaaaaaa cca                                1008
Asn Val
    295
```

Oligo Index

<210> 456
<211> 295
<212> PRT
<213> Corynebacterium glutamicum

<400> 456

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Met Thr Ile Ser Ala Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu
  1               5                  10                  15

Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
             20                  25                  30

Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
         35                  40                  45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
     50                  55                  60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65                  70                  75                  80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
                 85                  90                  95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
            100                 105                 110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
        115                 120                 125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
    130                 135                 140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
145                 150                 155                 160

Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
                165                 170                 175
```

```
Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
            180                 185                 190

Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln
        195                 200                 205

Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val
    210                 215                 220

Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly
225                 230                 235                 240

Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser
                245                 250                 255

Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp
            260                 265                 270

Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile
        275                 280                 285

Val Leu Ala Pro Gly Asn Val
    290                 295


<210> 457
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<212> DNA
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<222> (101)..(985)
<223> FRXA00178

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gcgaataatc cacggacggt cacagaagaa aacctcactg cgctgcttac cacagcgctc 60

aacggcgacg atccagcaac tttgaattaa ggagaccaac atg act att tca gca   115
                                            Met Thr Ile Ser Ala
                                              1               5

caa cag caa gca gtg gaa gaa gac ctt gta gag cgc gta ctc gca tct   163
Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu Arg Val Leu Ala Ser
                  10                  15                  20

ttt gat tcg tgt gaa aac cct cgc ctc aaa cta gtg atg aaa tcc ctg   211
Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu Val Met Lys Ser Leu
              25                  30                  35

act gtg cat ctc cat gat ttc atc cgc gat gtt cga ctc act gaa gaa   259
Thr Val His Leu His Asp Phe Ile Arg Asp Val Arg Leu Thr Glu Glu
          40                  45                  50

gag tgg aac tac gcc att gat ttc ctc acc aag gtt ggg cat atc acc   307
Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys Val Gly His Ile Thr
      55                  60                  65

gac gat aag cgc caa gaa ttc gtg ttg ctc tct gac acc ttg ggt gca   355
Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser Asp Thr Leu Gly Ala
```

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 70                  75                  80                  85

tcc atg cag acc atc gct gtt aat aac gaa gca tat gaa gac gct acc   403
Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala Tyr Glu Asp Ala Thr
                 90                  95                 100

gaa gca aca gtc ttt ggc ccc ttc ttt gtc gat gat gcg cca ctg gtc   451
Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp Asp Ala Pro Leu Val
            105                 110                 115

caa aac gga gat gac att gcc ttt ggc gca gtc ggc cag ccg gca tgg   499
Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val Gly Gln Pro Ala Trp
        120                 125                 130

gtg gag gga acg gtc aaa gac act gaa gga aac ccc att ccc aat gca   547
Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn Pro Ile Pro Asn Ala
    135                 140                 145

cgc att gaa gta tgg gaa tgc gat gaa gat gga ctt tat gat gtg caa   595
Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly Leu Tyr Asp Val Gln
150                 155                 160                 165

tac gcc gat gag cgc agt gct gga cgc gca cac ctg tat tca gat gaa   643
Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His Leu Tyr Ser Asp Glu
                170                 175                 180

aac ggc gaa tac cac ttc tgg gga cta act ccc gtg cca tat ccc atc   691
Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro Val Pro Tyr Pro Ile
            185                 190                 195

cca cac gat ggt cca gta gga caa atg ctc caa gca gtt ggt cgt tcc   739
Pro His Asp Gly Pro Val Gly Gln Met Leu Gln Ala Val Gly Arg Ser
        200                 205                 210

ccc gtt cgt tgc gcg cac cta cac ttc atg gtg act gcg cca gag aag   787
Pro Val Arg Cys Ala His Leu His Phe Met Val Thr Ala Pro Glu Lys
    215                 220                 225

cga acc ttg gta acc cat atc ttc gtt gag ggc gat ccg cag cta gag   835
Arg Thr Leu Val Thr His Ile Phe Val Glu Gly Asp Pro Gln Leu Glu
230                 235                 240                 245

atc ggc gat tcc gtg ttt ggc gtg aag gac tca ctg att aag aaa ttc   883
Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser Leu Ile Lys Lys Phe
                250                 255                 260

gtt gag caa cct gca gga acc gca act cca gat ggt cgc gat gtg ggt   931
Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp Gly Arg Asp Val Gly
            265                 270                 275

gat caa acc tgg gca cgc aca cgt ttt gat att gtg ctc gcc ccc ggc   979
Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile Val Leu Ala Pro Gly
        280                 285                 290

aat gtc taagtagaag cagcaaaaaa cca                                1008
Asn Val
    295
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<210> 458
<211> 295

<212> PRT
<213> Corynebacterium glutamicum

<400> 458

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Met Thr Ile Ser Ala Gln Gln Gln Ala Val Glu Glu Asp Leu Val Glu
  1               5                  10                  15

Arg Val Leu Ala Ser Phe Asp Ser Cys Glu Asn Pro Arg Leu Lys Leu
             20                  25                  30

Val Met Lys Ser Leu Thr Val His Leu His Asp Phe Ile Arg Asp Val
         35                  40                  45

Arg Leu Thr Glu Glu Glu Trp Asn Tyr Ala Ile Asp Phe Leu Thr Lys
     50                  55                  60

Val Gly His Ile Thr Asp Asp Lys Arg Gln Glu Phe Val Leu Leu Ser
 65                  70                  75                  80

Asp Thr Leu Gly Ala Ser Met Gln Thr Ile Ala Val Asn Asn Glu Ala
                 85                  90                  95

Tyr Glu Asp Ala Thr Glu Ala Thr Val Phe Gly Pro Phe Phe Val Asp
            100                 105                 110

Asp Ala Pro Leu Val Gln Asn Gly Asp Asp Ile Ala Phe Gly Ala Val
        115                 120                 125

Gly Gln Pro Ala Trp Val Glu Gly Thr Val Lys Asp Thr Glu Gly Asn
    130                 135                 140

Pro Ile Pro Asn Ala Arg Ile Glu Val Trp Glu Cys Asp Glu Asp Gly
145                 150                 155                 160

Leu Tyr Asp Val Gln Tyr Ala Asp Glu Arg Ser Ala Gly Arg Ala His
                165                 170                 175

Leu Tyr Ser Asp Glu Asn Gly Glu Tyr His Phe Trp Gly Leu Thr Pro
            180                 185                 190

Val Pro Tyr Pro Ile Pro His Asp Gly Pro Val Gly Gln Met Leu Gln
        195                 200                 205

Ala Val Gly Arg Ser Pro Val Arg Cys Ala His Leu His Phe Met Val
    210                 215                 220

Thr Ala Pro Glu Lys Arg Thr Leu Val Thr His Ile Phe Val Glu Gly
225                 230                 235                 240

Asp Pro Gln Leu Glu Ile Gly Asp Ser Val Phe Gly Val Lys Asp Ser
                245                 250                 255

Leu Ile Lys Lys Phe Val Glu Gln Pro Ala Gly Thr Ala Thr Pro Asp
            260                 265                 270

Gly Arg Asp Val Gly Asp Gln Thr Trp Ala Arg Thr Arg Phe Asp Ile
        275                 280                 285

Val Leu Ala Pro Gly Asn Val
    290                 295
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<210> 459
<211> 1407
<212> DNA
<213> Corynebacterium glutamicum

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<221> CDS
<222> (101)..(1384)
<223> RXA02111

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gcttgcggga acaccgcacc gcccacccaa actgttcaga ttccaaagat aaattctgac 60

gctcattcca gcccaccgtt tagaagaaaa gaccccaatc atg acc acc tca atc 115
Met Thr Thr Ser Ile
1 5

acc cca tct gtc aac ctt gca ttg aaa aat gcc aat agc tgc aac agt 163
Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala Asn Ser Cys Asn Ser
10 15 20

gaa ctc aaa gac gga ccc tgg ttc ctc gac cag ccc gga atg ccg gat 211
Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln Pro Gly Met Pro Asp
25 30 35

gtc tac ggc ccc ggc gcg tca caa aac gat ccg atc cct gcg cat gct 259
Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro Ile Pro Ala His Ala
40 45 50

ccg cgc cag cag gtt ctc ccc gag gag tac cag cgc gca agt gat gac 307
Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln Arg Ala Ser Asp Asp
55 60 65

gaa ctg cat cgt agg atc cgg gaa gcg aaa gac acc ctg ggt gac aaa 355
Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp Thr Leu Gly Asp Lys
70 75 80 85

gtg gtt atc cta gga cac ttc tac cag cgc gat gaa gtt atc caa cac 403
Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp Glu Val Ile Gln His
90 95 100

gca gat ttt gtt ggt gac tct ttc caa ctt gcc cgc gct gcc aaa acc 451
Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala Arg Ala Ala Lys Thr
105 110 115

cga ccc gag gcg gaa gcg att gtg ttc tgc ggt gtg cac ttc atg gct 499
Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly Val His Phe Met Ala
120 125 130

gaa acc gct gat ctg tta tcc acg gat gaa caa tca gtg atc ctc ccc 547
Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln Ser Val Ile Leu Pro
135 140 145

aac ctt gcc gca ggt tgc tcc atg gca gac atg gct gac ctt gat tcc 595
Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met Ala Asp Leu Asp Ser
150 155 160 165

gtc gaa gac tgc tgg gag caa ctc acc tca att tat ggc gat gac acc 643
Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile Tyr Gly Asp Asp Thr
170 175 180

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ctg atc cct gtg acc tac atg aat tcc tct gca gcg ctc aaa ggt ttc   691
Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala Ala Leu Lys Gly Phe
            185                 190                 195

gtg ggt gag cac ggc gga att gta tgc acc tcc tca aat gca cgt tcc   739
Val Gly Glu His Gly Gly Ile Val Cys Thr Ser Ser Asn Ala Arg Ser
        200                 205                 210

gta ttg gag tgg gcg ttt gaa cgc ggc caa cga gtc ctg ttc ttc ccc   787
Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg Val Leu Phe Phe Pro
    215                 220                 225

gat cag cac ttg ggt cga aac acc gcg aaa gcc atg ggc att ggg atc   835
Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala Met Gly Ile Gly Ile
230                 235                 240                 245

gat caa atg ccc ctg tgg aat ccc aac aaa cca ctg ggt ggc aac acc   883
Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro Leu Gly Gly Asn Thr
                250                 255                 260

gtt tcc gag cta gaa aac gca aag gta ctg ctc tgg cat ggt ttc tgc   931
Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu Trp His Gly Phe Cys
            265                 270                 275

tct gta cac aag cgc ttt act gtc gag cag atc aac aaa gcc cgc gcc   979
Ser Val His Lys Arg Phe Thr Val Glu Gln Ile Asn Lys Ala Arg Ala
        280                 285                 290

gag tac ccc gac gtt cac gtc atc gtg cac cct gaa tcc ccc atg cca   1027
Glu Tyr Pro Asp Val His Val Ile Val His Pro Glu Ser Pro Met Pro
    295                 300                 305

gtt gtt gac gcc gcc gac tca tcc gga tcc act gac ttc att gtg aaa   1075
Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr Asp Phe Ile Val Lys
310                 315                 320                 325

gcc att caa gca gca ccg gca gga tct acc ttt gcg atc ggc acc gaa   1123
Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe Ala Ile Gly Thr Glu
                330                 335                 340

atc aac ttg gtt cag cgc ctg gca gcc cag tac ccg cag cac acc atc   1171
Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr Pro Gln His Thr Ile
            345                 350                 355

ttc tgc ctc gac cct gtc atc tgc cca tgc tcc acc atg tat cgc att   1219
Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser Thr Met Tyr Arg Ile
        360                 365                 370

cac cct ggt tac ctg gcc tgg gca ctt gag gag ttg gtg gct gga aac   1267
His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu Leu Val Ala Gly Asn
    375                 380                 385

gtg att aac cag att tct gtc tct gaa tcc gtg gcg gca ccg gcg cga   1315
Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val Ala Ala Pro Ala Arg
390                 395                 400                 405

gtc gct ttg gaa agg atg cta tct gtt gtt cca gca gct cct gtt act   1363
Val Ala Leu Glu Arg Met Leu Ser Val Val Pro Ala Ala Pro Val Thr
                410                 415                 420
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cct agc tcc tcg aag gat gcg taatttatga ctacccatat tga 1407
Pro Ser Ser Ser Lys Asp Ala
425

<210> 460
<211> 428
<212> PRT
<213> Corynebacterium glutamicum

<400> 460
Met Thr Thr Ser Ile Thr Pro Ser Val Asn Leu Ala Leu Lys Asn Ala
1 5 10 15

Asn Ser Cys Asn Ser Glu Leu Lys Asp Gly Pro Trp Phe Leu Asp Gln
20 25 30

Pro Gly Met Pro Asp Val Tyr Gly Pro Gly Ala Ser Gln Asn Asp Pro
35 40 45

Ile Pro Ala His Ala Pro Arg Gln Gln Val Leu Pro Glu Glu Tyr Gln
50 55 60

Arg Ala Ser Asp Asp Glu Leu His Arg Arg Ile Arg Glu Ala Lys Asp
65 70 75 80

Thr Leu Gly Asp Lys Val Val Ile Leu Gly His Phe Tyr Gln Arg Asp
85 90 95

Glu Val Ile Gln His Ala Asp Phe Val Gly Asp Ser Phe Gln Leu Ala
100 105 110

Arg Ala Ala Lys Thr Arg Pro Glu Ala Glu Ala Ile Val Phe Cys Gly
115 120 125

Val His Phe Met Ala Glu Thr Ala Asp Leu Leu Ser Thr Asp Glu Gln
130 135 140

Ser Val Ile Leu Pro Asn Leu Ala Ala Gly Cys Ser Met Ala Asp Met
145 150 155 160

Ala Asp Leu Asp Ser Val Glu Asp Cys Trp Glu Gln Leu Thr Ser Ile
165 170 175

Tyr Gly Asp Asp Thr Leu Ile Pro Val Thr Tyr Met Asn Ser Ser Ala
180 185 190

Ala Leu Lys Gly Phe Val Gly Glu His Gly Gly Ile Val Cys Thr Ser
195 200 205

Ser Asn Ala Arg Ser Val Leu Glu Trp Ala Phe Glu Arg Gly Gln Arg
210 215 220

Val Leu Phe Phe Pro Asp Gln His Leu Gly Arg Asn Thr Ala Lys Ala
225 230 235 240

Met Gly Ile Gly Ile Asp Gln Met Pro Leu Trp Asn Pro Asn Lys Pro
245 250 255

Leu Gly Gly Asn Thr Val Ser Glu Leu Glu Asn Ala Lys Val Leu Leu
260 265 270

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Trp His Gly Phe Cys Ser Val His Lys Arg Phe Thr Val Glu Gln Ile
        275                 280                 285

Asn Lys Ala Arg Ala Glu Tyr Pro Asp Val His Val Ile Val His Pro
    290                 295                 300

Glu Ser Pro Met Pro Val Val Asp Ala Ala Asp Ser Ser Gly Ser Thr
305                 310                 315                 320

Asp Phe Ile Val Lys Ala Ile Gln Ala Ala Pro Ala Gly Ser Thr Phe
                325                 330                 335

Ala Ile Gly Thr Glu Ile Asn Leu Val Gln Arg Leu Ala Ala Gln Tyr
            340                 345                 350

Pro Gln His Thr Ile Phe Cys Leu Asp Pro Val Ile Cys Pro Cys Ser
        355                 360                 365

Thr Met Tyr Arg Ile His Pro Gly Tyr Leu Ala Trp Ala Leu Glu Glu
    370                 375                 380

Leu Val Ala Gly Asn Val Ile Asn Gln Ile Ser Val Ser Glu Ser Val
385                 390                 395                 400

Ala Ala Pro Ala Arg Val Ala Leu Glu Arg Met Leu Ser Val Val Pro
                405                 410                 415

Ala Ala Pro Val Thr Pro Ser Ser Ser Lys Asp Ala
            420                 425


<210> 461
<211> 951
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(928)
<223> RXA00644

<400> 461
ttgtcgacgc cgtctcccag aatgatctcg agaccgcgag aacaatcatt cgtgaacacg 60

cggagcacgg cattgacact atggttaagg ccctcgagaa atg agc gcg cca gta   115
                                              Met Ser Ala Pro Val
                                                1               5

gga caa ggc atc gaa ggt cgc ccc act cac gtc acc ccg gaa cgc ttc   163
Gly Gln Gly Ile Glu Gly Arg Pro Thr His Val Thr Pro Glu Arg Phe
                10                  15                  20

ttt ggc cag ggt gtt gtg gtt acc gga gcg gct caa ggc atc ggc atg   211
Phe Gly Gln Gly Val Val Val Thr Gly Ala Ala Gln Gly Ile Gly Met
            25                  30                  35

gca gtg gca cac cgc atc gca tat gag gat ggc aac cta gtg ttg gtg   259
Ala Val Ala His Arg Ile Ala Tyr Glu Asp Gly Asn Leu Val Leu Val
        40                  45                  50
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gac cgt tcc ccg ctg gtg cat gaa gtt gcc gaa gag ctg cgt aaa gca   307
Asp Arg Ser Pro Leu Val His Glu Val Ala Glu Glu Leu Arg Lys Ala
     55                  60                  65

ggc gcc gga acg gtg gat tct ttc atc gcc gat ctg gaa acc ttt gaa   355
Gly Ala Gly Thr Val Asp Ser Phe Ile Ala Asp Leu Glu Thr Phe Glu
 70                  75                  80                  85

ggc gca act gat gct ttg gaa ttt gcc ggg cag aag ttg aag aac ctt   403
Gly Ala Thr Asp Ala Leu Glu Phe Ala Gly Gln Lys Leu Lys Asn Leu
                 90                  95                 100

gat gtg gtg atc aac aac gtt ggt ggc acc atc tgg gcg aag cct tat   451
Asp Val Val Ile Asn Asn Val Gly Gly Thr Ile Trp Ala Lys Pro Tyr
            105                 110                 115

cag gaa tac tct gag gaa gag atc cgc aag gaa atc aac cga agc ctc   499
Gln Glu Tyr Ser Glu Glu Glu Ile Arg Lys Glu Ile Asn Arg Ser Leu
        120                 125                 130

ttc ccc acc ttg tgg atg tgc cgg gcc gcg ttg cca att ctg atc gga   547
Phe Pro Thr Leu Trp Met Cys Arg Ala Ala Leu Pro Ile Leu Ile Gly
    135                 140                 145

aat ggt ggt gga acg atc gtt aat gtg tcc tcc atc gcg acc ggt ggt   595
Asn Gly Gly Gly Thr Ile Val Asn Val Ser Ser Ile Ala Thr Gly Gly
150                 155                 160                 165

atc aac cgt gtt cct tat gct gca gca aag ggt ggc gtc aac ggc att   643
Ile Asn Arg Val Pro Tyr Ala Ala Ala Lys Gly Gly Val Asn Gly Ile
                170                 175                 180

gtt tct gcc atg gcc cgc gaa gct gca ccg cat aat gtg cgc gtg gtg   691
Val Ser Ala Met Ala Arg Glu Ala Ala Pro His Asn Val Arg Val Val
            185                 190                 195

gca acg gct ccc ggt ggc acg ctc gct ccg gaa cgt gcc gtc aaa cga   739
Ala Thr Ala Pro Gly Gly Thr Leu Ala Pro Glu Arg Ala Val Lys Arg
        200                 205                 210

ggc cct ggg cca gag ggc gaa ttg gaa gaa aag tgg tat cag caa atc   787
Gly Pro Gly Pro Glu Gly Glu Leu Glu Glu Lys Trp Tyr Gln Gln Ile
    215                 220                 225

gtt gat caa acc att gat tcc agt ttg atg aag cgc tac ggc acc cta   835
Val Asp Gln Thr Ile Asp Ser Ser Leu Met Lys Arg Tyr Gly Thr Leu
230                 235                 240                 245

gag gag cag gtc gcg ccg atc tgt ttc ctc gct tct gag gaa gct tcc   883
Glu Glu Gln Val Ala Pro Ile Cys Phe Leu Ala Ser Glu Glu Ala Ser
                250                 255                 260

tac atc act gga tca gtc atg cca gtc ggt gga ggc gac cag gga       928
Tyr Ile Thr Gly Ser Val Met Pro Val Gly Gly Gly Asp Gln Gly
            265                 270                 275

taacccttgg tcaatcttag gga                                        951

<210> 462
<211> 276
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<212> PRT
<213> Corynebacterium glutamicum

<400> 462

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Met Ser Ala Pro Val Gly Gln Gly Ile Glu Gly Arg Pro Thr His Val
  1               5                  10                  15

Thr Pro Glu Arg Phe Phe Gly Gln Gly Val Val Val Thr Gly Ala Ala
             20                  25                  30

Gln Gly Ile Gly Met Ala Val Ala His Arg Ile Ala Tyr Glu Asp Gly
         35                  40                  45

Asn Leu Val Leu Val Asp Arg Ser Pro Leu Val His Glu Val Ala Glu
     50                  55                  60

Glu Leu Arg Lys Ala Gly Ala Gly Thr Val Asp Ser Phe Ile Ala Asp
 65                  70                  75                  80

Leu Glu Thr Phe Glu Gly Ala Thr Asp Ala Leu Glu Phe Ala Gly Gln
                 85                  90                  95

Lys Leu Lys Asn Leu Asp Val Val Ile Asn Asn Val Gly Gly Thr Ile
            100                 105                 110

Trp Ala Lys Pro Tyr Gln Glu Tyr Ser Glu Glu Glu Ile Arg Lys Glu
        115                 120                 125

Ile Asn Arg Ser Leu Phe Pro Thr Leu Trp Met Cys Arg Ala Ala Leu
    130                 135                 140

Pro Ile Leu Ile Gly Asn Gly Gly Gly Thr Ile Val Asn Val Ser Ser
145                 150                 155                 160

Ile Ala Thr Gly Gly Ile Asn Arg Val Pro Tyr Ala Ala Ala Lys Gly
                165                 170                 175

Gly Val Asn Gly Ile Val Ser Ala Met Ala Arg Glu Ala Ala Pro His
            180                 185                 190

Asn Val Arg Val Val Ala Thr Ala Pro Gly Gly Thr Leu Ala Pro Glu
        195                 200                 205

Arg Ala Val Lys Arg Gly Pro Gly Pro Glu Gly Glu Leu Glu Glu Lys
    210                 215                 220

Trp Tyr Gln Gln Ile Val Asp Gln Thr Ile Asp Ser Ser Leu Met Lys
225                 230                 235                 240

Arg Tyr Gly Thr Leu Glu Glu Gln Val Ala Pro Ile Cys Phe Leu Ala
                245                 250                 255

Ser Glu Glu Ala Ser Tyr Ile Thr Gly Ser Val Met Pro Val Gly Gly
            260                 265                 270

Gly Asp Gln Gly
        275
```

<210> 463
<211> 1191

<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1168)
<223> RXN00177

<400> 463
ctattccaca gcagtggacg ctgaacaact tcaaacacag attaagcagc tatcggatct 60

acttcacctc aactcagttg tcggagcata ggagctaaaa atg tct tta cag ttc 115
Met Ser Leu Gln Phe
1 5

gat cat gaa acc ctc ggt caa cga gtt ctg ttc ggt tca ggt gag gcg 163
Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe Gly Ser Gly Glu Ala
10 15 20

gcg caa aat ctc gcc gct gaa att agc cga ctc gat gcc aaa aac gtc 211
Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu Asp Ala Lys Asn Val
25 30 35

atg gtg gtt gcc ggt gat ttc gag ctt ccc atg gca cgg caa gta gca 259
Met Val Val Ala Gly Asp Phe Glu Leu Pro Met Ala Arg Gln Val Ala
40 45 50

gca gat att gat gtc aag gtg tgg cat tca aat gtc gtg atg cat gtg 307
Ala Asp Ile Asp Val Lys Val Trp His Ser Asn Val Val Met His Val
55 60 65

ccc atc gaa aca gca gaa gaa gca cgc agt gtt gcg aaa gaa aac gac 355
Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val Ala Lys Glu Asn Asp
70 75 80 85

att gat gtt gtg gtg tgt gtg ggc ggt gga tcc aca aca ggt cta gct 403
Ile Asp Val Val Val Cys Val Gly Gly Gly Ser Thr Thr Gly Leu Ala
90 95 100

aaa gcg att gcc atg acc acc gca ttg ccg atc att gcg gta ccc act 451
Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile Ile Ala Val Pro Thr
105 110 115

act tat gca ggt tct gaa gca aca aat gtg tgg gga ttg acc gaa gcc 499
Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp Gly Leu Thr Glu Ala
120 125 130

gcg cgc aaa aca act ggt gtt gat aac aaa gtg ctg cca gtg aca gtt 547
Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val Leu Pro Val Thr Val
135 140 145

atc tac gat tca gcg tta acc atg tct ttg ccg gta gaa atg tcg gtt 595
Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro Val Glu Met Ser Val
150 155 160 165

gct tct ggt ctc aat ggt ttg gct cac tgc att gat tct ttg tgg gga 643
Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu Trp Gly
170 175 180

ccg aag gcg gat ccc atc aat gcg gct atg gct gct gag gga att cga 691
Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala Ala Glu Gly Ile Arg

```
            185                 190                 195

gca ctt tct gct ggc ctt ccc aag att gtg gca gat gct cag gac gta   739
Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala Asp Ala Gln Asp Val
        200                 205                 210

gat ggt cgc gat gaa gcg ctc tac ggt gcc tac ctg gct gcg gtg tct   787
Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala Val Ser
    215                 220                 225

ttt gcc tct gct ggc tct ggt ctc cac cac aag atc tgc cac gtg ttg   835
Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His Val Leu
230                 235                 240                 245

ggt gga act ttt aac ctt cca cac gcg caa acc cat gca aca gta ctg   883
Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr Val Leu
                250                 255                 260

cct tat gtt ctt gcc ttc aac gcg cca tat gcg cca cag gca gaa caa   931
Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu Gln
            265                 270                 275

cgc gca gcg gca gct ttc ggt tct gcg aca gca ctt gaa gga ttg caa   979
Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu Gln
        280                 285                 290

cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac gga   1027
Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr Gly
    295                 300                 305

ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag aaa   1075
Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu Lys
310                 315                 320                 325

gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act gcg   1123
Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr Ala
                330                 335                 340

ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat       1168
Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
            345                 350                 355

taaggagacc aacatgacta ttt                                        1191


<210> 464
<211> 356
<212> PRT
<213> Corynebacterium glutamicum

<400> 464
Met Ser Leu Gln Phe Asp His Glu Thr Leu Gly Gln Arg Val Leu Phe
  1               5                  10                  15

Gly Ser Gly Glu Ala Ala Gln Asn Leu Ala Ala Glu Ile Ser Arg Leu
             20                  25                  30

Asp Ala Lys Asn Val Met Val Val Ala Gly Asp Phe Glu Leu Pro Met
         35                  40                  45

Ala Arg Gln Val Ala Ala Asp Ile Asp Val Lys Val Trp His Ser Asn
```

```
     50                  55                  60

Val Val Met His Val Pro Ile Glu Thr Ala Glu Glu Ala Arg Ser Val
 65                  70                  75                  80

Ala Lys Glu Asn Asp Ile Asp Val Val Val Cys Val Gly Gly Gly Ser
                85                  90                  95

Thr Thr Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile
            100                 105                 110

Ile Ala Val Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp
        115                 120                 125

Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Asn Lys Val
    130                 135                 140

Leu Pro Val Thr Val Ile Tyr Asp Ser Ala Leu Thr Met Ser Leu Pro
145                 150                 155                 160

Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile
                165                 170                 175

Asp Ser Leu Trp Gly Pro Lys Ala Asp Pro Ile Asn Ala Ala Met Ala
            180                 185                 190

Ala Glu Gly Ile Arg Ala Leu Ser Ala Gly Leu Pro Lys Ile Val Ala
        195                 200                 205

Asp Ala Gln Asp Val Asp Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr
    210                 215                 220

Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys
225                 230                 235                 240

Ile Cys His Val Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr
                245                 250                 255

His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala
            260                 265                 270

Pro Gln Ala Glu Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala
        275                 280                 285

Leu Glu Gly Leu Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg
    290                 295                 300

Leu Ser Asp Tyr Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu
305                 310                 315                 320

Ile Ile Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu
                325                 330                 335

Glu Asn Leu Thr Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro
            340                 345                 350

Ala Thr Leu Asn
        355
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Sequence Listing

<210> 465

<211> 311
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(288)
<223> FRXA00177

<400> 465

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ctg cct tat gtt ctt gcc ttc aac gcg cca tat gcg cca cag gca gaa   48
Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu
  1               5                  10                  15

caa cgc gca gcg gca gct ttc ggt tct gcg aca gca ctt gaa gga ttg   96
Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu
             20                  25                  30

caa cag ctg cgt gcc caa gtg gga gca cca cag cga cta tcc gat tac   144
Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr
         35                  40                  45

gga ttc acc gca gca gga atc cca gag gca gtg gaa atc atc ttg gag   192
Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
     50                  55                  60

aaa gta ccg gcg aat aat cca cgg acg gtc aca gaa gaa aac ctc act   240
Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
 65                  70                  75                  80

gcg ctg ctt acc aca gcg ctc aac ggc gac gat cca gca act ttg aat   288
Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
                 85                  90                  95

taaggagacc aacatgacta ttt                                        311
```

<210> 466
<211> 96
<212> PRT
<213> Corynebacterium glutamicum

<400> 466

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Leu Pro Tyr Val Leu Ala Phe Asn Ala Pro Tyr Ala Pro Gln Ala Glu
  1               5                  10                  15

Gln Arg Ala Ala Ala Ala Phe Gly Ser Ala Thr Ala Leu Glu Gly Leu
             20                  25                  30

Gln Gln Leu Arg Ala Gln Val Gly Ala Pro Gln Arg Leu Ser Asp Tyr
         35                  40                  45

Gly Phe Thr Ala Ala Gly Ile Pro Glu Ala Val Glu Ile Ile Leu Glu
     50                  55                  60

Lys Val Pro Ala Asn Asn Pro Arg Thr Val Thr Glu Glu Asn Leu Thr
 65                  70                  75                  80

Ala Leu Leu Thr Thr Ala Leu Asn Gly Asp Asp Pro Ala Thr Leu Asn
                 85                  90                  95
```

<210> 467
<211> 1212
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1189)
<223> RXA02448

<400> 467
agcattcacc ggccagatct tcaagaaggc ttaaaccccc tccgatctct ttggctagca 60

cctaacaaac caccacacct tttagaaagt gattctcgct gtg aac aac tca ctc 115
Val Asn Asn Ser Leu
1 5

gca ttc aac cac gac acc ctc cca cag aaa gtc atg ttt gga tat ggc 163
Ala Phe Asn His Asp Thr Leu Pro Gln Lys Val Met Phe Gly Tyr Gly
10 15 20

aag tcc agt gca ttc tta aag cag gaa gtt gaa cgc cgc ggc tca gcc 211
Lys Ser Ser Ala Phe Leu Lys Gln Glu Val Glu Arg Arg Gly Ser Ala
25 30 35

aag gtc atg gtc att gcg ggt gaa cga gaa atg tcg atc gcc cat aag 259
Lys Val Met Val Ile Ala Gly Glu Arg Glu Met Ser Ile Ala His Lys
40 45 50

gtg gcc tca gaa att gag gtg gcg atc tgg cac gac gaa gtt gtc atg 307
Val Ala Ser Glu Ile Glu Val Ala Ile Trp His Asp Glu Val Val Met
55 60 65

cac gtg ccc atc gaa gta gcc gaa cgt gcg cgt gca gtg gca acc gac 355
His Val Pro Ile Glu Val Ala Glu Arg Ala Arg Ala Val Ala Thr Asp
70 75 80 85

aat gag att gat ctg ctg gtg tgt gtt ggc ggc gga tcc acc ata ggt 403
Asn Glu Ile Asp Leu Leu Val Cys Val Gly Gly Gly Ser Thr Ile Gly
90 95 100

ttg gcc aaa gca att gcc atg acc act gcc ctg ccc atc gtc gcg atc 451
Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu Pro Ile Val Ala Ile
105 110 115

ccc acc acc tac gca gga tcg gaa gca acc aac gtg tgg ggt ctg acg 499
Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn Val Trp Gly Leu Thr
120 125 130

gaa gca gcg cgc aaa aca acc ggt gtt gat ctg aag gtg ctc ccc gaa 547
Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Leu Lys Val Leu Pro Glu
135 140 145

aca gtc att tac gat tcc gaa ctc acc atg tcg ctt cca gtg gag atg 595
Thr Val Ile Tyr Asp Ser Glu Leu Thr Met Ser Leu Pro Val Glu Met
150 155 160 165

```
tcc gtg gca tcc gga ctc aac ggc ctg gcg cac tgc att gat tct ttg   643
Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His Cys Ile Asp Ser Leu
                170                 175                 180

tgg gga ccc aac gcc gat ccc atc aac gca gtg ctt gca gcc gaa gga   691
Trp Gly Pro Asn Ala Asp Pro Ile Asn Ala Val Leu Ala Ala Glu Gly
            185                 190                 195

atc cgc gca ctc aac cag gga ctg ccg aaa att gtt gcg aac ccg cac   739
Ile Arg Ala Leu Asn Gln Gly Leu Pro Lys Ile Val Ala Asn Pro His
        200                 205                 210

agc atc gaa gga cgc gac gaa gcc ctc tac ggc gcc tac ctc gca gca   787
Ser Ile Glu Gly Arg Asp Glu Ala Leu Tyr Gly Ala Tyr Leu Ala Ala
    215                 220                 225

gta tcc ttc gcc tcc gca ggc tcc gga cta cac cac aaa atc tgc cac   835
Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His His Lys Ile Cys His
230                 235                 240                 245

acc ttg gga ggc acc ttc aac ctc ccc cac gcc caa acc cac gca acc   883
Thr Leu Gly Gly Thr Phe Asn Leu Pro His Ala Gln Thr His Ala Thr
                250                 255                 260

gtg ctg ccg tat gtt ttg gca ttc aac gca ggc gac gca cca gaa gct   931
Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Gly Asp Ala Pro Glu Ala
            265                 270                 275

gaa cgc cgc gca gcc gca gcc ttt gga act gac acc gca cta gaa ggc   979
Glu Arg Arg Ala Ala Ala Ala Phe Gly Thr Asp Thr Ala Leu Glu Gly
        280                 285                 290

ctg caa cgc ctc cgc ttg tca gtc aac gca ccg aaa cga ctt tcc gac   1027
Leu Gln Arg Leu Arg Leu Ser Val Asn Ala Pro Lys Arg Leu Ser Asp
    295                 300                 305

tac ggc ttc gag gct tca gga att gct gag gca gtg gac gtc acg ttg   1075
Tyr Gly Phe Glu Ala Ser Gly Ile Ala Glu Ala Val Asp Val Thr Leu
310                 315                 320                 325

gag aaa gtt ccc gcc aac aat cct cgc cca gtg acc cgg gaa aac ctc   1123
Glu Lys Val Pro Ala Asn Asn Pro Arg Pro Val Thr Arg Glu Asn Leu
                330                 335                 340

agc aga ttg ctc gaa gca gca ctc aac ggt gag gat ccg gca gtt ctt   1171
Ser Arg Leu Leu Glu Ala Ala Leu Asn Gly Glu Asp Pro Ala Val Leu
            345                 350                 355

agc gca gta ctc agt aac taacccggcg atttttcaag gag                1212
Ser Ala Val Leu Ser Asn
        360
```

<210> 468
<211> 363
<212> PRT
<213> Corynebacterium glutamicum

<400> 468

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Val Asn Asn Ser Leu Ala Phe Asn His Asp Thr Leu Pro Gln Lys Val
  1               5                  10                  15
```

Met Phe Gly Tyr Gly Lys Ser Ser Ala Phe Leu Lys Gln Glu Val Glu
20 25 30

Arg Arg Gly Ser Ala Lys Val Met Val Ile Ala Gly Glu Arg Glu Met
35 40 45

Ser Ile Ala His Lys Val Ala Ser Glu Ile Glu Val Ala Ile Trp His
50 55 60

Asp Glu Val Val Met His Val Pro Ile Glu Val Ala Glu Arg Ala Arg
65 70 75 80

Ala Val Ala Thr Asp Asn Glu Ile Asp Leu Leu Val Cys Val Gly Gly
85 90 95

Gly Ser Thr Ile Gly Leu Ala Lys Ala Ile Ala Met Thr Thr Ala Leu
100 105 110

Pro Ile Val Ala Ile Pro Thr Thr Tyr Ala Gly Ser Glu Ala Thr Asn
115 120 125

Val Trp Gly Leu Thr Glu Ala Ala Arg Lys Thr Thr Gly Val Asp Leu
130 135 140

Lys Val Leu Pro Glu Thr Val Ile Tyr Asp Ser Glu Leu Thr Met Ser
145 150 155 160

Leu Pro Val Glu Met Ser Val Ala Ser Gly Leu Asn Gly Leu Ala His
165 170 175

Cys Ile Asp Ser Leu Trp Gly Pro Asn Ala Asp Pro Ile Asn Ala Val
180 185 190

Leu Ala Ala Glu Gly Ile Arg Ala Leu Asn Gln Gly Leu Pro Lys Ile
195 200 205

Val Ala Asn Pro His Ser Ile Glu Gly Arg Asp Glu Ala Leu Tyr Gly
210 215 220

Ala Tyr Leu Ala Ala Val Ser Phe Ala Ser Ala Gly Ser Gly Leu His
225 230 235 240

His Lys Ile Cys His Thr Leu Gly Gly Thr Phe Asn Leu Pro His Ala
245 250 255

Gln Thr His Ala Thr Val Leu Pro Tyr Val Leu Ala Phe Asn Ala Gly
260 265 270

Asp Ala Pro Glu Ala Glu Arg Arg Ala Ala Ala Ala Phe Gly Thr Asp
275 280 285

Thr Ala Leu Glu Gly Leu Gln Arg Leu Arg Leu Ser Val Asn Ala Pro
290 295 300

Lys Arg Leu Ser Asp Tyr Gly Phe Glu Ala Ser Gly Ile Ala Glu Ala
305 310 315 320

Val Asp Val Thr Leu Glu Lys Val Pro Ala Asn Asn Pro Arg Pro Val
325 330 335

```
Thr Arg Glu Asn Leu Ser Arg Leu Leu Glu Ala Ala Leu Asn Gly Glu
            340                 345                 350

Asp Pro Ala Val Leu Ser Ala Val Leu Ser Asn
        355                 360
```

<210> 469
<211> 1782
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1759)
<223> RXA00048

<400> 469

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gcgaaggcgt gggcataggg aaaaccttag ctgatctgcg gtgacttaaa tataaggggg 60

tggaatgggg gtattgtaaa atctgaaccc ttgttcattt atg aat cat gat tca   115
                                          Met Asn His Asp Ser
                                            1               5

gaa tgt gat cta gat aat gtt gtt cag ttc act att caa gaa ggg tta   163
Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr Ile Gln Glu Gly Leu
                10                  15                  20

gat ccc atg tca ccc aat aac ttc gat acc gat gtc tgc atc gtc ggt   211
Asp Pro Met Ser Pro Asn Asn Phe Asp Thr Asp Val Cys Ile Val Gly
            25                  30                  35

gga ggt cct acc gga acg ctc ctt gca gta ctg ctc ggc caa aaa ggt   259
Gly Gly Pro Thr Gly Thr Leu Leu Ala Val Leu Leu Gly Gln Lys Gly
        40                  45                  50

cac cgc gtc acc atc ctg gaa aag tgg cca aca ttc tac gaa cga cct   307
His Arg Val Thr Ile Leu Glu Lys Trp Pro Thr Phe Tyr Glu Arg Pro
    55                  60                  65

cgt gca gtc acc ttt gac cac gaa atc gca cgg atc ctt gga tac att   355
Arg Ala Val Thr Phe Asp His Glu Ile Ala Arg Ile Leu Gly Tyr Ile
70                  75                  80                  85

ggc att gat tct gaa aac gac gaa gcc atc gat tac cac tcc gac agc   403
Gly Ile Asp Ser Glu Asn Asp Glu Ala Ile Asp Tyr His Ser Asp Ser
                90                  95                  100

tac gac tgg aag aac gca gcg ggg gag acg ctt ttg gaa gtc gat tgg   451
Tyr Asp Trp Lys Asn Ala Ala Gly Glu Thr Leu Leu Glu Val Asp Trp
            105                 110                 115

acc tcc atg aca gat tcc gga tgg cgc acc cga tac tgg ttc tac cag   499
Thr Ser Met Thr Asp Ser Gly Trp Arg Thr Arg Tyr Trp Phe Tyr Gln
        120                 125                 130

cca gaa ctt gaa aag cgt ctg cgc gat ctg gcc ctg acc atg gat ttt   547
Pro Glu Leu Glu Lys Arg Leu Arg Asp Leu Ala Leu Thr Met Asp Phe
    135                 140                 145

gta gat att cgc tgt ggc ttc acc gct gtc gga ttg tcc caa gat gaa   595
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```
Val Asp Ile Arg Cys Gly Phe Thr Ala Val Gly Leu Ser Gln Asp Glu
150                 155                 160                 165

aac tcc gcc atc att cac ggc att gtc act gat acc cca gag aac att   643
Asn Ser Ala Ile Ile His Gly Ile Val Thr Asp Thr Pro Glu Asn Ile
                170                 175                 180

cca gca gat gct cag cgc gaa gat atc cga gcg aag tat gtc atc ggt   691
Pro Ala Asp Ala Gln Arg Glu Asp Ile Arg Ala Lys Tyr Val Ile Gly
            185                 190                 195

gca gac gga gct aac agt ttc gtg cgt aac tcc ctt ggc tta gag atg   739
Ala Asp Gly Ala Asn Ser Phe Val Arg Asn Ser Leu Gly Leu Glu Met
        200                 205                 210

aat gat ctt gga tac ttc ttc gac tgg ctg atc ctg gac ctc aag cca   787
Asn Asp Leu Gly Tyr Phe Phe Asp Trp Leu Ile Leu Asp Leu Lys Pro
    215                 220                 225

act cag gac att gac tac gga aca gat cac tgg caa ctg tgt gat ccc   835
Thr Gln Asp Ile Asp Tyr Gly Thr Asp His Trp Gln Leu Cys Asp Pro
230                 235                 240                 245

aag cgc cca acc acc atc gtt cct gga ggc ccc ggc cgc cga cgt tgg   883
Lys Arg Pro Thr Thr Ile Val Pro Gly Gly Pro Gly Arg Arg Arg Trp
                250                 255                 260

gaa ttc atg gcg ctg cct ggt gaa gat ctc aag gaa ctc gct tct gaa   931
Glu Phe Met Ala Leu Pro Gly Glu Asp Leu Lys Glu Leu Ala Ser Glu
            265                 270                 275

gaa agc gcg tgg aat cta ctt gag cca tgg gat gtc aca cct ggc aag   979
Glu Ser Ala Trp Asn Leu Leu Glu Pro Trp Asp Val Thr Pro Gly Lys
        280                 285                 290

gcc att ctc gag cgc tcc gca gtg tat cga ttc caa gct cgc tgg gcc   1027
Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe Gln Ala Arg Trp Ala
    295                 300                 305

cag gaa tgg cgc tcc gga aga gct ctc atc gca ggc gat gcc gct cac   1075
Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala Gly Asp Ala Ala His
310                 315                 320                 325

ctc atg cca cct ttc gca ggt gaa ggc atg tgc gct ggc ctg aga gac   1123
Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys Ala Gly Leu Arg Asp
                330                 335                 340

tca ctg gcg ttg gca tgg cgt ctt gat ttg gtg ctg agc gga aaa tca   1171
Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val Leu Ser Gly Lys Ser
            345                 350                 355

gat gat gca ttg cta gac acc tac gga gaa gaa cgc cgc gaa cac gtc   1219
Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu Arg Arg Glu His Val
        360                 365                 370

cac tac tac att gat ttc tcc atg gac ctg ggc aat gtc atc tgc att   1267
His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly Asn Val Ile Cys Ile
    375                 380                 385

act gat gaa gat gaa gca cgt ttg cgc gat gag cgc atg att aaa gag   1315
Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu Arg Met Ile Lys Glu
```

```
390                 395                 400                 405

ctt gaa gca caa gac ggg gtc cct gtt aat acc gat gtc gca cac ttg   1363
Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr Asp Val Ala His Leu
                410                 415                 420

gga ccg gga att tgg gat aaa gat tct tcc cat ggt ggc gag cta gcg   1411
Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His Gly Gly Glu Leu Ala
            425                 430                 435

aag cag ggc ata gtg gaa tac caa ggt cga aag gcg cgt ttc gac gac   1459
Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys Ala Arg Phe Asp Asp
        440                 445                 450

gca gtc ggc cgt ggc tgg gca gtt tta ggc ctc aac act gat cca cga   1507
Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu Asn Thr Asp Pro Arg
    455                 460                 465

gaa gtg ctt gat gag gat tcg ctt gtg gca ctt gac gcc atc ggt gca   1555
Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu Asp Ala Ile Gly Ala
470                 475                 480                 485

atc gtc gaa tca gta ggt gat gca act tcc gca gtt tta gat gtt gaa   1603
Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala Val Leu Asp Val Glu
                490                 495                 500

ggt ctt tac act cgc tgg ctc aag gaa gcc ggg gca aca ttt att att   1651
Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly Ala Thr Phe Ile Ile
            505                 510                 515

acc cgc ccc gat ttc tac gtc tat tcc aca gca gtg gac gct gaa caa   1699
Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala Val Asp Ala Glu Gln
        520                 525                 530

ctt caa aca cag att aag cag cta tcg gat cta ctt cac ctc aac tca   1747
Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu Leu His Leu Asn Ser
    535                 540                 545

gtt gtc gga gca taggagctaa aaatgtcttt aca                        1782
Val Val Gly Ala
550
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<210> 470
<211> 553
<212> PRT
<213> Corynebacterium glutamicum

<400> 470

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Met Asn His Asp Ser Glu Cys Asp Leu Asp Asn Val Val Gln Phe Thr
  1               5                  10                  15

Ile Gln Glu Gly Leu Asp Pro Met Ser Pro Asn Asn Phe Asp Thr Asp
             20                  25                  30

Val Cys Ile Val Gly Gly Gly Pro Thr Gly Thr Leu Leu Ala Val Leu
         35                  40                  45

Leu Gly Gln Lys Gly His Arg Val Thr Ile Leu Glu Lys Trp Pro Thr
     50                  55                  60
```

```
Phe Tyr Glu Arg Pro Arg Ala Val Thr Phe Asp His Glu Ile Ala Arg
 65                  70                  75                  80

Ile Leu Gly Tyr Ile Gly Ile Asp Ser Glu Asn Asp Glu Ala Ile Asp
                85                  90                  95

Tyr His Ser Asp Ser Tyr Asp Trp Lys Asn Ala Ala Gly Glu Thr Leu
            100                 105                 110

Leu Glu Val Asp Trp Thr Ser Met Thr Asp Ser Gly Trp Arg Thr Arg
        115                 120                 125

Tyr Trp Phe Tyr Gln Pro Glu Leu Glu Lys Arg Leu Arg Asp Leu Ala
    130                 135                 140

Leu Thr Met Asp Phe Val Asp Ile Arg Cys Gly Phe Thr Ala Val Gly
145                 150                 155                 160

Leu Ser Gln Asp Glu Asn Ser Ala Ile Ile His Gly Ile Val Thr Asp
                165                 170                 175

Thr Pro Glu Asn Ile Pro Ala Asp Ala Gln Arg Glu Asp Ile Arg Ala
            180                 185                 190

Lys Tyr Val Ile Gly Ala Asp Gly Ala Asn Ser Phe Val Arg Asn Ser
        195                 200                 205

Leu Gly Leu Glu Met Asn Asp Leu Gly Tyr Phe Phe Asp Trp Leu Ile
    210                 215                 220

Leu Asp Leu Lys Pro Thr Gln Asp Ile Asp Tyr Gly Thr Asp His Trp
225                 230                 235                 240

Gln Leu Cys Asp Pro Lys Arg Pro Thr Thr Ile Val Pro Gly Gly Pro
                245                 250                 255

Gly Arg Arg Arg Trp Glu Phe Met Ala Leu Pro Gly Glu Asp Leu Lys
            260                 265                 270

Glu Leu Ala Ser Glu Glu Ser Ala Trp Asn Leu Leu Glu Pro Trp Asp
        275                 280                 285

Val Thr Pro Gly Lys Ala Ile Leu Glu Arg Ser Ala Val Tyr Arg Phe
    290                 295                 300

Gln Ala Arg Trp Ala Gln Glu Trp Arg Ser Gly Arg Ala Leu Ile Ala
305                 310                 315                 320

Gly Asp Ala Ala His Leu Met Pro Pro Phe Ala Gly Glu Gly Met Cys
                325                 330                 335

Ala Gly Leu Arg Asp Ser Leu Ala Leu Ala Trp Arg Leu Asp Leu Val
            340                 345                 350

Leu Ser Gly Lys Ser Asp Asp Ala Leu Leu Asp Thr Tyr Gly Glu Glu
        355                 360                 365

Arg Arg Glu His Val His Tyr Tyr Ile Asp Phe Ser Met Asp Leu Gly
    370                 375                 380

Asn Val Ile Cys Ile Thr Asp Glu Asp Glu Ala Arg Leu Arg Asp Glu
```

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```
385                 390                 395                 400

Arg Met Ile Lys Glu Leu Glu Ala Gln Asp Gly Val Pro Val Asn Thr
                405                 410                 415

Asp Val Ala His Leu Gly Pro Gly Ile Trp Asp Lys Asp Ser Ser His
            420                 425                 430

Gly Gly Glu Leu Ala Lys Gln Gly Ile Val Glu Tyr Gln Gly Arg Lys
        435                 440                 445

Ala Arg Phe Asp Asp Ala Val Gly Arg Gly Trp Ala Val Leu Gly Leu
    450                 455                 460

Asn Thr Asp Pro Arg Glu Val Leu Asp Glu Asp Ser Leu Val Ala Leu
465                 470                 475                 480

Asp Ala Ile Gly Ala Ile Val Glu Ser Val Gly Asp Ala Thr Ser Ala
                485                 490                 495

Val Leu Asp Val Glu Gly Leu Tyr Thr Arg Trp Leu Lys Glu Ala Gly
            500                 505                 510

Ala Thr Phe Ile Ile Thr Arg Pro Asp Phe Tyr Val Tyr Ser Thr Ala
        515                 520                 525

Val Asp Ala Glu Gln Leu Gln Thr Gln Ile Lys Gln Leu Ser Asp Leu
    530                 535                 540

Leu His Leu Asn Ser Val Val Gly Ala
545                 550


<210> 471
<211> 583
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (1)..(564)
<223> RXA01126

<400> 471
tcc gca gaa tca ctg cca cca acc ctg ttc ctg aag cca cca aca gct   48
Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala
  1               5                  10                  15

gtc acc gga cca gag tcc cca atc cga atc cct tcc ttt gcc acc aag   96
Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys
             20                  25                  30

gtg gaa ttc gaa ggt gag ctc gca gta gtt atc ggc aag ccc tgc aag   144
Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys
         35                  40                  45

aac gtc aag gct gat gac tgg aag tct gtc gtt ttg ggc ttc acc atc   192
Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile
     50                  55                  60

atc aac gac gtc tcc tcc cgt gac ctc cag ttc gct gac ggc cag tgg   240
```

```
Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp
 65                  70                  75                  80

gca cgc gct aag ggc att gac acc ttc ggc ccc atc gga cca tgg att   288
Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile
                85                  90                  95

gaa act gac atc aac tcc atc gac ttg gac aac ctg ccc atc aag gca   336
Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala
            100                 105                 110

cgc ctc acc cac gac ggc gaa acc caa ttg aag cag gac tcc aac tcc   384
Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser
        115                 120                 125

aac cag atg atc atg aag atg ggc gaa att atc gag ttc atc acc gcc   432
Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala
    130                 135                 140

tcc atg acc ctg ctc cca ggc gac gtt att gca acc ggt tct cca gca   480
Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala
145                 150                 155                 160

ggc acc gaa gca atg gtt gac ggc gac tac atc gaa atc gaa att cca   528
Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro
                165                 170                 175

ggc atc ggc aag ctg ggc aac cca gtt gtg gac gcc taaaatggat        574
Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala
            180                 185

caccaccat                                                        583


<210> 472
<211> 188
<212> PRT
<213> Corynebacterium glutamicum

<400> 472
Ser Ala Glu Ser Leu Pro Pro Thr Leu Phe Leu Lys Pro Pro Thr Ala
  1               5                  10                  15

Val Thr Gly Pro Glu Ser Pro Ile Arg Ile Pro Ser Phe Ala Thr Lys
             20                  25                  30

Val Glu Phe Glu Gly Glu Leu Ala Val Val Ile Gly Lys Pro Cys Lys
         35                  40                  45

Asn Val Lys Ala Asp Asp Trp Lys Ser Val Val Leu Gly Phe Thr Ile
     50                  55                  60

Ile Asn Asp Val Ser Ser Arg Asp Leu Gln Phe Ala Asp Gly Gln Trp
 65                  70                  75                  80

Ala Arg Ala Lys Gly Ile Asp Thr Phe Gly Pro Ile Gly Pro Trp Ile
                85                  90                  95

Glu Thr Asp Ile Asn Ser Ile Asp Leu Asp Asn Leu Pro Ile Lys Ala
            100                 105                 110
```

```
Arg Leu Thr His Asp Gly Glu Thr Gln Leu Lys Gln Asp Ser Asn Ser
        115                 120                 125

Asn Gln Met Ile Met Lys Met Gly Glu Ile Ile Glu Phe Ile Thr Ala
    130                 135                 140

Ser Met Thr Leu Leu Pro Gly Asp Val Ile Ala Thr Gly Ser Pro Ala
145                 150                 155                 160

Gly Thr Glu Ala Met Val Asp Gly Asp Tyr Ile Glu Ile Glu Ile Pro
                165                 170                 175

Gly Ile Gly Lys Leu Gly Asn Pro Val Val Asp Ala
            180                 185


<210> 473
<211> 864
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(841)
<223> RXA01117

<400> 473
tacgaaatct ggcgattgtt cgaccatccc atcaactcct ctttttgttc gcattgcgaa 60

cccttgtgca tatgatgaac attacgttag catgtctcac atg att aac aag agc   115
                                          Met Ile Asn Lys Ser
                                            1               5

att tct tcc act gct gaa gcg gtg gcc gat atc cca gac ggt gcg tcc   163
Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile Pro Asp Gly Ala Ser
                10                  15                  20

atc gcc gtc ggt ggt ttc ggc ctc gtg ggc atc ccc act gca ttg atc   211
Ile Ala Val Gly Gly Phe Gly Leu Val Gly Ile Pro Thr Ala Leu Ile
            25                  30                  35

ctc gcc ctc cgc gaa caa ggc gca ggc gat ctg acc atc att tcc aac   259
Leu Ala Leu Arg Glu Gln Gly Ala Gly Asp Leu Thr Ile Ile Ser Asn
        40                  45                  50

aac cta ggc acc gac ggt ttc ggc ctc gga ctg ttg ctt ttg gat aag   307
Asn Leu Gly Thr Asp Gly Phe Gly Leu Gly Leu Leu Leu Leu Asp Lys
    55                  60                  65

aag atc tcc aag tcc atc ggc tcc tac ctt ggc tcc aac aag gaa tat   355
Lys Ile Ser Lys Ser Ile Gly Ser Tyr Leu Gly Ser Asn Lys Glu Tyr
70                  75                  80                  85

gca cgc cag tac ctg gaa gga gaa ctc acc gtc gag ttc acc ccg cag   403
Ala Arg Gln Tyr Leu Glu Gly Glu Leu Thr Val Glu Phe Thr Pro Gln
                90                  95                  100

ggc acc ttg gct gaa cgc ctc cgc gca ggt ggc gcc ggc atc cct gcg   451
Gly Thr Leu Ala Glu Arg Leu Arg Ala Gly Gly Ala Gly Ile Pro Ala
            105                 110                 115
```

```
ttt tac acc acc gca ggc gtg ggc acc cag gtc gca gaa ggc gga ctc   499
Phe Tyr Thr Thr Ala Gly Val Gly Thr Gln Val Ala Glu Gly Gly Leu
        120                 125                 130

cca cag cgc tac aac acc gac ggc acc gtc gcc gtg gtg tcc cag cca   547
Pro Gln Arg Tyr Asn Thr Asp Gly Thr Val Ala Val Val Ser Gln Pro
    135                 140                 145

aag gaa acc cgc gaa ttc aac ggc cag ctc tac gtc atg gaa gag ggc   595
Lys Glu Thr Arg Glu Phe Asn Gly Gln Leu Tyr Val Met Glu Glu Gly
150                 155                 160                 165

atc cgc gcc gat tac gca ctc gtg cac gca cac aaa gca gat cgc ttt   643
Ile Arg Ala Asp Tyr Ala Leu Val His Ala His Lys Ala Asp Arg Phe
                170                 175                 180

ggc aac ctg gtg ttc cgc aag acc gcg cag aac ttc aac cca gat gca   691
Gly Asn Leu Val Phe Arg Lys Thr Ala Gln Asn Phe Asn Pro Asp Ala
            185                 190                 195

gca atg agc ggc aag atc acc att gct cag gtc gag cac ttt gta gac   739
Ala Met Ser Gly Lys Ile Thr Ile Ala Gln Val Glu His Phe Val Asp
        200                 205                 210

gaa ctc cac cca gat gag atc gat ctg cca gga att tac gtc aac cgc   787
Glu Leu His Pro Asp Glu Ile Asp Leu Pro Gly Ile Tyr Val Asn Arg
    215                 220                 225

gtc gtc cac gtt gga ccg cag gaa acc gga atc gaa aac agg acg gtg   835
Val Val His Val Gly Pro Gln Glu Thr Gly Ile Glu Asn Arg Thr Val
230                 235                 240                 245

tct aac taatgacttg ggatcataac caa                                864
Ser Asn
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09054-0099

<210> 474
<211> 247
<212> PRT
<213> Corynebacterium glutamicum

<400> 474

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Met Ile Asn Lys Ser Ile Ser Ser Thr Ala Glu Ala Val Ala Asp Ile
  1               5                  10                  15

Pro Asp Gly Ala Ser Ile Ala Val Gly Gly Phe Gly Leu Val Gly Ile
             20                  25                  30

Pro Thr Ala Leu Ile Leu Ala Leu Arg Glu Gln Gly Ala Gly Asp Leu
         35                  40                  45

Thr Ile Ile Ser Asn Asn Leu Gly Thr Asp Gly Phe Gly Leu Gly Leu
     50                  55                  60

Leu Leu Leu Asp Lys Lys Ile Ser Lys Ser Ile Gly Ser Tyr Leu Gly
 65                  70                  75                  80

Ser Asn Lys Glu Tyr Ala Arg Gln Tyr Leu Glu Gly Glu Leu Thr Val
                 85                  90                  95
```

```
Glu Phe Thr Pro Gln Gly Thr Leu Ala Glu Arg Leu Arg Ala Gly Gly
            100                 105                 110

Ala Gly Ile Pro Ala Phe Tyr Thr Thr Ala Gly Val Gly Thr Gln Val
        115                 120                 125

Ala Glu Gly Gly Leu Pro Gln Arg Tyr Asn Thr Asp Gly Thr Val Ala
    130                 135                 140

Val Val Ser Gln Pro Lys Glu Thr Arg Glu Phe Asn Gly Gln Leu Tyr
145                 150                 155                 160

Val Met Glu Glu Gly Ile Arg Ala Asp Tyr Ala Leu Val His Ala His
                165                 170                 175

Lys Ala Asp Arg Phe Gly Asn Leu Val Phe Arg Lys Thr Ala Gln Asn
            180                 185                 190

Phe Asn Pro Asp Ala Ala Met Ser Gly Lys Ile Thr Ile Ala Gln Val
        195                 200                 205

Glu His Phe Val Asp Glu Leu His Pro Asp Glu Ile Asp Leu Pro Gly
    210                 215                 220

Ile Tyr Val Asn Arg Val Val His Val Gly Pro Gln Glu Thr Gly Ile
225                 230                 235                 240

Glu Asn Arg Thr Val Ser Asn
                245
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Sequence Listing

<210> 475
<211> 1629
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(1606)
<223> RXA00772

<400> 475

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gtcgcattct gcttgctgaa gtggcacacc tatgtgttct gcttgggtat agcagtgcgg 60

gaaaaatttg aaaaagtccg attacctgag gaggtattca atg tct gat cgc att   115
                                                Met Ser Asp Arg Ile
                                                  1               5

gct tca gaa aag ctg cgc tcc aag ctc atg tcc gcc gac gag gcg gca   163
Ala Ser Glu Lys Leu Arg Ser Lys Leu Met Ser Ala Asp Glu Ala Ala
                  10                  15                  20

cag ttt gtt aac cac ggt gac aag gtt ggt ttc tcc ggc ttc acc ggc   211
Gln Phe Val Asn His Gly Asp Lys Val Gly Phe Ser Gly Phe Thr Gly
             25                  30                  35

gct ggc tac cca aag gca ctg cct acg gca atc gct aac cgg gct aaa   259
Ala Gly Tyr Pro Lys Ala Leu Pro Thr Ala Ile Ala Asn Arg Ala Lys
         40                  45                  50

gaa gca cac ggt gca ggc aac gac tac gca atc gac ctg ttc act ggc   307
```

```
Glu Ala His Gly Ala Gly Asn Asp Tyr Ala Ile Asp Leu Phe Thr Gly
     55                  60                  65

gca tcg acc gcc cct gac tgc gat ggc gta ctt gca gaa gct gac gct   355
Ala Ser Thr Ala Pro Asp Cys Asp Gly Val Leu Ala Glu Ala Asp Ala
 70                  75                  80                  85

atc cgc tgg cgc atg cca tac gca tct gat cca atc atg cgt aac aag   403
Ile Arg Trp Arg Met Pro Tyr Ala Ser Asp Pro Ile Met Arg Asn Lys
                90                  95                 100

atc aac tcc ggc tcc atg gga tac tcc gat atc cac ctg tcc cac tcc   451
Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile His Leu Ser His Ser
            105                 110                 115

ggc cag cag gtt gaa gag ggc ttc ttc ggc cag ctc aac gta gct gtc   499
Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln Leu Asn Val Ala Val
        120                 125                 130

att gaa atc acc cgc atc act gaa gag ggc tac atc atc cct tct tcc   547
Ile Glu Ile Thr Arg Ile Thr Glu Glu Gly Tyr Ile Ile Pro Ser Ser
    135                 140                 145

tcc gtg ggt aac aac gtt gag tgg ctc aac gct gca gag aag gtc atc   595
Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala Ala Glu Lys Val Ile
150                 155                 160                 165

ctc gag gtt aac tct tgg cag tct gaa gac ctc gaa ggt atg cac gac   643
Leu Glu Val Asn Ser Trp Gln Ser Glu Asp Leu Glu Gly Met His Asp
                170                 175                 180

atc tgg tct gtt cct gcc ctg cca aac cgc att gcc gtg cca atc aac   691
Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile Ala Val Pro Ile Asn
            185                 190                 195

aag cca ggc gac cgc atc ggt aag acc tac atc gag ttc gac acc gac   739
Lys Pro Gly Asp Arg Ile Gly Lys Thr Tyr Ile Glu Phe Asp Thr Asp
        200                 205                 210

aag gtt gtt gct gtt gtt gag acc aac acc gca gac cgc aac gca cca   787
Lys Val Val Ala Val Val Glu Thr Asn Thr Ala Asp Arg Asn Ala Pro
    215                 220                 225

ttc aag cct gtc gac gac atc tct aag aag atc gct ggc aac ttc ctc   835
Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile Ala Gly Asn Phe Leu
230                 235                 240                 245

gac ttc ctg gaa agc gaa gtt gct gca ggt cgc ctg tcc tac gcg ggc   883
Asp Phe Leu Glu Ser Glu Val Ala Ala Gly Arg Leu Ser Tyr Ala Gly
                250                 255                 260

tac atc atg cag tcc ggc gtg ggc aac gtg cct aac gcg gtg atg gca   931
Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro Asn Ala Val Met Ala
            265                 270                 275

ggc ctg ctg gaa tcc aag ttt gag aac atc cag gcc tac acc gaa gtt   979
Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln Ala Tyr Thr Glu Val
        280                 285                 290

atc cag gac ggc atg gtg gac ctc atc gac gcc ggc aag atg acc gtt  1027
Ile Gln Asp Gly Met Val Asp Leu Ile Asp Ala Gly Lys Met Thr Val
```

```
    295                 300                 305

gca tcc gca act tcc ttc tcc ctg tct cct gag tac gca gag aag atg   1075
Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu Tyr Ala Glu Lys Met
310                 315                 320                 325

aac aac gag gct aag cgt tac cgc gag tcc att atc ctg cgc cca cag   1123
Asn Asn Glu Ala Lys Arg Tyr Arg Glu Ser Ile Ile Leu Arg Pro Gln
                330                 335                 340

cag atc tct aac cac cca gag gtc atc cgc cgc gtt ggc ctg atc gcc   1171
Gln Ile Ser Asn His Pro Glu Val Ile Arg Arg Val Gly Leu Ile Ala
            345                 350                 355

acc aac ggt ctc atc gag gct gac att tac ggc aac gtc aac tcc acc   1219
Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly Asn Val Asn Ser Thr
        360                 365                 370

aac gtt tct ggc tcc cgc gtc atg aac ggc atc ggc ggc tcc ggc gac   1267
Asn Val Ser Gly Ser Arg Val Met Asn Gly Ile Gly Gly Ser Gly Asp
    375                 380                 385

ttc acc cgt aac ggc tac atc tcc agc ttc atc acc cct tca gag gca   1315
Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile Thr Pro Ser Glu Ala
390                 395                 400                 405

aag ggc ggc gca atc tct gcg atc gtt cct ttc gca tcc cac atc gac   1363
Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe Ala Ser His Ile Asp
                410                 415                 420

cac acc gag cac gat gtc atg gtt gtt atc tct gag tac ggt tac gca   1411
His Thr Glu His Asp Val Met Val Val Ile Ser Glu Tyr Gly Tyr Ala
            425                 430                 435

gac ctt cgt ggt ctg gct cca cgt gag cgc gtt gcc aag atg atc ggc   1459
Asp Leu Arg Gly Leu Ala Pro Arg Glu Arg Val Ala Lys Met Ile Gly
        440                 445                 450

ctg gct cac cct gat tac cgc cca ctg ctc gag gag tac tac gct cgc   1507
Leu Ala His Pro Asp Tyr Arg Pro Leu Leu Glu Glu Tyr Tyr Ala Arg
    455                 460                 465

gca acc tcc ggt gac aac aag tac atg cag acc cct cat gat ctt gca   1555
Ala Thr Ser Gly Asp Asn Lys Tyr Met Gln Thr Pro His Asp Leu Ala
470                 475                 480                 485

acc gcg ttt gat ttc cac atc aac ctg gct aag aac ggc tcc atg aag   1603
Thr Ala Phe Asp Phe His Ile Asn Leu Ala Lys Asn Gly Ser Met Lys
                490                 495                 500

gca taagtttttt cttggtttag aaa                                    1629
Ala
```

<210> 476
<211> 502
<212> PRT
<213> Corynebacterium glutamicum

<400> 476

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Met Ser Asp Arg Ile Ala Ser Glu Lys Leu Arg Ser Lys Leu Met Ser
 1               5                  10                  15

Ala Asp Glu Ala Ala Gln Phe Val Asn His Gly Asp Lys Val Gly Phe
            20                  25                  30

Ser Gly Phe Thr Gly Ala Gly Tyr Pro Lys Ala Leu Pro Thr Ala Ile
        35                  40                  45

Ala Asn Arg Ala Lys Glu Ala His Gly Ala Gly Asn Asp Tyr Ala Ile
    50                  55                  60

Asp Leu Phe Thr Gly Ala Ser Thr Ala Pro Asp Cys Asp Gly Val Leu
65                  70                  75                  80

Ala Glu Ala Asp Ala Ile Arg Trp Arg Met Pro Tyr Ala Ser Asp Pro
                85                  90                  95

Ile Met Arg Asn Lys Ile Asn Ser Gly Ser Met Gly Tyr Ser Asp Ile
            100                 105                 110

His Leu Ser His Ser Gly Gln Gln Val Glu Glu Gly Phe Phe Gly Gln
        115                 120                 125

Leu Asn Val Ala Val Ile Glu Ile Thr Arg Ile Thr Glu Glu Gly Tyr
    130                 135                 140

Ile Ile Pro Ser Ser Ser Val Gly Asn Asn Val Glu Trp Leu Asn Ala
145                 150                 155                 160

Ala Glu Lys Val Ile Leu Glu Val Asn Ser Trp Gln Ser Glu Asp Leu
                165                 170                 175

Glu Gly Met His Asp Ile Trp Ser Val Pro Ala Leu Pro Asn Arg Ile
            180                 185                 190

Ala Val Pro Ile Asn Lys Pro Gly Asp Arg Ile Gly Lys Thr Tyr Ile
        195                 200                 205

Glu Phe Asp Thr Asp Lys Val Val Ala Val Val Glu Thr Asn Thr Ala
    210                 215                 220

Asp Arg Asn Ala Pro Phe Lys Pro Val Asp Asp Ile Ser Lys Lys Ile
225                 230                 235                 240

Ala Gly Asn Phe Leu Asp Phe Leu Glu Ser Glu Val Ala Ala Gly Arg
                245                 250                 255

Leu Ser Tyr Ala Gly Tyr Ile Met Gln Ser Gly Val Gly Asn Val Pro
            260                 265                 270

Asn Ala Val Met Ala Gly Leu Leu Glu Ser Lys Phe Glu Asn Ile Gln
        275                 280                 285

Ala Tyr Thr Glu Val Ile Gln Asp Gly Met Val Asp Leu Ile Asp Ala
    290                 295                 300

Gly Lys Met Thr Val Ala Ser Ala Thr Ser Phe Ser Leu Ser Pro Glu
305                 310                 315                 320

Tyr Ala Glu Lys Met Asn Asn Glu Ala Lys Arg Tyr Arg Glu Ser Ile
```

SEQUENCE LISTING

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                325                 330                 335

Ile Leu Arg Pro Gln Gln Ile Ser Asn His Pro Glu Val Ile Arg Arg
            340                 345                 350

Val Gly Leu Ile Ala Thr Asn Gly Leu Ile Glu Ala Asp Ile Tyr Gly
        355                 360                 365

Asn Val Asn Ser Thr Asn Val Ser Gly Ser Arg Val Met Asn Gly Ile
    370                 375                 380

Gly Gly Ser Gly Asp Phe Thr Arg Asn Gly Tyr Ile Ser Ser Phe Ile
385                 390                 395                 400

Thr Pro Ser Glu Ala Lys Gly Gly Ala Ile Ser Ala Ile Val Pro Phe
                405                 410                 415

Ala Ser His Ile Asp His Thr Glu His Asp Val Met Val Val Ile Ser
            420                 425                 430

Glu Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ala Pro Arg Glu Arg Val
        435                 440                 445

Ala Lys Met Ile Gly Leu Ala His Pro Asp Tyr Arg Pro Leu Leu Glu
    450                 455                 460

Glu Tyr Tyr Ala Arg Ala Thr Ser Gly Asp Asn Lys Tyr Met Gln Thr
465                 470                 475                 480

Pro His Asp Leu Ala Thr Ala Phe Asp Phe His Ile Asn Leu Ala Lys
                485                 490                 495

Asn Gly Ser Met Lys Ala
            500
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<210> 477
<211> 498
<212> DNA
<213> Corynebacterium glutamicum

<220>
<221> CDS
<222> (101)..(475)
<223> RXA01288

<400> 477
tgctcaattt cacaccacac gacatcactg gaaaaacctg acatcgccgg ctgatatata 60

tggaaatatc aactccaccc acgttgcggg tacgcgcgtg atg aat ggt atc ggc 115
                                                Met Asn Gly Ile Gly
                                                  1   5

ggc tcg ggc gat ttc acg cgt aac gcc ttt gct tcc aca ttt atc tct 163
Gly Ser Gly Asp Phe Thr Arg Asn Ala Phe Ala Ser Thr Phe Ile Ser
                10   15   20

ccc tcg gca gcc aaa gtt gat gcg att tcc gcg att gtg cct ttc gcg 211
Pro Ser Ala Ala Lys Val Asp Ala Ile Ser Ala Ile Val Pro Phe Ala
            25   30   35

```
tcc cat atc gat cac acg gaa cat gat gcg atg gtt gtc att act gaa   259
Ser His Ile Asp His Thr Glu His Asp Ala Met Val Val Ile Thr Glu
         40                  45                  50

tat ggc tac gca gac ctg cgc ggg cta tcg cca aaa caa cga gtc ccc   307
Tyr Gly Tyr Ala Asp Leu Arg Gly Leu Ser Pro Lys Gln Arg Val Pro
     55                  60                  65

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APPENDIX A: DNA SEQUENCES

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>RXA00231
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>RXA00249
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>RXA00277
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>RXA00299
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>RXA00372-upstream

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>RXA00372
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>RXA00470
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>RXA00621
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>RXA01126
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>RXA01151-upstream
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>RXA01151
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>RXA01571
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>RXA01161-upstream
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>RXA01161
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>RXA01182-upstream
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>RXA01182
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>RXA01189-upstream
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>RXA01189
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>RXA01192-upstream
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>RXA01192
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>RXA01214-upstream
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>RXA01214
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>RXA01224
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>RXA01232-upstream
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>RXA01232
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>RXA01236
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>RXA01250
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>RXA01254
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>RXA01257-upstream
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>RXA01257
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>RXA01270
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>RXA01277-upstream
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>RXA01277
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>RXA01288
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>RXA01302
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>RXA01303
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>RXA01307
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>RXA01324
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>RXA01340-upstream
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>RXA01354
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>RXA01358-upstream
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>RXA01358
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>RXA01385
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>RXA01412
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>RXA01428
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>RXA01430-upstream
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>RXA01435
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>RXA01461
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>RXA01462
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>RXA01465
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>RXA01466-upstream
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>RXA01499-upstream
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>RXA01499
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>RXA01509
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>RXA01589
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>RXA01967
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>RXA02048-downstream
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>RXA02052-upstream
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>RXA02052
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>RXA02064
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>RXA02083
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>RXA02092
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>RXA02098-upstream
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>RXA02098
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>RXA02101-upstream
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>RXA02101
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>RXA02105-upstream
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>RXA02105
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>RXA02111
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>RXA02118-upstream
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>RXA02118
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>RXA02120
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>RXA02126
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>RXA02192
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>RXA02214
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>RXA02215
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>RXA02264-upstream
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>RXA02264
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>RXA02265
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>RXA02274
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>RXA02317-upstream
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>RXA02317
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>RXA02448
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>RXA02470
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>RXN00621-downstream
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>RXN00622-upstream
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>RXN00622
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>RXN00658
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>RXN00675
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>RXN00787-upstream
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>RXN00877
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>RXN03088
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>RXN03091-upstream
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>RXN03091
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>RXN03091-downstream
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>RXN03092-upstream
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>RXN03092
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>RXN03092-downstream
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>RXN03094-upstream
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>RXN03094
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>RXN03094-downstream
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>RXN03128
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>RXN03128-downstream
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>RXN03131-upstream
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>RXN03131
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>RXN03133-upstream
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>RXN03133
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CTTCTCAAAGAGGGGACGCCACTTCCTGCTGGTTTCCGACTAGATGTTGTTCTACACGCC
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>RXN03133-downstream
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>RXN03145-upstream
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>RXN03145
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>RXN03145-downstream
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>RXN03178
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>RXN03178-downstream
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>RXN02021-upstream

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>RXN02021
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>RXN02021-downstream
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RXC00110 - 5′-Region
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CGCTAATTTTAAACACTGGAGGAGCTTCCAC

RXC00110 - coding Region
GTGAGCAACAAAGACGGCCTTTTTACTGACGGTAACAGCACGTTTGCACCTAAGGTGGATTCAATTCCC
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CAAATGTCCAGCCTTTTCCGCGCAGAAGTTGAGCTGGCGAAGACTGAACTCGCAGGCGAAGCCAAGAAA
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RXC00110 - 3′-Region
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RXC01971 - 5′-Region
AGGTCTTGTTTATTTCGGCTACTGATTCAGTAGCTGCGCTCCGATAGGATTCTTAGTTTTCAGTTCAGT
ATCTTTGAGCCACGGCTAGAATGTGAATCCT

RXC01971 - coding Region
ATGTCTAAGAAGAAGCCTCGCCCCATTCCGGTTCCTGCCCAATTTATCCCTGGTCTCATTGATGCGCAT
ACACATTTGGCATCGTGTGGAGGAGATCTTGCAGGGTTGGTGGAAAGGGCCAAGGAGGCGGGCGTCGAA
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CTA

RXC01971 - 3'-Region
TAACGTGAGGTAGCTCACAGTCA

RXS00004 - 5'-Region
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GAAGTATTTTCCAATTCCCGATGTAGGGTCA

RXS00004 - coding Region
GTGCTGACTCAATTGATTGAATCATCGATTTTCGACAACGTTGCGAGCAGGGAGTCCTCTGAATTTCTC
GGCCATGCTGCCATCGATCTACTTGCTGGCCTTGTCTATGAAAAAGCCACTCCCTATGCTCCAGATGAA
GCACTTAGAGTGGCAGTTTATGGCTATATTCGGGAGAACCTTGGATCCTCACAACTTACGGTCGCAGCT
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GCGGAATTAATCCGACACCTCCGATTAGAGGCAGTATATGAAGACCTTCGGGATCCTCGCCTCCAGAAC
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RXS00004 - 3'-Region
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RXS00156 - 5'-Region
ACCGAGAGCGTGGTACGCCTCATTTAGTTTCCTCCTATGAATCTTGATGTGGTTCATGCGTTTTTATGC
AATATCAACCAAAAGTTGGTACGATCCTCAT

RXS00156 - coding Region
ATGAATGAACGCACATCGGATGCATTTGACGCCCTCCTTGTGCTCTCCTTCGGTGGTCCCGAAGGGCAC
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AATGTGGAAAAAGAATTGGCGTCTCGCGATCACAAGCTGCCTGTTTATTTTGGTAACCGCAACTGGAAG
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GCTACCGTTGGCCCCACCGATGAATTCGCAGCCCTTGTGGTTGATCTCATCGAGGAGGCAGAGCTCAAG
CGCGTTATCGAGCGCCTTGGAAAGCTGCCAGCACGCGGAAGTTCCGTCAACGGCGCACCGTGTGGCGAC
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GCCAAC

RXS00156 - 3'-Region
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RXS00166 - 5'-Region
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CGATGTCCGACCTGGATATCCGGCTGAGGCC

RXS00166 - coding Region
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CTAACAGCTGATCAGGTCCTAGCCCTTGATCCAAGCATGGACATGTTGCGGGTGTTTCGCTCCGCGCTT
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CCTGAGGGTGCAGTCCTGCTCGTGTGGAATAACCTGGACACCTCCATCGCGTGGGTACACCGACTCAGT
CGCATTATGCATGCCGGCGATGTACTCAAGCCGGGATTCACCCCAGAAACCGCAGCTCCCTGGATAATT
GATCGAGAAATTCGCACCACGTGGAATCAGCACCTCACCCCTGAAGAAATCATCCAGCTCGCTCACACG
AGGTCCTACTGGTTAAACGCGTCAGAGAAAATCAAAGAGCGTGTTGATCAGAACCTTCAGTGGTATCTC
TACGAGCATTTGGGTTTCAGTCCCGACAATCCAGTGGAACTTCCCTATCGCTGTGATGCATTTTTACTT
TCACGTTCCGGTACCCTGGCAGGCAGATCTTCCAATCTT

RXS00166 - 3′-Region
TAGGAGCCCTCGCCATGTACCTG

RXS00197 - 5′-Region
GTCGATGATATTTTGGCAACCGAATCTGAGGCACGCGCGCGTGCGAATGCTTTGATCAACCGGTTGGCA
ACCAACTTGTAAGCTAAGGAGCTTCCGCCTC

RXS00197 - coding Region
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ATTGTCGCCGATGTGGTCAATCCCATCCGACTCTTTGGC

RXS00197 - 3′-Region
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RXS00288 - 5′-Region
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TGAAACGTACCCAAGGGCTAACATCGGGGGC

RXS00288 - coding Region
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CCTAAAATTTTAGGTTTTGATGCTGCAGGTGAGGTGGTGGCTGTTGGATCGCAGGTCACGCTCTTCAAT
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CAGTTTGAGTCCGTGACAGCAACGGTGCTGGATGGGCTCAACGCTGCAAACATCATGGAGGGGCACCGG
CTCGTTGAGCAGGGTAAAACCTCAGGAAAAATTGTTGTGAGGGTA

RXS00288 - 3′-Region
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RXS00624 - 5′-Region
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GACAACGGCCGGACATGCGACAATACAATGC

RXS00624 - coding Region
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ATTTCAGACCTGCGAGCCGACGGCATCGAGGTCTCATTACTTGTCGCACCCCGCATCGATGGGGACTGG

CGTCTCGCCAAAGACAAAGGGACCCTCGCGTGGATGGAACAACAACGCGAACGCGGCCACGAACTCATC
CTCAACGGTTTCGACCAAGCAGTTCAGGGACGTCGCTCAGAATTCGCCAACCTTGAACGGCACGAAGCA
CGTCTTCGCCTTACCGGTGCCATTAGGCAAATGCAGAAAATTGGCTTCGAATTCCAAATCTTTGCCCCA
CCTCGTTGGAGAATGTCAGAAGGCACCTTCGCGGTACTCCCAGAATTTGATTTCAACGTCGCCGCCTCG
ACCAGGGGATTACATAACCTCGACACCGGCGAATTCTTGGCGTGTAGAAACCTCTCCGTGGGTGAAGGT
TTTGGTGCTGCAAAATGGTGGCGCAAGAATGTCATCAAGGCTGTCACTCGTGGAGCGGAAAAAGGAAAT
ACAGTGCGCTTGTCCGCATCGGCGCGAAATCTCACCAACCCTAAAGTCGCAGCTGACTTCCGGGAAGCT
GCATTAGCTGCCTTGGATTTGGGTGCTCAGGTGCAAACCTATTCTCAGGCGGCCGCACAACTGGCC

RXS00624 - 3′-Region
TAGTTGGGGAGGTTCGGGGCACC

RXS00949 - 5′-Region
GCTCAAGGATCCTTCCTGGGCAAACCAAGCAGCCCTCGCACTAGGTGCGGAACCCAGGTATGTTCACCA
ATACGACTACGTACTTTAAAGGAGAGTTGAC

RXS00949 - coding Region
ATGAAGGTTTTCATCATCGGCGCTGCGGGTGGCATCGGCAATCGACTTTCCAGCCTGCTTCACGCCAGG
GGAGATGCAGTTAGCGGCATGCACCGCAATCTTGAGCAGGCCTCAAAAATCACAGACACTGGGGCAACT
GCCGTACTCGGGGATCTCATCCACAACAGCACGGAGGAGCTTGCGGAGCTTTTCCGCGGTCACGATGCC
ATCGTATTTTCTGCAGGCGCCCACGGAACAGGGCAAGAAAATACCACGCTTATCGACGGCGCCGGCCTC
CGTAAAGCCGCCGACGCTGCCAGCGCGGCCAACGTTTCACGCTTCATCTTGGTCTCTGCGTTTCCGGAA
TCCTCCCGCGGGGAGAACACCACCGAGAACTTTGAGCACTATATGAAGGTGAAGAAGTCCGCCGATGTC
TACCTCAGTCACACTGACCTAGACTGGGTTATTGTCCGACCAGGCGTGCTTCAAGATGAGGCAGGGGAT
GGTTTAGTCACTGCTGGCTTAGCGATTAATTACGGCAATGTTGCTCGCGATAATGTCGCAGCGTTCATT
GATGAAGCTCTGCATCAACCGCAGTTGTCAAAGATCATTGTTGAACTCACCGACGGTTCAACTCCGGTG
GCGGAAGCCGTAGAACGCCTCATCAAG

RXS00949 - 3′-Region
TAAAGACGAAAAGAGGGAGAATG

RXS01000 - 5′-Region
CTTTCTATGCCTACGCGGATGTTTCCGTGATCATTCTGGAAATCCTCATCGTGGTGATTGTCATTGAAG
TAATCTCCAACGCACTTCGAAAGAGGCTGGT

RXS01000 - coding Region
ATGAGCACCTTAACCTCTCACCGCACAGTACCGGCCCCCAGCTCTCCCCCGGCGCGCCCCAACAAACTG
GCGCGCAATATCGTTGCAATTGTCGCTGCGCTGATTGTCCTTATAGCTACCGGCACGCTCAAGATCGAG
TGGAATGAGCTTCCGCAGATGCCCGCGCAGGTGTGGCATTACTTAGAGCTGATGTTTAGCGATCCCGAT
TGGTCGAAGTTTGGCCGCGCCGTCCAGGAAATGTGGCGTTCCATCGCCATGGCGTGGTTGGGTGCCATT
TTATGCGTGGTGGTCTCTGTCCCTCTGGGAATGTTGGCTGCCCGCGGGGTGGGACCTTATTGGCTGCGT
ACCGTTTTACGGTTCGTGTTCGCGGTGATTCGTGCGTTCCCCGAAGTGGTTATCGCAATTATTTTGCTA
ACTGTCACCGGCCTAACTCCTTTTACTGGTGCGCTCGCATTGGGTATCTCCGGTATTGGACAACAGGCA
AAGTGGACCTATGAAGCCATTGAGTCCACTCCCACCGGCCCGTCAGAGGCAGTGCGTGCAGCGGGTGGA
ACTACGCCGGAGGTTCTGCGGTGGGCGTTGTGGCCACAGGTTGCGCCATCCATTGCATCTTTTGCCCTG
TACCGCTTTGAGATCAACATCCGTACCTCTGCGGTATTGGGCATCGTTGGTGCAGGTGGTATCGGTAGT
ATGCTTGCCAATTACACCAACTACAGGCAGTGGGACACCGTGGGCATGCTGCTCATCGTCGTGGTTGTC
GCAACGATGATCGTCGATCTCATCTCCGGCACCATCCGCCGCCGCATCATGAAGGGGGCTAGTGACCGT
GTCGTGGCACCAAGCAAC

RXS01000 - 3′-Region
TGACGCTCCACCAAGCATCCGCA

RXS01002 - 5′-Region
GACTGCTGATACCGCACAGGATGAAATCACTCGTTACGGCGAGATCCTGAAGAAGTTCTCCAACTAATT
TCCCTGTTTCCAATACTCAAGGTGTGCGCAT

RXS01002 - coding Region
ATGAATTCTGATGCTTCGGCTACCACCAACTCCTGGGCTATCAACTTCGACCATGTGTCGGTGACGTAT
CCCAATGGGACGAAAGCCCTCGATGATGTTTCCCTCACCATCAATCCCGGTGAGATGGTTGCCATCGTG
GGTCTGTCAGGATCGGGTAAATCCACGCTGATTCGCACGATCAACGGTCTTGTCCGCGCTACGGAAGGC

ACCGTGACGGTGGGGCCGCATCAGATCAACACCTTGAAGGGGAAAGCACTGCGTGATGCCCGTGGGCAG
ATCGGCATGATTTTCCAGGGGTTCAACCTGTCGGAACGCAGCAGTGTGTTCCAGAATGTTTTGGTGGGC
CGCTTCGCGCACACAGCGTGGTGGCGTAACCTCCTCGGGTTTCCCACGGAGCACGACAAGCAGATTGCT
TTTCACGCGTTGGAGTCCGTGGGCATTTTGCACAAAGTGTGGACCCGAGCTGGTGCTTTGTCGGGTGGA
CAGAAACAGCGCGTTGCTATTGCGCGCGCCTTATCGCAAGATCCGTCTGTCATGCTGGCAGATGAGCCT
GTGGCAAGCCTTGATCCGCCAACCGCGCATTCCGTGATGCGCGATCTAGAAAACATCAACAACGTGGAA
GGCCTCACCGTGTTGGTGAACTTGCACTTGATTGATTTGGCTCGTCAATACACCACAAGGCTTGTGGGT
TTGCGTGCCGGCAAGCTGGTCTATGACGGTCCTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATC
TATGGTCGCCCCATCCAGGCTAAAGACCTGCTAGGTGATCGCGCA

RXS01002 - 3′-Region
TGACCACGCCTTCTTCTACACTT

RXS01003 - 5′-Region
AGCTGGTCTATGACGGTCCTATCTCTGAGGCCACCGATAAAGACTTTGAAGCTATCTATGGTCGCCCCA
TCCAGGCTAAAGACCTGCTAGGTGATCGCGC

RXS01003 - coding Region
ATGACCACGCCTTCTTCTACACTTATCCCACAAAAGCCTCGGGCTGGGGTAAAGACCTATCTCATCATC
GGCGCCATCGTTGTCTTCACCGTGGCAACAGCAACCCCAGCGCTAGGTGGCATTGAGCTTGATTTCGCT
TCCATTGCTGCGAATTGGCGCAATGGTGCCAACAAACTCCTGCAAATGCTGCAGCCCAACTTTGCGTTC
TTGCCTCGTACGTGGCTTCCCATGTTGGAAACCCTGCAGATGGCGCTTGTTGGAGCTGTCTTGTCTGCT
GCCGTATCGGTGCCTTTGACGTTGTGGGCAGCGCAGGCAACCAACACCAGTGCGATTGGTCGTGGCATT
GTCCGCACCATCATTAACGTGGTGCGCTCTGTCCCCGACTTGGTGTATGCCACCATCTTGGTCGCCATG
GTTGGTGTCGGCGCATTACCTGGCATTTTGACGCTGTTTCTGTTCAACCTGGGCATCGTGGTCAAGCTT
GTCTCTGAGGCCATTGATTCCACTGAGCATCCCTATATGGAAGCAGGACGCGCAGCAGGTGGATCACAG
TTCCAAATCAACCGAGTCTCCGCGCTTCCTGAAGTCATGCCGCTCTTTGCCAACCAATGGCTCTACACC
CTAGAGCTGAATGTACGCATCTCCGCCATCCTTGGCATCGTGGGCGCAGGTGGCATCGGCAGGCTGCTT
GATGAACGCCGAGCTTTCTATGCCTACGCGGATGTTTCCGTGATCATTCTGGAAATCCTCATCGTGGTG
ATTGTCATTGAAGTAATCTCCAACGCACTTCGAAAGAGGCTGGTA

RXS01003 - 3′-Region
TGAGCACCTTAACCTCTCACCGC

RXS01114 - 5′-Region
TTCGGTGGAAGATATCCGCAAGCTGGTGCTGCCGCAGCTTTTAGAAACGGCTCAAGCAATTTCGACAGA
TCTCTCTGCACTCTAAATTAAGGATCAAAAA

RXS01114 - coding Region
ATGAACCCTCAAGATATTGTCATCTGTTCCCCATTGCGCACCCCAGTTGGTGCTTACGGCGGATCCTTC
ACCGGCGTCCCTGTTGAAGAATTGGCCACCACCGTGATCAACGCGATCGTTGAGGCAACCGGCATCACC
GGCGACGATGTGGACGATCTGATCCTCGGCCAGGCATCCCCCAACGGTGCGGCTCCAGCACTGGGCCGT
GTTGTTGCTCTAGATTCCAAGCTTGGCCAAAACGTTCCAGGCATGCAGCTTGATCGCCGCTGTGGTTCC
GGCCTGCAGGCAATCGTCACCGCTGCTGCACACGTTGCATCCGGCGCTGCTGATCTGATCATCGCAGGT
GGCGCAGAATCCATGAGCCGCGTTGAGTACACCGTGTCCGGCGATATCCGTTGGGGTGTCAAGGGCGGC
GACATGCAGCTTCGTGACCGCCTTGCAGAAGCACGCGAAACCGCTGGCGGACGCAACCACCCGATCCCT
GGTGGCATGATCGAGACCGCTGAGAACCTGCGTCGCGAATACGGCATCTCCCGCGAGGAGCAGGACAAG
ATCTCCGCAGCGTCCCAGCAGCGTTGGGGCAAGGCTGCTGATGCGGGGCTTTTCGACGACGAGATCGTG
CCAGTCACCGTCCCTGCCAAGAAGCGCGGCCAGGAGCCAACCATCGTTTCTCGAGACGAGCATGGTCGA
CCAGGAACAACCGTCGAAAAGCTTGCTGCTTTGCGCCCCATCATGGGCCGCCAGGATGCGGAAGCAACC
GTCACCGCTGGCAACGCGTCCGGCCAAAATGATGGCGCTGCTGCCGTCATCGTGACCACTCGCGCCAAG
GCCGAGGAGAAGGGCCTGCGCCCAGTCATGCGTTTGGCTGGCTGGTCTGTGGCTGCTGTTCCCCCAGAG
ACCATGGGTATTGGACCTGTTCCTGCCACCAAGAAGGTCCTGGATCGTTTGGGCCTTACCCTGGAGGAC
ATCGGCGCGATCGAACTCAACGAAGCTTTCGCAGCTCAGGCACTGTCTGTGCTGAAGGAATGGAACATT
TCTTGGGAAGATGAGCGCGTCAACCCACTGGGTTCCGGTATTTCCATGGGACACCCAGTCGGTGCCACC
GGTGCTCGCATGGCAGTAACCTTGGCTCACCGCATGCAGCGTGAAAACACTCAGTACGGACTGGCCACC
ATGTGCATCGGTGGCGGCCAGGGTCTTGCAGCTGTCTTTGAAAAGGAGAAC

RXS01114 - 3′-Region
TAAAAATGGCTATTTTGCACAGC

RXS01205 - coding Region
GTATCGGCCTATCCGCCGGCCATCATCGCAGCGGCTCTCGTAGGAATTTGCGCGGGAGTTTTGCCCCAT
AATTTTGAACCCTCGCGAATATTTATGGGCGATTCCGGCTCCATGCTCATCGGCCTGCTGTTGGCTGCA
GCATCGACCTCAGCGTCAGGAAAAATCAACATGAGCCTGTATGGCGCAGCTGATTTTATCGCATTGATC
TCACCCATCATCGTTGTTCTCGCCGCCGTGGCCATCCCACTGCTCGACCTCGTGATGGCAGTGGTTAGG
CGCGTGGGCAGGGGAGCATCACCCTTTTCCCCGGACAAAATGCATCTGCACCACCGACTGCTGTCCATC
GGACACACCCATAGGCGCGTGGTCCTAGTGCTCTACACCTGGGCGAGCGCCGTGGCATTCGGCGCAGTG
AGCTTCTCCGTCGTTCCGCCACTGTTTGCCACCGGATCGAGCATCTGTGGCATCCTCATCGCCGTCGCT
GTCACAGCCGTGCCAGTGATGAAAAGCCGGCGAGCCGCCAAACTTGAT

RXS01205 - 3′-Region
TAAGTGATTGTCACTTTGGATTG

RXS01223 - 5′-Region
GCGGGAGTGGACGGGCCGCCAGCCATCGGGGCGACAATCACGGGAGTTTTCAACGTGTCAAGGATGCTC
ATGGCACCATCCTAGGCGCGCCTGCCATAGG

RXS01223 - coding Region
ATGACTTCCGTGAGTTTTTTGTCTAAAATCCAAGCACTGTTTGCCCCCAAGCCTGAACTTCCCGCCGCC
AAATGGCTGGTCGTGGGCCTGGGCAACCCCGGCGCCAAGTACGAATCCACCCGACACAACGTCGGTTAC
ATGTGCCAAGACATGCTTATCGACGCCCACCAGCAGCAGCCCCTCACCCCCGCCACGGGCTACAAGGCC
CTCACAACGCAGCTCGCACCAGGGGTGCTCGCCGTTCGATCCACCACTTTTATGAACCACTCCGGCCAA
GGTGTCGCACCGATCGCCGCAGCGTTGGGTATCCCAGCAGAGCGCATCATCGTGATCCACGACGAGCTC
GATCTGCCCGCTGGAAAAGTACGCCTGAAAAAGGGCGGAAACGAAAACGGTCACAACGGCCTGAAATCC
CTCACGGAAGAGCTCGGCACCAGAGACTACCTGCGCGTCCGCATCGGCATTTCACGACCACCAGCAGGA
ATGGCCGTGCCCGACTACGTTTTGGAACCAGTCGATCACGACCAACCAGGCATTGAACTTGCCGCCGAG
GCAGTGGATTTGCTGCTGGCCCAGGGATTATCTGCTGCGCAAAACGCTATCCACAGCCGC

RXS01223 - 3′-Region
TAGATTGCTAGAGATTCCCGCAC

RXS01269 - 5′-Region
GATTATCTCTGCGCCGATTCAGCTGGCAATAGCAGCAGTTGTATTGAGAGCTCATGGTCGTCCGATTCT
ATTTCGTCAACCACGACCTGGGAAAGACGGT

RXS01269 - coding Region
GTGGTATTTGAGATGATTAAGTTTCGAACCATGCTTGAACCAGATGAAAAACATGTAACTGATGAACAG
CGTCTAACTAAAGTTGGAAAGCTTCTGCGGGAAACGAGTTTAGATGAGTTACCTACACTCTGGAATGTA
TTTAAAGGTGATATGAGCCTTGTAGGGCCTCGACCTTTGCTTGTTAGCTATCTGGAACATTACTCTTCT
GAACAAGCTCGACGCCATGAAGTTCGTCCTGGGATTACTGGTTTGGCTCAGGTGAATGGCCGTAATCAA
ACTACTTGGGATGAACGACTTAAGTTGGATGTCGAATATGTGGATCGCTGTAGTTTGAAACTAGATTTC
AAAATATTAATCGCCACTGTAAAAACAGTTCTTTCTAAAAAGGGCATTAGTAATGAAGGTCATGTCACG
ATGCCATCCTTCATTGAAGAAAGAAAA
RXS01269 - 3′-Region
TAGCAGGTAAAAATTTTACTTTC

RXS01421 - 5′-Region
TTGATGCACGTGCAGAAATCGTCGGCGGTCCGTGGCACCCATCTGTTAAGGGAGACTCGGTTACTGCAG
GGATCCTGCGAGATCGAGTAAACGCCTAAAG

RXS01421 - coding Region
ATGACGTCGAAAAGCATTAGCGGCAAGCGCCCGAATCTGCCGTCGCTCACTGGAGCGCGGTGGCTCGCG
GCGCTCGCTGTTTATTTTTTGCATGCGTTGGTGTTTTTGTCGGTGTATCCGTTCCAGCAGTCGGAACTG
TTTGCCACAATCCATAAATTTGTCCCCATGCAGCTGGGTTCAGCTGGTGTAACCTTCTTCTTTATCTTG
TCCGGATTTTTGATCTATTGGTCAAATAGCCAGCTCAAGGGCATGAAGAATGTGCTGTATTACTGCAAG
CGCCGCATCACCAAGATTTATCCCATGCACTTGATTGCGTTGCCGATGTTTATTGAGGCGTCGGCGAAG
TTCACGACTACAGGCATTACCTGGGTGCTGATTTTGCGCGAG

RXS01421 - 3′-Region
TAAAGCTGTGGCTGCGGAATGCG

RXS01491 - 5'-Region
AACGGTGTGAAACACATTGAAGTGTCGTTGGGTTATCCGCGCGAATGGGAGCATTGGTCTGGGCAGCAT
GTGTGGCCATATCCAGTGATGGAGGTGGACA

RXS01491 - coding Region
ATGCTGGATGAGTCTTTGTTTCCAAATTCGGCAAAGTTTTCTTTCATTAAAACTGGCGATGCTGTTAAT
TTAGACCATTTCCATCAGTTGCATCCGTTGGAAAAGGCACTGGTAGCGCACTCGGTTGATATTAGAAAA
GCAGAGTTTGGAGATGCCAGGTGGTGTGCACATCAGGCACTCCAAGCTTTGGGACGAGATAGCGGTGAT
CCCATTTTGCGTGGGGAACGAGGAATGCCATTGTGGCCTTCTTCGGTGTCTGGTTCATTGACCCACACT
GACGGATTCCGAGCTGCTGTTGTGGCGCCACGATTGTTGGTGCGTTCTATGGGATTGGATGCCGAACCT
GCGGAGCCGTTGCCCAAGGATGTTTTGGGTTCAATCGCTCGGGTGGGGGAGATTCCTCAACTTAAGCGC
TTGGAGGAACAAGGTGTGCACTGCGCGGATCGCCTGCTGTTTTGTGCCAAGGAAGCAACATACAAAGCG
TGGTTCCCGCTGACGCATAGGTGGCTTGGTTTTGAACAAGCTGAGATCGACTTGCGTGATGATGGCACT
TTTGTGTCCTATTTGCTGGTTCGACCAACTCCAGTGCCGTTTATTTCAGGTAAATGGGTACTGCGTGAT
GGTTATGTCATAGCTGCGACTGCAGTGACT

RXS01491 - 3'-Region
TGAACTGGATGGAGAGGATACCT

RXS01572 - 5'-Region
CTGCTGTGCGCAGGCATCACCACCTACTCCCCAATCGCTCGCTGGAACGTTAAAGAAGGCGACAAAGTA
GCAGTCATGGGCCTCGGCGGGACTCGGACAC

RXS01572 - coding Region
ATGGGTGTCCAGATCGCTGCAGCCAAGGGTGCTGAGGTTACCGTTCTGTCCCGTTCCCTGCGCAAGGCA
GAACTTGCCAAGGAACTCGGCGCAGCTCGCACGCTTGCGACTTCTGATGAGGATTTCTTCACCGAACAC
GCCGGTGAATTCGACTTCATCCTCAACACCATTAGCGCATCCATCCCAGTCGACAAGTACCTGAGCCTT
CTCAAGCCACACGGTGTCATGGCTGTTGTCGGTCTGCCACCAGAGAAGCAGCCACTGAGCTTCGGTGCG
CTCATCGGCGGCGGAAAAGTCCTCACCGGATCCAACATTGGCGGCATCCCTGAAACCCAGGAAATGCTC
GACTTCTGTGCAAAACACGGCCTCGGTGCGATGATCGAAACTGTCGGCGTCAACGATGTTGATGCAGCC
TACGACCGTGTTGTTGCCGGCGACGTTCAGTTCCGCGTTGTCATTGATACTGCTTCGTTTGCTGAGGTT
GAGGCGGTT

RXS01572 - 3'-Region
TAGGTTTACTGAAGTTCAGACTT

RXS01642 - 5'-Region
TTGGAATCACTGTGTCTTGCAGCTAGTCTGCCACTCGCACTGCATTTGCTGGATGTATTTGGAATGCTG
CGCGGTCTTGATATTGGATTCGGTGGATAAG

RXS01642 - coding Region
ATGCGCAGACTCATCGCGGTTAGCTTGGCCGCTCTGTTTATGTTGGCTTCCACTCCAGCGACGAGGGCA
CAGGAAGTAGAAGCTCTCGCTTGCCCCGAGGTAGCGATCGCCGATCCTTCCTCCGCAGTTTTAGATGAA
CACCTTTCGCAGTCATTATCCCAAGCTCACCAACTAGCAACTGGCGCCGGTGTGATGGTGGCAGTCATC
GACACCGGAGTATCCCTGCATCCACGTCTGCCCCACTTAATTCCCGGCGGTGATTTCGTGGGCGCCCAC
CAAAGCCCCGATGTGCCAGGTGAACTTATCGATTGCGACGGCCACGGCACCATCGTCGCCGGAATCATC
GCCTCCCAAGGAAACCCCGGCACCGGCTGGCCATATGACGGCAGCTCCGATCCTTATATCGGTGTCGCC
CCAGATTCCGGAATCATCTCCATTAAACAAACCAGCTCATATGTGCGTACTCGTGAAGATTCCAACGTC
GGAACGCTGAGCACCCTGGCGGAATCCATCCACCGAGCTCTCGATTCCGGTGCCCACGTGATCAATATT
TCCGTGGTGTCCTGTTTGCCCCAATCACCCGACGAGGCCGCATCGTTCCAGCCTCTGACGGATGCTCTT
AACAGAGCAGAACTTCAAGGGGTGATAGTGGTGGCAGCAGCAGGAAACCTCGGGCAGGATTGTCCAGTT
GGATCTACCGTTTATCCTGCACATTCAGACACTGTGCTCTCTGTGTCGGCACGTTTTGATTCTCACACG
CTTGCAGAATATTCCATGCCTGGCAACCAACAAATCCTCTCTGCACCAAGCCACATTCAGGCTGGTCTA
TCACCGCGTGGCGACGGCTTCGCCAGCCACATGATCACCACCGCTGGCGAAAGCCCCTTCGAGGGCACC
AGTTTTGCCGCTCCAGTTGTCAGCGCCACAGCTGCACTGCTTCGCCAGCATTTTCCCTTTGCCACACCC
TATGAAATTCGTGCACGAATCTTCAACAGCATCGACCCTGCAAGAGGCGCTATTGATCCCTACCTGGCA
CTTACTCAAGAAATCTATCCCACCACTCCCCTGGTTCATGAGATCGCACTAAGTGTTCCCACGCCGCCG
GATGATTCTCCACGGGAGCGGGGCATCCTAGTTACCGCAATCATTGTTGGGTTGCTCGCAGTGTTAGCT
GTGCTGATGGGACTACGCCGAATTCATCATCACTCGGCCTTTCAAAAAGCTAGCTCAAGTGTTATCACT

RXS01642 - 3'-Region

TAATCTATGAGGCACCGTTCAGA

RXS01902 - 5'-Region
GGCTGGTCCGAAGTGCAAACCTTCAACACCGGCACCTACGGTGACAACTGGAACTTCCTCTTCTTCGGC
GACACCCAGCTGTACAACACCCACTCCAACC

RXS01902 - coding Region
GTGCAGAAGAAGTCCAGAACTGGGCAAACAACCTGGAACGGCGGCCCACCAATCGAAAACCCAGGAACC
TCCTTCATCCTCTCCGCGGGTGATCAGGCAAACCACTCCAGCTGGGACGAGCACTCCGCATACATCTCC
CCAGAAACCCTGCGCAACTACCGTCTGGCCGTGAACAATGGAAACCACGACCAGTACAACTACGACGCC
TACAACGCGATGTACCCACGCCCTAACCAGGTCGATGAGAACTACTTCTTCGAGTACAACAATGCACTC
TTCCTGTCCCTGGACTCCAACGACTACTTGGACATCGACGACGACATCGCATTCCTTCGCGACACCGTC
GCAGCACACGGTGACGACAAGGACTGGATCGTCCTGACCTACCACCATTCCACTTTCTCCCAGGCCTAC
CACATGGATGACGCTCGCATTAAGTACCAGCGCGAACGCCTCACCCCAGTGATCTCTGAACTGAACGTT
GACTTGGTTCTCGGTGGACACGACCACATCTACACCCGCTCCCACCTGATGAACGGCTTCACCCCAGTC
GATGCAGGCCGCGAAGCAGTTGTCGGTGAAACTCTGAACCCTAAGGCCGGCGAAGTTGTTTACCTTGCA
ACCAACTCTTCCTCAGGCTCCAAGTTCTACGACTTCTACGACTTCCAGCTCGGCCAGCGTTACGACACC
GGACTGGATTTCCAGGAAACCGTCGATCAGAAGAAGATCCGCACCTACACCGCAGTCTGGAACCAGGAC
CAGGTTCAGGACTACACCAACGTTGAACTGACCCCAGAAGGCCTGACTGTGACCACTAAGGACGCAGTC
TCCGGCGAGCTGGTTGACCAGTTCACCCTGAGCAAGCAGGACCGCGACGAAGAATCTGAAGTCCCAGTT
GAAGATGACAAGGACGGAGACAACGCGACCGGCTCCTCCAACCTTGGTCTAGCTGCTATCTTGGCTCCA
GTTCTGGCCATCTTCGGTTTCGTCGGTGGACTCTTTGTTGGCGGCGGCTCCCTCGCTGAGTTCTTTGCC
AACCTCGGCGTGAAGATGCCTTTC

RXS01902 - 3'-Region
TAATACTGTCTGAGATTCAAGCA

RXS02453 - 5'-Region
AACCAACAAAGGTCATCTCAACCGGCTTAAGAAAATTCTGCCAGCTTTCTGCTGATTGAATCGTGCCAG
CTCAGGGCATATCTCACCTAAAGTAAACACC

RXS02453 - coding Region
ATGAAATCAATCTTCATTTCCGGTGCGGCGAACGGAATTGGCAAAGCTGTGGCGTTGAAATTTCTTCAC
GAAGGTTGGCTCGTTGGAGCCTACGACCTCGCGGAAATCACCTACTCACACCCCAATCTTCGCTGGGGC
TACCTCAATGTTCGACAGTCCGAGTCGTGGGACAAAGCCCTAGAAGACTTTGCGACGCACACCGGAGGC
ACCATCGATGTGGTGGACAATAATGCCGGCGTAATTATTGAGGGACCGCTGCAGGACGCAGAGGAGGGG
AGCGTCGACAAGCTTCTTGCAATCAACGTCAATGGCGTGACTCTTGGTGCCCGCGCCGCTCATCCTTAT
TTGGCGCGCACGCCGGGCGCCCAGTTGTTAAACATGTCCTCGGCGTCGGCGGTGTACGGGCAGCCCCAG
ATCGCGGTGTATTCGGCTTCGAAGTTTTACGTCGCAGGTCTTACTGAGGCGCTGAATTTGGAGTGGCGG
AAAGACGATATTCGCGTGGTCGATGTTTGGCCTTTGTGGGCGAAAACCGATTTGGTGAACGGCGTGAAG
GCTAAGTCACTGAAGCGTTTGGGTGTCCGGATCACTCCGGAACAGGTGGCACAGGCGGTATGGGATGCG
GTGCATCCGAAATCTCGGTGGGCGAAGGGAAAGGTGCATCACGGGGTGTCAAAGTTGGATAAGGCGCTG
TATCTCATGAAATCTCTGTCGCCTGATCGGGTAGCGATGTGTTTTGCGCGACTAATCGCCGGA
RXS02453 - 3'-Region
TAAATGAATTGATTATTTTAGGC

RXS02474 - 5'-Region
TGCTGGTCTATTGTGGCGACCGAGGGCCTTTGAAGGTTCGACAAACTGTATAAGGCCTTGAATCTTGAG
AATTTATTTTGAGGAAGCAAGAGGAAGTGTC

RXS02474 - coding Region
ATGAGCAAAGTTGCAATGGTTACCGGTGGTGCACAAGGCATCGGTCGTGGAATTTCAGAGAAGCTGGCA
GCAGATGGTTTCGATATTGCCGTAGCCGACCTGCCACAACAGGAAGAACAAGCTGCAGAGACCATCAAG
TTGATTGAAGCTGCAGGTCAAAAGGCTGTATTCGTTGGATTAGATGTCACCGATAAGGCTAATTTCGAC
AGTGCAATTGATGAGGCAGCAGAGAAACTTGGCGGCTTCGATGTGCTAGTAAACAACGCCGGCATCGCA
CAAATTAAGCCACTTCTGGAAGTCACCGAAGAAGACCTAAAGCAGATCTACTCCGTGAACGTTTTTAGC
GTATTTTTTGGTATTCAAGCAGCATCCCGAAAGTTCGATGAGCTTGGCGTAAAAGGCAAGATCATCAAC
GCTGCATCAATCGCTGCTATCCAAGGTTTCCCAATCTTGAGCGCCTACTCCACCACCAAATTCGCGGTT
CGTGGCCTCACCCAGGCTGCTGCGCAAGAACTCGCACCCAAGGGTCACACCGTGAATGCCTACGCACCT
GGCATCGTGGGCACCGGAATGTGGGAGCAAATCGATGCCGAGCTTTCCAAGATCAACGGCAAGCCAATC
GGTGAGAACTTCAAGGAGTACTCCTCCTCAATCGCATTGGGCCGACCATCAGTACCTGAGGATGTAGCC

GGTCTGGTTTCGTTCCTGGCTTCTGAAAACTCCAACTACATCACCGGACAGGTCATGCTTGTCGACGGC
GGCATGCTCTACAAC

RXS02474 - 3'-Region
TAGGGGTTGCTTTCCCGCACTCA

RXS02485 - 5'-Region
CGGTGGTCAGTGCTTGGTGCACCTTGCCGACGGGCTGATTGATCGTAATGGTGTTTTCTGTACGCGTTG
CCATGAGGATAAGACTACCGTTAGTGGGGTG

RXS02485 - coding Region
TTGGATTCATCGCTAGCCCAGGAAATCGCCGCGATCGACGGCGTCGAACTCGATTCGGAAGTCACTTTC
GCCGATCTGACGACCCTCCGCATCGGCGGAAAACCCCGCAGCGCCGTACGTTGCCAGACCACGGAGGCG
CTGGTCAGCGCCATAAAATTGCTTGACGACGCCTCCCTCCCCCTCCTCATTGTCGGCGGCGGGTCCAAT
CTCGTCGTGGCCGACGGCGATCTGGATGTTATTGCCGTCATCATCGAAACCGACGACGTCTCCATCAAC
CTCACCGACGGTCTCCTCACCGCCGATGCAGGCGCTGTTTGGGACGATGTTGTCCACCTTTCGGTGGAT
GCCGGCCTCGGTGGAATTGAATGCCTCTCCGGAATCCCCGGCTCCGCCGGCGCCACCCCAGTCCAAAAC
GTGGGCGCCTACGGCACGGAAGTTTCCGATGTACTCACCCGCGTCCAGCTTCTCGACCGCACCACCCAC
CAAGTCTCCTGGGTCGACGCCTCCGAACTCGACCTCTCTTACCGATACTCCAATCTCAAATTCACCAAC
CGCGCAGTCGTCTTGGCGATCGAACTCCAGCTCCTCACCGACGGATTGTCCGCGCCGCTACGTTTTGGT
GAATTGGGACGTCGATTAGCGATCTCCGAGGCCGAACCCCACCCACGTCGCCCCGTCCGCATGGTCCGC
GACGCCGTCCTAGAACTCCGCCGCGCCAAAGGCATGGTCGTGGAACACACCGACCACGACACCTGGTCC
GCCGGATCCTTCTTCACCAACCCAATCGTCGACCCAGCCCTTGCCGACGCAGTCTTTGAAAAAGTCGGC
GAACCCACCATGCCCCGCTTCCCAGCCGGCGATGGCAAAGAAAAACTCTCCGCAGCCTGGCTCATCGAA
CGCGCCGGCTTCAAAAAGGGACACCCCGGCGCAGGCGCAAAAGCCTCCCTGAGCACCAAACACACCCTC
GCACTCACCAACCGTGGCGACGCCCGCGCCTCCGACCTCGTCGCATTAGCCAAAGAAATCCGCGACGGA
GTCCTCGAAACCTTCGGCGTCACCCTCGTCCCAGAACCCGTCTGGATTGGAATCAGCATCGATGAC

RXS02485 - 3'-Region
TGAATTTTCCGACGTCCCTGGCA

RXS02539 - 5'-Region
GGCTGCTAAGCGTGCGAATGTGCGCGTTGTCACAATCGTTGACCAAGTGTCACCTGACGCACAGGTAGT
GCTCAGGTGGAGGTGGCCCAAAGGAGACCCA

RXS02539 - coding Region
ATGACTGTCTACGCAAATCCAGGAACCGAAGGCTCGATCGTTAACTATGAAAAGCGCTACGAGAACTAC
ATTGGTGGCAAGTGGGTTCCACCGGTAGAGGGCCAGTACCTTGAGAACATTTCACCTGTCACTGGTGAA
GTTTTCTGTGAGGTCGCACGTGGCACCGCAGCGGACGTGGAGCTTGCACTGGATGCTGCACATGCAGCC
GCTGATGCGTGGGGCAAGACTTCTGTCGCTGAACGTGCTCTGATCCTGCACCGCATTGCGGACCGCATG
GAAGAGCACCTGGAAGAAATCGCAGTTGCAGAAACCTGGGAGAACGGCAAGGCAGTCCGTGAGACTCTT
GCTGCAGATATCCCACTGGCAATCGACCACTTCCGCTACTTTGCTGGCGCGATCCGTGCTCAGGAAGAT
CGTTCCTCACAGATCGACCACAACACTGTTGCTTACCACTTCAACGAGCCAATCGGTGTTGTTGGTCAG
ATCATTCCTTGGAACTTCCCAATCCTCATGGCTACCTGGAAGCTCGCACCGGCACTTGCTGCAGGTAAC
GCGATCGTCATGAAGCCAGCTGAGCAGACCCCAGCATCCATTTTGTATCTGATTAACATCATCGGCGAT
CTCATCCCAGAGGGCGTCCTCAACATCGTCAACGGACTCGGCGGTGAAGCAGGCGCTGCACTGTCCGGC
TCTAATCGGATTGGCAAGATTGCTTTCACCGGTTCCACCGAGGTCGGCAAGCTGATCAACCGCGCTGCA
TCCGACAAGATCATTCCTGTCACCCTGGAGCTCGGCGGTAAGTCCCCATCCATCTTCTTCTCCGATGTT
CTGTCACAGGATGACGCCTTCGCAGAGAAGGCAGTTGAAGGCTTCGCGATGTTCGCCCTCAATCAGGGT
GAAGTTTGTACCTGTCCTTCCCGTGCACTTGTTCATGAGTCCATCGCTGATGAATTCCTCGAGCTTGGC
GTGAAGCGAGTTCAGAACATCAAGCTGGGTAACCCACTTGATACTGAAACCATGATGGGTGCTCAGGCG
TCCCAGGAGCAGATGGACAAGATCTCCTCCTACCTGAAGATCGGCCCAGAAGAAGGCGCTCAAACCCTC
ACTGGTGGCAAGGTCAACAAGGTTGATGGCATGGAGAACGGTTACTACATTGAGCCAACCGTTTTCCGC
GGCACCAACGACATGAGGATCTTCCGCGAGGAAATCTTCGGACCAGTCCTTTCTGTTGCTACCTTCAGC
GACTTCGATGAGGCCATCCGTATTGCAAACGACACCAACTACGGCCTCGGCGCTGGTGTCTGGAGCCGT
GACCAAAACACCATTTATCGTGCAGGTCGCGCAATCCAGGCTGGTCGAGTTTGGGTCAACCAGTACCAC
AACTACCCAGCGCACTCCGCTTTCGGTGGATACAAGGAGTCCGGCATCGGCCGTGAGAACCACCTCATG
ATGCTGAACCACTACCAGCAGACCAAGAACCTGTTGGTCTCCTACGATCCAAACCCAACCGGACTGTTC

RXS02539 - 3'-Region
TGATCTAAGCGTTAAGTCCTAGA

RXS02554 - 5'-Region
GCTTTTGAAGTGTGTCGCGTGTGCGGACTGAAATAGTTTCCGCTTCAACTTGGTTGCTAAGGATAGGCT
CCATAAAAATAACCAAAGGCGGAAAATTTCA

RXS02554 - coding Region
ATGTCACACACTAAGCCATCCATTGCCATCCTCGGTGCTGGCCGAGTGGGTTCTTCACTTGCCAGGTCA
GCGGTCGCCGCAGGCTATGAGGTAAAGGTTGCTGGTTCAGGTGCTGTGGACAAAATCGCTCTTACCGCT
GAGATCCTTATGCCCGGCGCGGTTCCAAGCACTGCTGACCAGGCTGTAAAGGATGCAGATATTGTGTTC
TTGGCTGTTCCCCTGCATAAATTCCGCAGTGTCAATCCAGCCACTTTAGAGGGCAAGATCGTTATTGAC
ACGATGAACCACTGGGTTCCGGTCAATGGTGAGTTGGAGGAAATTGATCAGGATCCGCGCAGCACTTCG
GAGATTATTGCGGAGTTTTTCGCGGGATCAACCATGGTGAAGTCTTTTAACCACATTGGTTATCACGAG
ATTGAGCAGGATGCGGGTACCGGGCGTGCGATTGCGTATGCCACGGATGATGTGGATGCAGGTGCCCAG
GTTGCACAGCTAATTAAGAGTTTTGGGTTTGTTCCTTTAAATATTGGCGCATTGGAAAACGGCCGTATT
CTGGAACCTGGCCAAGAAGCTTTCGGCGCGCACCTTAATAAAGATTCGCGCCTAGAACTTGTTAATCAG
CGG

RXS02554 - 3'-Region
TAGTACCTCGATCTTCAGCCAAC

RXS02560 - 5'-Region
TTGGGGCAAGCCAGCTAACGCATTTCTTGTGGAAACCGCAGACATTGAGGCCGCCCACGCGGAACTTCT
AAGAGCAGTGGAATGAAATAATCCGGTGCTG

RXS02560 - coding Region
ATGCAGGGCAACTCGCTTAATCTGGCAGACAACAGCGAGAGAAAGAAGCCCATGCCGTCACCAGGAGAA
CTTTTAGCCGCCCGCTACGGACAACCTGCAACCTGGACGCCACCGCAGTGGAATGAGACGCTTGATGTC
ATTCACCAGCATCGATCAGTTCGCAGGTGGTTGGATAAACCGGTTGATGATGACACCATCCGCACCATT
ATTTCCGCCGCACAATCGGCTGGAACCTCTTCCAATAAGCAGGTCATTTCTGTCATCGTGGTTAAAGAT
CCTGAGCTGAGGAAAGGCCTCGCGGGGATCACTCGCCAGATGTTTCCGCACCTTGAGCAGGTTCCCGCG
GTGCTGATTTGGTTGATTGATTATTCCCGAATCAGTGCGGTGGCAGCCAGAGAAGATCTCCCAACAGGG
GCTCTTGATTATCTCGATGAGGCCGCGTGGGGGTTCCTCGACGCCGGAATCGCAGCTCAAAACGCTGCA
ATTGCTGCGGAGTCACTTGGATTGGGAACGCTCTATTTGGGTTCGGTGCGCAACGATGCGGAAGCCGTG
CACAAATTGCTTGGCCTTCCACCTGAGATCGTGCCTGTCGTGGGCTTGGAAATGGGGCATGCGGATCCG
CCTGAACCTGCCGGAATTAAACCTCCCCTGCCACAAGAAGCCATTGTTCACTGGGATACCTACACCGAG
AAAAACCTCGAACTTATCGATTCCTACGACCGCGCCCTCGACACTTACTATTCTCGCTACGGCCAGCAC
CAGCTCTGGTCGAAGCAGACGGCGCATAGGGCGGCGTCGAAAAGCTTTTCAAAAACCAACAGGCAGTTC
CTTAGGGGCGTGTTTGAGCGCGCCGGGTTTGGGCTGAGA

RXS02560 - 3'-Region
TAAAAGCATGATTATGGACGCCT

RXS02578 - 5'-Region
GGCAAAAATGAGGAACAGCACGCCCGCAATAATGAGGACCGTTGCAGATCGCTTCATAAAAACAGCCCA
CACCTTTCCGCTAAACTCGCATGTTGAAATA

RXS02578 - coding Region
ATGTCTACCCAATCATATGCACCCATCCGCCATCGCGGATTCATCAGCTCACTCGAGGGACTACGCGCA
ATCGCCTCCCTGGGAGTCTTGGCGACCCACGTTGCATTCCAAACCTCCGTCGACCCCGCCAGCAACATC
GGTGCAGTACTCGCGCGTTTCGACTTTTTCGTCGCCGTCTTCTTCGCCCTCTCCGCCTTCGTTCTTTGG
CGACGCCGCGCCGGGCAACCAGTGGGACTGTACTACCTCAAACGCCTAGCCCGCATCATGCCCGCATAC
TGGGCAACGGTCATTGCAGTCCTGCTGTTTATTCCCACCGGCCCCTGGTTAGCCAACCTGACGATGACC
CAAATCTACTGGCCAGACGGGCTCATGACAGGCCTCACCCACCTTTGGTCCCTGTGCGTGGAAGTGGCG
TTTTACCTGGTGATGCCGCTTCTCGCGTGGGTGTTGGATAGGTTTGGTCGGCCGGTGCGCATCCTGTTG
ATTGTTGGTGGGGCAGTGTTGAGTCTGGCGTGGCCGTGGATTCCCCTTGTGGAGCATGCGTTGGACGAG
GGGTGGGCGAACATGCAGATCTGGCCACCCGCTTACGCTTGCTGGTTTGCAGTCGGCATGATCGCCGCA
GAAATTGAAGGAGTTCGATTCCCACGGGTTCCGAGCTTTGTGTGGGTGGGTTTAGCTTTAGTGGTCGCT
TGGATCGCGGGCCAAGAATGGTTCGGACCACTAGGTTTAGTGCACCCCAGCCCCTGGGAATTCAACTTA
AGAGTCCTCGCGGGCACACTTTTCGCTGTATTTCTGGTGGTTCCCTACGCGCTGGGTACGCCCTCTCGG
CTTCTTGATTCCAGTTGGATGAAAACGCTCGGCACCTGGTCGTATTCCATCTTCCTCTGGCACCTTCCC
GTGCTGACGATTGTGTTCCCACTGCTCGGGTTGCCTTTATTTAGTGGAAATTTCCTGTTGGTGTTCATC

GTGACGGTCTTGTTGACGATCCCAGTTGCCGCCATCAGCTACACCTTCATCGAAGAGCCCATCAGCGGT
GGACCCGGCGCGCCATTCAGGCTGGGGGTCGTTAGGATTCACCATTTTTCTGGGGGTAGGTCTGGAAAA

RXS02578 - 3′-Region
TGATGAATTGGCACCACGTCAAG

RXS02741 - 5′-Region
ACTGGTCACCTGGTTTGGTCTGCACTCTGACTCCCCTCAAAAGGGCACAATTTGGTCAATTTCCCAACC
TTGTCTTTCAGTCATGGTTAGTGTGGGAACC

RXS02741 - coding Region
ATGAAGGCAATCTTAGTTTCCCGCACCGGCGGACCAGAGGTGTTGGAGTTCACCGACACTGACGCCCCA
AAGCCCACTGATGATCAGGTTTTAGTTGAAGTTGATATGGCTGGCGTCAACTTTATTGATACTTACTAT
CGCCAGGGTGAATATCACGCTCGCCTGCCGTTTATCCCAGGTTTTGAAGGCACTGGTCGGGTGTTGGAG
GATCCGCAGGGGTTGATTGCGGCGGGTACCAAGGTGGCGTGGTGTGATGCCATGGGTTCGTATGCTCAG
CAGGTGTGTGTGCCGCGGGATCGCTTGGTGGCGGTTCCCGAGGGCGTGAGTTCGGAAGTGGCTGCGTCG
ATGTTGATGCAGGGAATCACTGCGCATTATCTAACCAATGGTGTGTATGAGCTTGAAGAGGGCGATTCT
TGCCTCATCACTGCTGGCGCGGGTGGTGTTGGATTGTTGGCTACGCAGATGGCGGCGGCCAAGGGAGTG
CGCGTGTACAGCGTGGTGTCCACGGATGAAAAAGCTGAGCTTGCTTTGGATGCCGGTGCTTATGAGGTG
TTTCGTTATTCCGATAATTTGGCGGAGCAGGTTCGTCGGCACAACGGGGGTCGCGGAGTTGATGTGGTG
TATGACGGTGTCGGCCAGTCCACGTTCAATGAGTCCTTAGAGGCTGTTCGTCCGCGCGGCACTGTGTGT
TTGTTTGGTGCGGCGTCGGGTCCTGTGGAGCCTTTTGATCCGCAGCTGTTGAACACTCACGGTTCGATC
TTCTTGACCCGCCCAAGCATTGGCGCGTGGACGTCTGAGGAGGGCGAATTTGCCAAGCGTGCACAGGCG
GTCACGCAGGCCATCGTCGAAGGCACCTTGCGGGTTCGCGTTACTGGCACATATTCGCTTGCCGACGCC
TACATCGCCCACCGCGACCTTCAGGCGCGTAGCACGAGCGGTTCTTTGGTCTTGGAAATCCCGAAGGAC

RXS02741 - 3′-Region
TAAACACGCATAAAAAGATCCTG

RXS03058 - 5′-Region
ACGAGCTTCCGCTCTGCACAAGCCGCTAGAAGCCCCGCATAGCCCTAATGTAGAGCTCATGCCCATTTG
GAATCACAACACCGCATATCGGCCATGGCTG

RXS03058 - coding Region
GTGTCAAAGCTCAAAGGCTCAAGATCGCTTCTCGACGTCGGCTCCGGCGATCACTCCTTCGCCGACCTG
GCCGGCCGCCAGGTCGCGCATGTCGATGTCGTGGATCCTCTTATTAATACAACCTTTGAAGAATTCCAG
CCGACCCAAAGCTACGATGCCATCACGTTCATCGCGTCCCTCCATCACATGAACGCGGAAGAAGGACTT
AACAAAGCAGTCCGAATCCTCAATCCTGGCGGCAAGCTCCTCATCGTAGGCCTCGCCAAAAACAAAACC
GCCTCCGACTGGATCATCTCCGGACTACAAGCTTTTCTCTCCCGACCAATCAGCCTCATCAATAGGGAA
CAACAAATCTACCCCTTCCCTACCAAAGAACCCTCAGAGAGTCTCCACGAAATACGACAACTCACCAAG
CAGCTCCTCCCTCACCGCCGTATTCGCCGTGGAATCCACTTCCGATACCTCCTCGAGTGGACAAAGCCT

RXS03058 - 3′-Region
TAAACAGCCCTATAAACCAAAAA

RXS03061 - 5′-Region
CTGCCACCACTGGTCATTGCAGAGGACACTCTCCGTGATGGTCTTCAGGTGTTAGTCGCAGCCCTAGAG
CGCGAAACCGCGCACCAGAAGGTGGGCTAAA

RXS03061 - coding Region
GTGTCTTTGACCTTCCCAGTAATCAACCCCAGCGATGGCTCCACCATCACCGAGCTAGAAAACCACGAT
TCCACCCAGTGGATGTCCGCGCTCTCTGATGCAGTTGCAGCTGGTCCTTCATGGGCTGCGAAAACTCCC
CGCGAAAGATCCGTGGTACTCACCGCAATCTTCGAAGCACTGACCGAACGCGCCCAAGAACTTGCAGAG
ATCATCCACCTGGAAGCTGGAAAATCCGATGCAGAAGCTCTTGGTGAAGTCGCTTATGGTGCAGAATAC
TTCCGTTGGTTTGCGGAAGAAGCAGTGCGCCTGCCCGGCCGCTACGGACAGTCA

RXS03119 - 5′-Region
TGGGAGGTGTCGCACCAAGTACTTTTGCGAAGCGCCATCTGACGGATTTTCAAAAGATGTATATGCTCG
GTGCGGAAACCTACGAAAGGATTTTTTACCC

RXS03119 - coding Region

ATGGCTGTATACGAACTCCCAGAACTCGACTACGCATACGACGCTCTCGAGCCACACATCGTCGCTGAA
ATCATGGAGCTTGACCAGTCCAAGGACCACGCAACCTACGTTGCGGGCGCAAATGCAGCACTC

RXS03119 - 3'-Region
TAGGCACTAGAGAAGGCACGCGA

RXS03120 - 5'-Region
CTGGGCAGTTCTTGGGTACGACCACATATCCGGTCGCCTGGTTATCGAGCAGCTCACCGACCAGGAGGG
CAACATCTCCTTCGACATCACCCCAGTTCTG

RXS03120 - coding Region
ATGCTCGATATGTGGGAGCACGCTTTCTACCTGCAGTACATGAACGTTAAGGCAGATTACGTCAAGGCT
GTTTGGAACGTCTTCAACTGGGACGACGCAAGAGCACGCTTCGCAGCAGCTTCCAAG

RXS03120 - 3'-Region
TAAGCATTTTTAGTCCGTGCAAT

RXS03150 - 5'-Region
TTTAACAGAGTGCGTTTCAATGCCTGTAGTGTTCCGGCAATTTTGAATGTCGTTACGGTTACCCAAGGC
TGAATTCCTGAGCTCACCTTGTACAAGATCA

RXS03150 - coding Region
GTGGAAGCCCAGTTCACCTCTCCCCTGCTCAACAATGGGCAAACCTGTTTCCTTGGTACCCGAATCCTT
GCTCCAAAATCACGTTACGCGGAAGTAGTCGATGCATTCACCGCTTTCGCTGGCAGCCTGCAGGTTGGA
GTCACGTCCTCCCCTGACACTCAGATCGGACCGATGGCGACTGCCCGGCAGCGTGAGCGCGTGGAATCC
TACATTTCCCAAGGCAAAAATGCTGGAGCCCGCATCACTGTCGGTGGCAGCCGTCCACGAGATCTTGAC
GCCGGATTCTTCGTTGAGCCAACAGTGTTCGCCGATGTAGACAATCGCGCAGCCATTGCCCAAGATGAA
ATCTTCGGACCGGTGCCCTCTGTTGTTTCCTACCAAGACGATGAACACGCCATCCAACTAGCCAACGAT
TCCGAATTCGGTCTCGGCGGAACTGTCTGGACGAGCGATCCCGAGCGCGGCGCTGCATTGGCCCGCCGA
GTTCACACAGGAACCATTGGCATCAACCGCTATATCCCTGATCCCGCCGCACCATTTGGAGGTGTGAAA
AACAGTGGCCTTGGCAGAGAACTCGGCCCCGAAGGTCTTGCTTCCTACCAAGAAACCCAAACCATTTAT
CTC

RXS03150 - 3'-Region
TAATCCAAACTGCACCTATATAT

RXS03218 - 5'-Region
TTGGTACGGGGGTTAACAACCTAGCTTTGTATCTGAAGGCTTCGGAGATTTCCTGTATACATCAACAAT
TGCCCTTTAACCAGGAGTATTCTTAGCTTCT

RXS03218 - coding Region
ATGACTCCTGATCTTGCAGCTTTTCTGGACAAACTTTATGCCGAGGGGCAGGAATTTGATGCAGAGCAA
CCGGATCGGCTTGATCGCAGGAGAAACCTTGAATCTGAAAGCGCTGCGCTACTTCGCTCGCTCATCTAC
GGAATTAGTCCAAAGTCAGTTCTCGAGCTAGGCACATCCAATGGTTACTCGACTATTTGGATGGCAGAT
GTCGTGAATTTAACAACAGTAGACAATGATCCTGAGCGGTCTTTGGATGCTGCAGCAAACCTTCGCGCC
GCTGGAGTTGAAGAAAAAGTTCAACGAATCGTCGCCGATGGAGCAACCGTACTTGCCGATTCCGCCGAT
GAACAATGGGATTTCATTTTCCTTGATGCCGAACAATCACTCTATGTAAATTGGTGGCCTGACCTGCAA

RXS03218 - 3'-Region
TGAGTTCTAGCAAATGGCGGCTTGTTAGTG

APPENDIX B: AMINO ACID SEQUENCES

> RXA00009 (1-900, translated) 300 residues
MAFGYVLREA VRGMGRNVTM TIALIITTSI SLALLATGFL VTNMTDRTKD IYLDRVEVMI
QLDEDTSAND PECTAESCTE VRDVLEGLDG IDSITYRSRE ASYERFVEVF KDTDPVLVAE
TSPDALPAAF HVRLEDPLAV EILDPVRDLP QVSNVIDQVD DLRGATENLD SIRNATFLIA
AVQVLASIFL IANMVQIAAF NRREETEIMR IVGASRFYTQ GPFVFEAILS TLIGAVFAVG
ALFLGKELVI DKALRGLYDS QLIAPVTTTD IWLVAPIISG IGVVIAGIIA QLTLRFYVRK

> RXA00010 (1-687, translated) 229 residues
VITFENVTKN YKTSTRPALD NVSLHIEKGE FVFLIGPSGS GKSTFLRLMT REENVSSGSL
TLADFQVNKL RGTQVNKLRQ RIGYVFQDFR LLKNKNVYDN VAFALEVIGK KKDKIQELVP
ETLEMVGLAG KANRMPNELS GGEQQRVAIA RAFVNRPLVL LADEPTGNLD PDTSDEIMIL
LNRINRLGTT VVMSTHNART VDDMRRRVIE LQLGKLVRDD AHGVYGEMR

> RXA00024 (1-945, translated) 315 residues
MEHGVTVIKG TEFDVFPLNL GGNTFGWTSN REQTFAVLDA FVAAGGNFVD TADSYSAWVE
GNEGGESERE LGAWIKERGA DKLIIATKSG ALEPVAGRSR EATFKAVEGS LERLGVESID
IFYYHYDDEA VSIDEQVAIA NDLIAQGKIK HLALSNYSAE RLAEFFEKSV GTPAQPVALQ
PHYNLVSRKD YEENVQPLAE KHGVAVFPYF ALAAGLLTGK YTSKEDISGK ARAGQLDRYA
SDEAFAVVTE LRAVADELGV APTTVALAWL VAHGVTAPIA SVSKVEQLKD LMAVKDVELS
AEQLARLDKV SEPFA

> RXA00026 (1-1386, translated) 462 residues
MSTDNFSPQV PSTVYLDYME QGIAARKAEA ESNASTKGES PDYPGQQVIW RLIQEAGESL
RDELRTLAFT LHDHPEEAFE EVFATEEITK LLQNHGFEVQ SGVYGVKTAL ETSFETPGYD
PAQHPSIAIL AEYDALPEIG HACGHNIIAA AGVGAFLAVT NMIKTAEVKG VDHLDFEGRI
VLLGTPAEEG HSGKEYMIRN GAFDGIDASI MMHPFGFDLA EHVWVGRRTM TATFHGVSAH
ASSQPFMGKN ALDAASLAYQ GFGVLRQQMP PSDRLHAIIT EGGNRPSIIP DTATMSLYVR
SLLPEALKDI SKRVDDVLDG AALMAGVGVE KQWDVHPASL PVRNNHVLAR RWAKTQNLRG
RTALSEGILP DTLAASTDFG NVSHLVPGIH PMVKISPENV ALHTKEFAAY ARTEEAIDAA
VDAAIGLAQV AVDALADPQM LIDATLEFTN SGDVLKVGDY LA

> RXA00048 (1-1659, translated) 553 residues
MNHDSECDLD NVVQFTIQEG LDPMSPNNFD TDVCIVGGGP TGTLLAVLLG QKGHRVTILE
KWPTFYERPR AVTFDHEIAR ILGYIGIDSE NDEAIDYHSD SYDWKNAAGE TLLEVDWTSM
TDSGWRTRYW FYQPELEKRL RDLALTMDFV DIRCGFTAVG LSQDENSAII HGIVTDTPEN
IPADAQREDI RAKYVIGADG ANSFVRNSLG LEMNDLGYFF DWLILDLKPT QDIDYGTDHW
QLCDPKRPTT IVPGGPGRRR WEFMALPGED LKELASEESA WNLLEPWDVT PGKAILERSA
VYRFQARWAQ EWRSGRALIA GDAAHLMPPF AGEGMCAGLR DSLALAWRLD LVLSGKSDDA
LLDTYGEERR EHVHYYIDFS MDLGNVICIT DEDEARLRDE RMIKELEAQD GVPVNTDVAH
LGPGIWDKDS SHGGELAKQG IVEYQGRKAR FDDAVGRGWA VLGLNTDPRE VLDEDSLVAL
DAIGAIVESV GDATSAVLDV EGLYTRWLKE AGATFIITRP DFYVYSTAVD AEQLQTQIKQ
LSDLLHLNSV VGA

> RXA00070 (1-432, translated) 144 residues
VGINRISQGS APKLGVRSTR QRKAVIDVLE EIDNFASAKE IHHELSTREH NVGLTTVYRT
LQSLADIGAV DVLTVTGGET LYRQCHDEGH HHHLVCTNCG RTVEIDGGPV ETWAQEIATK
NGFALSSHEA EIFGLCADCK EKVT

> RXA00072 (1-441, translated) 147 residues
MSFQLVNALK NTGSVKDPEI SPEGPRTTTP LSPEVAKHNE ELVEKHAAAL YDASAQEILE
WTAEHAPGAI AVTLSMENTV LAELAARHLP EADFLFLDTG YHFKETLEVA RQVDERYSQK
LVTALPILKR TEQDSIYGLN LYRSNPA

> RXA00078 (1-414, translated) 138 residues
MKADLTPYRQ FNGNAKEAME FYQTVFGGEL QMMPFSAMHS EEEVGGDGEK IMHAELVVDG
QKLLFASDIP RVMQRMKGED TPLSLTGGAE LEEEIRGYWE KLSEGGTVTM PLEAVPWGAV
YGALEDRFGT HWMFNIGG

> RXA00088 (1-1014, translated) 338 residues
MVKNRFKLVS IATVAALALV GCSSTDSTSS ESSSAAESTA AASTLTIEDN HGTEGISLPI
EGVAATDNRA FELLDRWGVE LVAAPLQLVP FTVTGYTEEG GVANLGSHRE PDLEALAAAQ
PSLIINGQRF AQYYDDIIAL NPDATVVELD PRDGEPLDQE LIRQAETLGE IFGEEEDAAK
IVADFESALE RAKTAYAAIS DQTVMAVNVS GGNIGYIAPS VGRTYGPIFD LVGLTPALEV
GNASSDHEGD DINVEAIAAA NPDLILVMDR DGGTSTRNEA DYVPAEQIVS DNEALANVKA
VTDGYVYYAP ADTYTNENII TYTEILNGMA DMFEKAAQ

> RXA00100 (1-600, translated) 200 residues
MILDWVISIM EALGAVGVGV AVFLENVFPP IPSEVVLPLA GFTTTQGDLN VWAALMWSVI
GSVSGAFLLY GLGRSIGAAR LRQVADWMWL VDATDVDKSL SWFEKYGKYS VFFGRLVPGV
RSLISIPAGV DKMNPVLFGV LTAVGSTIWN AVLIWTGVWL GAEWETVSMW FESYSTIIYV
GIALIXAYVL FGLVRRRIKT

> RXA00111 (1-993, translated) 331 residues
MAFFSFSTSP LTRLIPGSRS KATGAKRRLS STIASIERSP GIIALDGPFT HDHVSVRGIR
LHLAEAGSPT KPLVLLIHGA FGGWYDYREV IGPLADAGFH VAAIDLRGYG MSDKPPTGYD
LRHAAGELSS VIAALGHDDA LLVGSDTGAS IAWAIASMYP ERVRGLISLG AIHPLDMRRA
IRRKPHLHVS DLSRLAPFRL PSFLHNLFHF GITSEARREI VNNTSSSYQR SNAFTETVLL
RKKALSIDHT ITPIIRTNRY LVGSIPSKTV SAPVWLLRTN TRRWEHLANT ARTRTTGPFT
TIAIPGGYEL PYLENPSEFA ATIAEFARTT F

> RXA00112 (1-1191, translated) 397 residues
LSPSLVVDAV IVLVMAFALW GGWRQGAFTS LLSTVGVVSG LVVGAAAAPF VMGLTDSTAL
RFLLAIGTVV LLVGLGNLIG AHLGAAIRDN IKFRSSRTLD SGLGAIFQVL ATLIVVWLVA
IPLATGLPGT VASGIRDSRI LGFVDKYTPQ GLDTLPSKIA AMLSESGLPP LISPFTGGSS
VEVDAPEINV TNVDLVEAMR PSVIHVMGDA QECSRRLMGS GFVASPDYVV TNAHVVAGTS
TVSLDTMIGT RSAEVVFYDP NLDIAVLYSP DLGLDPLPWA STPLDTGDEA IVMGFPQSGP
FNASPARVRE RIMITGSNIY ANGQHEREAY SVRGSIQSGN SGGPMTNEMG EVVGVVFGAA
IDGSDTGYVL TAEEVQERIG DITALTQPVD TMQCAVS

> RXA00133 (1-813, translated) 271 residues
MLFVRRLTSL KTATGIPVTM FATVLQDNRL QITQWVGLRT PALQNLVIEP GVGVGGRVVA
TRRPVGVSDY TRANVISHEK DSAIQDEGLH SIVAVPVIVH REIRGVLYVG VHSAVRLGDT
VIEEVTMTAR TLEQNLAINS ALRRNGVPDG RGSLKANRVM NGAEWEQVRS THSKLRMLAN
RVTDEDLRRD LEELCDQMVT PVRIKQTTKL SARELDVLAC VALGHTNVEA AEEMGIGAET
VKSYLRSVMR KLGAHTRYEA VNAARRIGAL P

> RXA00135 (1-1254, translated) 418 residues
VKDKFLVTGG AQLQGAVKVY GAKNSVLKLM AAALLAEGTT TLTNCPEILD VPLMRDVLVG
LGCDVTIDGS TVTITTPAEL SSNADFPAVT QFRASVCVLG PLTARCGRAV VSLPGGDAIG
SRPLDMHQSG LEKLGATTRI SHGAVVAEAE KLVGANITLD FPSVGATENI LTASVMAEGR
TVLDNAAREP EIVDLCRMLR SMGANIEGEG SPPITIEGVE KLTPTQHEVI GDRIVAGTWA
YAAAMTRGDI TVGGIAPRYL HLPLEKLKIA GAKVETYENG FRVQMDKQPE ATDYQTLPFP
GFPTDLQPMA IGINAVSNGT SVITENVFES RFRFVDEMLR LGADANVDGH HVVIRGIEQL
SSTSVWSSDI RAGAGLVLAA LCADGVTEVH DVFHIDRGYP NFVENLQKLG ATIERVSS

> RXA00137 (1-1089, translated) 363 residues
MALADTRFAT RRRALAAKLA AQRIDSILVT SPIHVRYLSG FTGSNGALIV NKDLSAQICT
DGRYTTQIAE EVPDIEALIE RASATTLLAQ VEGPRRIAIE AAQTTLDQLD SLREATQEDV
ELIPVSGVVE SIRLTKDSFE LDRLRDVAAL ASQAFEDLLA AGELAEGRSE RQVAADLEYR
MRLLGAERPS FDTIVASGPN SAKPHHGAGD RILQRGDLVT IDFGAHARGF NSDMTRTLVM
GEAGEFEAEI YDIVLRSQLA GVEAAYSGAN LFDIDAACRK IIEDAGYGEY FVHSTGHGIG
LEVHEAPSAS KTSQGVLETG STLTIEPGIY VPGKGGVRIE DTLIITSGAP EIITKVSKDL
IVV

> RXA00139 (1-711, translated) 237 residues
LIEQEQREQN VSERRQDYKR HGSRYKARMR AVDILFEAES RDVDPVAIID DRHKLARDTN
PIVAPVAEYT ETIINGVAVE LDTLDVFLAE HIAETWTLGR LPSVDRAILR VASWEMIYNA
DVPVTTAIVE AVEIASEYSG DKSSAYINAT LDAMASKVET LRERAANPEA VLAEASESLD

DAPVAPWDDS DALDDSDEDF EAVDAAEVFE AEETVEVSEV AEDSEVSKVS EEKADES

> RXA00143 (1-1482, translated) 494 residues
MVWDWHTRKG AVARLTPPFI PLNPITQAER LADGTTIFSL PAGLKWVARH DLSGFLNGSR
FTDVCLTAPV KALANWRHVH NFVDQDGGTL ITDSVSTRLP ASTLTGMFAY RQTQLIEDLK
FLSRTSTLFD GSPLTVAITG SRGLVGRALT AQLQTGGHEV IQLVRKEPKP GQRFWDPLNP
ASDLLDGADV LVHLAGEPIF GRFNDSHKEA IRESRVLPTK FLAELVAEST QCTTMISASA
VGFYGHDRGD EILTEESESG DDFLAEVCRD WEHATAPASD AGKRVAFIRT GVALSGRGGM
LPLLKTLFST GLGGKFGDGT SWFSWIAIDD LTDIYYRAIV DAQISGPINA VAPNPVSNAD
MTKILATSMH RPAFIQIPSL GPKILLGSQG AEELALASQR TAPAALENLS HTFRYTDIGA
AIAHELGYEQ LADFAQQQEI EAERKQERAE LKAAKKIAKK APVLEESPTN LEDPEEVEQS
ILSSILNFRR KRND

> RXA00152 (1-1296, translated) 432 residues
MTGLILAIVF LVFVAVVVIK SIALIPQGEA AVIERLGSYT RTVSGGLTLL VPFVDRVRAR
IDTRERVVSF PPQAVITQDN LTVAIDIVVT FQINEPERAI YGVDNYIVGV EQISVATLRD
VVGGMTLEET LTSRDVINRR LRGELDAATT KWGLRISRVE LKAIDPPPSI QQSMEKQMKA
DREKRATILT AEGQREADIK TAEGEKQAKI LQAEGEKHAS ILNAEAERQA MILRAEGERA
ARYLQAQGEA RAIQKVNAAI KSAKLTPEVL AYQYLEKLPK IAEGNASKMW VIPSQFSDSL
EGFAKQFGAK DAEGVFRYEP NTVDEETRDI ANADNVEDWF STESDPEIAA AVAAANAVAN
KPVDPEPGEI LSKKTARRVE PEAVLEALQN GTTTQPEVEA APPTANFAQE FPAPQANPED
YSDQHRENPY GN

> RXA00177 (1-288, translated) 96 residues
LPYVLAFNAP YAPQAEQRAA AAFGSATALE GLQQLRAQVG APQRLSDYGF TAAGIPEAVE
IILEKVPANN PRTVTEENLT ALLTTALNGD DPATLN

> RXA00178 (1-885, translated) 295 residues
MTISAQQQAV EEDLVERVLA SFDSCENPRL KLVMKSLTVH LHDFIRDVRL TEEEWNYAID
FLTKVGHITD DKRQEFVLLS DTLGASMQTI AVNNEAYEDA TEATVFGPFF VDDAPLVQNG
DDIAFGAVGQ PAWVEGTVKD TEGNPIPNAR IEVWECDEDG LYDVQYADER SAGRAHLYSD
ENGEYHFWGL TPVPYPIPHD GPVGQMLQAV GRSPVRCAHL HFMVTAPEKR TLVTHIFVEG
DPQLEIGDSV FGVKDSLIKK FVEQPAGTAT PDGRDVGDQT WARTRFDIVL APGNV

> RXA00191 (1-1419, translated) 473 residues
MSFKRRSLAI TCAITSSIVL AGISGTAAAQ SSYVSGSSGL LSSSELHPET PAPLDAPKNI
IYMIGDGMGY NHVSATNLFE TGQTMHQVEG EPGSVTPVEG GTPVQAFEGA EWTQLAQSTF
QDGNSYDPER AWADHNYVNE NFTDSAAAGT AMATGVKTTN GMIGINPANE PAKNTSEYAI
EKGKAAGVVS SVPFNHATPA AWAAHNSNRN DLHAMAEEMI NSDLNVIMGA GHPFFDNNGN
PITEADEDYM QASQYERLAS GETDFTFVEE DADFEALANG QVESDKYFGL AQVEDPLQHD
RDGDSVTPYD VPLNDVVDLS TMSKAALNVL NQDEDGFHIM IEGGAIDWAG HANDMARDIE
EVQEFNKAVE TVIEWVETNS SWDETLVIVT ADHETGYMTG PNDDPNWSAM TGAAGIVPNH
GWHSGNHINQ LVPVFARGAG VSDIVAAADQ VDPIRGNYID NIEIANLTFN KWW

> RXA00226 (1-825, translated) 275 residues
MNLSMPAFAT WVLILDFSRT LMAAHNLQGK NALIFRADAL QPASRGADVI IADPARRAGG
KRITNPAQLL PPLPSLLDAW INQPLAVKCA PGLDFSEWPG LVSIASVDGG VKEACLYTTD
LADGETREAI VIKDGLIDRI TNFEDDATGQ DLAAAPGEFI IDPDGAIVRA GLVRHYAVRE
QLWMLDERIA YLTGNRIPEG TSGFRFIEEV PLKKLKSAMA AHDAGAVEIL VRGVDVDPDQ
LRKRLQLKGT KAMSVVITRI GSRGVALICG PRERA

> RXA00231 (1-789, translated) 263 residues
DRLRKVSFTG STPVGQQLLK KAADKVLRTS MELGGNAPFI VFEDADLDLA IEGAMGAKMR
NIGEACTAAN RFLVHESVAD EFGRRFAARL EEQVLGNGLD EGVTVGPLVE EKARDSVASL
VDAAVAEGAT VLTGGKAGTG AGYFYEPTVL TGVSTDAAIL NEEIFGPVAP IVTFQTEEEA
LRLANSTEYG LASYVFTQDT SRIFRVSDGL EFGLVGVNSG VISNAAAPFG GVKQSGMGRE
GGLEGIEEYT SVQYIGIRDP YAG

> RXA00249 (1-954, translated) 318 residues
GVFTFQGVVL LVDARHGVVE QTRRHLSVSA LLGVRTVILA VNKIDLVDYS EEVFRNIEKE
FVGLASALDV TDTHVVPISA LKGDNVAEPS THMDWYTGPT VLEILENVEV SHGRAHDLGF

RFPIQYVIRE HATDYRGYAG TINAGSVSVG DTVYLPEGRT TQVTHIDSAD GSLQTASVGE
AVVLRLAQEI DLIRGELIAG EDRPESVRSF NATVVGLADR TIKPGAAVKV RYGTELVRGR
VAAIERVLDI DGVNDNEAPE TYGLNDIAHV RIDVAGELEV EDYAARGAIG SFLLIDQSSG
DTLAAGLVGH RLRNNWSI

> RXA00277 (1-1584, translated) 528 residues
MKDNEDFDPD SPATEAVAFN PFDDDDEDDS PATSAVAFNP FEDDDDDDEF QGEGLEFLLR
DLDNLRATQG QMVVEQPAVE DSLGSASAHT ETTAASLRPR PEVDPSERSR RQAISLFRER
RRVRRQSRPV ADGMVELPFI TPKPEDELLI DPEKKRKPGV AAPQLVAGDI VAEQYEVLGV
IAHGGMGWIY LANDRNVSGR IVVLKGMMAQ SSVQDQGTAE AEREFLADIT HPGIVKAYNF
IDDPRVPGGF IVMEYVNGPS LKDRCKAQPD GVLRVDLAIG YILELLPAMD YLHQRGVVYN
DLKPENVIAT EDQVKLIDLG AVTGIGAFGY IYGTKGFQAP EVATHGPSIS SDIFTIGRTL
AALTMPLPVE DGVLAPGIPS PKNSPLLRRH LSFYRLLQRA TADDPQHRFR NVSELRTQLY
GVLREILAVR DGKQYPPQHS LFSPQRSTFG TKHLVFRTDR IIDGIERQAR ITAPEIVSAL
PVPLIDRTDP GARMLSGSSY AEPSETLETL RNSMEDEQYR QSIEIPLG

> RXA00299 (1-744, translated) 248 residues
MLPNHSPYVI AEQFGTLAEL YPDRIDLGMG RAPGTDMNTL RALRRDPQSA ENFPSDVVEL
NSYLTGRSRL PGVNAIPGKG TNVPLYILGS SLFGAQLAAQ LGMPYSFASH FAPTHLEHAV
QTYRDNYQPS EQHPEPYVIA AVNVTASDST EQAHDDFYKV ARARVKNMAL RGRQVTDEQL
DELMDSPAAR QIVDMLHYTA IGTGSEVKEY LDGFVKTAQA DELMISLQSP NTEATTRNME
ILADAWIN

> RXA00332 (1-702, translated) 234 residues
MAFNKAYDAL RAPQITLGLM TPNGPELGRS EMVPTENSIE LAIQAEAQGF RGMWVRDVPL
AVPQGITVTD KQATYLDDPF LMLGAMASVT STIALGTAAT VLPLRHPLHV AKSALTLDRL
SHGRFVLGIG SGDRPEEFEI FGKSLDNRRA DIQSGWAILR AALSPDPAMR ADLEFAPTTP
PEAQIPMIAV GSARQTVQWI ARNADGWATY YRPAEAQVGR LDLWDKARGG TRPC

> RXA00354 (1-636, translated) 212 residues
GLIGANGGYV ESAQESVFHR RLSGEETRHI VEWLYNRGLE FYLESNNGLY ASRGFREASK
PVLSRLSEKT DVTVDSMYPD MFWGASLDRD DVNKISYIFN SQEDLDAARE AFPNLEHTTW
GGQTGALFGT IGVSVNKKIG VDRLLKYLNA DRANTIAFGD SDEDLSLFEA SAYGVAMGEA
TESLKAAADL VTDAVGQDGL RNAFLKLELI DA

> RXA00372 (1-1077, translated) 359 residues
MSSKHPLKRT AVTVFALGAS AALLVACSEP SEDVSTAETT TASSSANASD AAGEKVTITV
YTSEPEEKVD EINKAFMEAN PDIEVEVYRA GTGDLTARIE AEKASGSIEA DVLWAADAAT
FETYAAQGDL AELEDVETSD IIEEALDAEN FYVGTRIIPT VIAYNTEVVD QAELPTSWAD
LTDPKYAGQL VMPDPAVSGA AAFNASVWKN DPALGEAWIT ALGENQPMIA QSNGPTSQEI
AGGGHPVGIV VDYLVRDLAA AGSPIDTIYA SEGSPYITEP AGVFADSEKK EAAERYINFL
LSVEGQEIAV EQAYLPVRED VGTPEGTPEL ADIELMTPDL EVVTADKAAA VEFFQNAMN

> RXA00470 (1-1200, translated) 400 residues
MIEDMSNTPA PYTPQPAGQA VPLYPTFTRS RDGRVVAGVA SGLAKHLNVS VFWVRALLIF
AALLSGAGLF AYALIWIFTR IEKKGSGEAS TSKRWVSWCL VLLAIGGAAA SVMLSTGFAV
GTLVPIGVVG VGLLMVWLAY DRGVESGPNL LIIATGGVLM LVAIVLIVMN WNTQDGFVMA
LVAVVLTLVG VAALGVPLWV RMWDQLGEER AEKAAAAERA DIASRLHDSV LQTLALIQKR
ADDPAEVARL ARGQERELRQ WLFDSQDKTP QTTGTVFTAL ERACGEVEDI YALRIVPVTV
GTDEALTEKT QAAVMAVREA LVNVAKHAGV ETADVYAEIM LGELNIFVRD RGAGFDPDNI
PDGHHGLAES VQGRVERAGG KVRIKSEIGE GTEVAITMDV

> RXA00471 (1-690, translated) 230 residues
MVDVFLVDDH SVFRSGVKAE LGNAVTVVGE AGTVADAVAG IKASKPEVVL LDVHMPDGGG
LAVLQQINDS DVDTIFLALS VSDAAEDVIA IIRGGARGYV TKSISGEELI EAINRVKSGD
AFFSPRLAGF VLDAFAAPDS AAGAGIVDAP EKDAAVESGK ILDDPVVDAL TRRELEVLRL
LARGYTYKEI GKELFISVKT VETHASNILR KTQQSNRHAL TRWAHSRDLD

> RXA00499 (1-957, translated) 319 residues
GNDILEKPTA EVVEYLSHLR ADGIVRDAEA LRKHLGVNQW NLLGQSFGGF TTLHYLSRHA
DSLDNVFITG GLSAIDRPAE DVYANCYNRM RRNSEEFYRR FPQLRETFRG LVNRARAGEI

VLPTGEVVSE TRLRSLGHLL GSNDGWFDLY NLLELDPTSN AFVHDLAGLL PFGNRNPIYY
VLHESSYADG VVTNWAAERV LPEDFREDPT LLTGEHVFQE WTDTVPSLK? WKDVALALAQ
QEWPKLYDAK ALENSQAKGA AAVYANDVFV PVDYSLETAQ HLPGVQLFIT SQHEHNGLRA
SSGAVLKHLF DLAHGREVR

> RXA00500 (1-675, translated) 225 residues
VLVLALDTST PDLIVGVVDS DTGNTRAETI IEDTRAHNEQ LTPTVQKTLL DANLSFSDID
AIVVGCGPGP FTGLRVGMVS GAAFGDALGI PVYGVCSLDA IAHNIGARNI PHALVATDAR
RREIYWATYR SGERDQGPDV IAPANIQISG AVDTISIPEH LVEKLPEELQ NVTMHSGKPA
PASLVAVADF SVEPQPLVPL YLRRPDAKEP KPKPKSAAIP EVDLS

> RXA00501 (1-507, translated) 169 residues
MSEQFELREL RREDAGRCAD LEQILFPGDN PWPRDVFAVE FSHPTNFYIG AFDEGYLVAY
AGLAMMGPAD DPEFEIHTIG VDPEFQRKGL GRVLMDQMMH AADSHDGPVF LEVRTDNVPA
ISMYEAFGFK TLAVRKNYYR PSGADAYTMQ RPRLSDRKDQ QTDTEGTPS

> RXA00502 (1-1032, translated) 344 residues
MIVLGIESSC DETGVGVVKL DGEGNLEILA DSVASSMQEH ARFGGVVPEI ASRAHLESMV
PVMREALRQA GVDRPDAVAA TVGPGLAGAL LVGASAAKAY AAAWGVPFYA VNHLGGHVAV
ANLEGETLPH AVALLVSGGH TQLLEVDAVG LPMKELGSTL DDAAGEAYDK VSRLLGLGYP
GGPIIDKLAR RGNPEAIAFP RGLMKKSDSR HDFSFSGLKT SVARYVEAAE RNGEVISVED
VCASFQEAVC DVLTFKAVRA CRDVGAKVLL LGGGVAANSR LRELAQERCD KADIELRVPR
FNLCTDNGVM IAALAAQRIH EGAQESPISV GTDPSLSVET PQVF

> RXA00566 (1-606, translated) 202 residues
MPTSRYVLPS FIEQSAYGTK ETNPYAKLFE ERIIFLGTQV DDTSANDIMA QLLVLEGMDP
DRDITLYINS PGGSFTALMA IYDTMQYVRP DVQTVCLGQA ASAAAVLLAA GAPGKRAVLP
NSRVLIHQPA TQGTQGQVSD LEIQAAEIER MRRLMETTLA EHTGKTAEQI RIDTDRDKIL
TAEEALEYGI VDQVFDYRKL KR

> RXA00567 (1-591, translated) 197 residues
MSDIRMAAQG GPGFGNDVFD RLMSERIIFL GSQVDDEIAN KLCAQILLLS AEDPTRDISL
YINSPGGSVT AGMAIYDTMK YSPCDIATYG MGLAASMGQF LLSGGTKGKR FALPHARIMM
HQPSAGVGGT AADIAIQAEQ FAATKREMAQ LIAEHTGQTF EQISKDSDRD RWFTAQEAKD
YGLVDHVITL AEGPISN

> RXA00569 (1-1026, translated) 342 residues
MRLKKQLLGS LLVVIVVLSI AVATTKQQKG FVTGQPTGAL NLSDILDSEE LGEYHLMSAA
IITGNTVDFS GLGAGPDDPF EIASITKIFT GELLRLQIER GEITESTAVG DVLGERVADS
LIRDITVEEL ANHTSGLPRL GNVGLRPFMA TFFDKNPYKD LSADRVISIS TTSKLNSRGE
FHYSNLGFAL LGQVLARNAG LTFDQLLDRD LLAPLNLNNT KLMTPESLAQ DAPQGFSTPG
KQVEAWEMDG FLPAAGLRST ARDMAVFCQY LFTKGPAPFT WQSLESAPEI VWHNGESFGY
SSVLFFNTAT TTAIFVAADV ATSVFPIGHE LLMANSTRQE SK

> RXA00594 (1-933, translated) 311 residues
VSTTNSLTKL VASTVAAGVL GALALVPFAS LSGVAVARTN DTMQTNLSDL TDGRGPGVTT
ITDSTDQPIA YIYAQRRFEV GGDQISTSMK DAIVSIEDRR FYEHDGVDLQ GFGRAILTNL
AAGGVEQGAS TINQQYVKNF LLLVEADDEA EQAAAVETSI PRKLREMKMA SDLEKTLSKD
EILTRYLNIV PFGNGAYGVE AAARTYFGTS AAELTIPQSA MLAGIVQSSS YLNPYTNHDA
VFERRNTVLG AMADAGAISP DEASAFQQEP LGVLETPQGL SNGCIGAGDR GFFCDYALQY
LSEQGITQDM L

> RXA00612 (1-1185, translated) 395 residues
AAAAIQQGAG LDTMLDVPSR YEVKGMGSGG AANCPANTYC VENAGSYAPR MTLQDALAQS
PNTAFVEMIE QVGVDTVVDL SVKLGLRSYT DEGSFDGESS IADYMKDNNL GSYTLGPTAV
NPLELSNVAA TIASGGMWCE PNPIASVHDR EGNEVYIDRP ACERAIDAET ASALAVGMSK
DTVSGTAASA ASMYGWSLPT AAKTGTTESN QSSAFMGFNS NFAAAPYIYN DGTSTTPLCS
GPVRQCSSGN LFGGNEPAQT WFNMASNVPA ASQGTLPSSS DSFRLGTSGE LLNQVVGQSE
ASARRTLEAK GYKVTTRSVS GAGSARGTVV SATPQGAVLI DGGTVILDIS DGTSPAPAAT
NNDDSDDGDT PAPSTNNRGT TIEDAINDAI NQFFR

> RXA00615 (1-582, translated) 194 residues
MTASVFYPVL SVVVLIDCIL PLIPSETVLA LAGAWSGARG TPNLWLVISV ATLAAIIGDN
LCYFFGTRLI NMVNRIPGES RRGKALEWAR KNLNERDVST IIIARFIPWA RWFVTIILGS
VGYSWSRFIV WDSIGALIWA TQATLLGYVG GWLFQEQPLI GLVAGAALGI FFGFFLQWLN
KMWERRRLAK VAAE

> RXA00621 (1-783, translated) 261 residues
MSERLNAPQA PIHPITRTHH GIDFVDNYEW LRDKESQETL DYLEAENAFT KQETEQLATL
RDNIYEEIKS RVKETDMSIP VRAGKHWYYS RTEEGKSYGY SCRIPVTEGS DAWTPPVIPE
GEPAQGETII MDANELAEGH EFFSMGASSV TTSGRYLAYS TDVTGEERFT LRIKDLETGE
LLPDTLTGIF YGATWVGEEY LFYQRVDDAW RPDTVWRHKV GTPVEEDVLV YHEPDERYST
WVGTTRSEKV HPFWLRLQDH L

> RXA00622 (1-1416, translated) 472 residues
MNVIPPGWAP LVQKKFILFG CASKITSEVR VLPFDQPEGT PEVLIPRAEG VEYDVDHAVV
DGSDIWLVTH NAEGPNFSVG WAGVDKLNSL DALAPLVAHK DDVRIEGVDT YRDFIILGYR
SGAIGQVAIM KLIDGTFGDF QQLEFDEEIY TVASGGNPEW DAPVIRLSYG SFTTPAQLFN
YWIESGERTL LKQQEVLGGY KPSDYVASRL WVTAKDGAQI PVSLVHRTDL DVSKPNPTLL
YGYGSYESSI DPGFSIARLS LMDRGMIFAI AHVRGGGEMG RGWYDNGKTT TKKNTFTDFI
DVADALIEQK ISAPEMLVAE GGSAGGMLMG AIANMAGDRF KAIEANVPFV DPLTSMLMPE
LPLTVIEWDE WGDPLHDKDV YEYMASYAPY ENIEAKNYPN ILAVTSLNDT RVLYVEPAKW
VAQLRATATG GEFLLKTEMV AGHGGVSGRY EKWRETAFEY GWLINQATGV TE

> RXA00636 (1-1029, translated) 343 residues
MMIDTPAVLI DRERLTANIS RMAAHAGAHE IALRPHVKTH KIIEIAQMQV DAGARGITCA
TIGEAEIFAG AGFTDIFIAY PLYLTDHAVQ RLNAIPGEIS IGVDSVEMAQ ATAGLREDIK
ALIEVDSGHR RSGVTATASE LSQIREALGS RYAGVFTFPG HSYGPGNGEQ AAADELQALN
NSVQRLAGGL TSGGSSPSAQ FTDAIDEMRP GVYVFNDSQQ ITSGACTEKQ VAMTVLSTVV
SRNVSDRRII LDAGSKILST DKPAWIDGNG FVLGNPEARI SALSEHHATI FWPDKVLLPV
IGEQLNIVPN HACNVINLVD EVYVREADGT FRTWKVVARG RNN

> RXA00639 (1-660, translated) 220 residues
MTSAEQIVDP TAHDSGNKAT DKFKANRVSS DTSKERANAI YVDLLAAIAQ VAHKHEVTYE
EYAVLKQWMI DVGEYGEWPL WLDVFVEHEI EEINYNRHDY TGTKGSIEGP YYVENSPKLP
WDAEMPMRDK DRACTPLIFE GQVTDLDGNG LDGAEVELWH ADEDGYYSQF APGIPEWNLR
GTIVTDEEGR YKIKTLQPAP YQIPHDGPTG WFIESYGGHP

> RXA00640 (1-249, translated) 83 residues
MSTPVSNLAS VQKTLDHALE DRPEEGIVRV NRNIFTDPEI FELEMRHIFE GIWMDMAHES
QIPNGGDYFT TYIGCQRIMI TRS

> RXA00641 (1-1041, translated) 347 residues
VRRVPKLESY RGFLFGSLND DVVSLEEHLG DTRTVIDMLV DQSPEGLEVL RGSSTYTYDG
NWKLQTENGA DGYHVSSTHW NYAATTSRRG TGESANETKA MDAGTWGKQG GGYFSYPYGH
MLLWMWWGNP EDRPLFERRD EFKKEFGEEK GEFMVGASRN LCLYPNVYLM DQFSSQIRHI
RPISVDQTEV TIYCIAPKGE SAEARANRIR QYEDFFNATG MATPDDLEEF RSCQKTYQAS
AFPWNDMTRG LGHQVQGPNE VAKGLGMNEV LSSGARTEDE GLYPIQHGFW HELMQEAVNK
QSIKEKELAD DTASSLATVA AAKIREEAKA AAKSDAGEPR RRRRTRG

> RXA00642 (1-492, translated) 164 residues
MSEITRSEIE AFLYYEARLL DDRKFEEWLE CYREDAEFWM PAWDDNGELT EDPQSEISLI
YYPNRGGLED RVFRIRTERS SATSLPEPRT GHSTTNVEIL ERRDGEVDIR FNWITFYYRY
NTTDTYFGTT FITLDVSGET PKIVKKKVVL KNDYIHHIVD IYHV

> RXA00643 (1-1536, translated) 512 residues
MTHQVALAFE DGITRFIDCE DDQTVADAAY QARINIPFDC RDGACGTCKA FCESGDFDEG
DYIDDALSED EAADGYCLPC QMTPKTDLIL QIATTSVLAK TGASTFDGEL KEINHFSDST
IGIEIELENR QDLAFLPGQY MNIQVPGSDQ TRSYSFSCAQ DSGNVQFLIK VTPGGLMTTY
LTDHAKVGDK LTLTGPMGSF FLREPVRPIL LLAGGTGLAP ILAILEKLSR DELLDVPIRL
VYGANFTHDL VELDRLDAFK DKFDFDYITV LSDKDTEHPR KGYVPAHLTG EYEPDEDTDV
YLCGPPPMVE AVRQFLGTLE HPPLDFYYEK FTSAAAPAAG KPEITVETSE VAEDFNLVEV

STPGMSSGEV HSSATQLQAR MALELGALEL AINKLGERDI ERFRNLADIA NSFIDGDKFI
DAVKFTEANA DFHEFLFRRA NNEALLAAYQ NLQVVQEMNA TLPGAEWIDP AIATEHLALV
DAVSQNDLET ARTIIREHAE HGIDTMVKAL EK

> RXA00644 (1-828, translated) 276 residues
MSAPVGQGIE GRPTHVTPER FFGQGVVVTG AAQGIGMAVA HRIAYEDGNL VLVDRSPLVH
EVAEELRKAG AGTVDSFIAD LETFEGATDA LEFAGQKLKN LDVVINNVGG TIWAKPYQEY
SEEEIRKEIN RSLFPTLWMC RAALPILIGN GGGTIVNVSS IATGGINRVP YAAAKGGVNG
IVSAMAREAA PHNVRVVATA PGGTLAPERA VKRGPGPEGE LEEKWYQQIV DQTIDSSLMK
RYGTLEEQVA PICFLASEEA SYITGSVMPV GGGDQG

> RXA00650 (1-636, translated) 212 residues
MIRVLLADDH EIVRLGLRAV LESAEDIEVV GEVSTAEGAV QAAQEGGIDV ILMDLRFGPG
VQGTQVSTGA DATAAIKRNI DNPPKVLVVT NYDTDTDILG AIEAGALGYL LKDAPPSELL
AAVRSAAEGD STLSPMVANR LMTRVRTPKT SLTPRELEVL KLVAGGSSNR DIGRILFLSE
ATVKSHLVHI YDKLGVRSRT SAVAAAREQG LL

> RXA00658 (1-318, translated) 106 residues
VRHDEHYPAA ANLIAFDKGW STLIAPQLED PEAEEFTAGF LTEYQDNLIT AGMEHQALAS
GFPVGRRFKS DIALRRCDAV TTHIGHEHSA DGHWRIYVFA GQATPQ

> RXA00659 (1-621, translated) 207 residues
VEASDGGTFD VENPATGETI ATLASATSED ALAALDAACA VQAEWARMPA RERSNILRRG
FELVAERAEE FATLMTLEMG KPLAEARGEV TYGNEFLRWF SEEAVRLYGR YGTTPEGNLR
MLTALKPVGP CLLITPWNFP LAMATRKVAP AIAAGCVMVL KPARLTPLTS QYFAQTMLDA
GLPAGVLNVV SGASASAISN PIMEDDR

> RXA00663 (1-996, translated) 332 residues
LGDNDTRILA VAKNLQEEGH NVVLVSKDLP MRIKASASGI AAQEYRAALA RDRGYTGMTH
ANITDDQLSE LYDTGEVRIE ELEKLPVNHG FTLKSNSGSA LGRMNSDKII ELVPGDQQVF
GISGRSAEQR VAIDLLNDDA VGIVSIGGPA GTGKSALALC AGLEAVMERR IQRKIIVFRP
LFAVGGQELG YLPGDQEEKM GPWAQAVFDT LSSMVSQNII DEALSRGLIE VLPLTHIRGR
SLHDAFVIVD EAQSLERNVL LTMLSRIGQN SRVVLTHDVA QRDNLRVGRY DGIVSVVEAL
KDHELFGHIT LQRSERSRIA ELVTQVLDAP SL

> RXA00675 (1-483, translated) 161 residues
CGATFDGWVG DSAWSFGIGE LDEDVQGLNL ATEWVLMEGM KAMVPGNRLT DVSHALEVAT
RKAESKFGVA LGIVDGYGGH GIGRHMHEEP YLANEGKAGK GPVIQEGSVL AIEPMLTLGT
EDSAVLEDDW TVVTLDGSWA SHWEHTVAAT KGGPRILTPR Y

> RXA00689 (1-627, translated) 209 residues
MRNTGQTCYI STRIIAPSSR YAEVVQTVAS TIAAGRQGDP YDEETVFGPV ASASQYSTVM
SYIDSAREEG ARVVAGGTRS ISLSEGLESG EFIQPTVFAD VTPDMRISRE EIFGPVISIL
KYDDTNGVSE AIALANNTKF GLGGLVFGAD EEQALEVARQ VDSGSVGINF FGSNHSAPFG
GRHESGMGVE YGIEGLSAYL TYKSIHRTI

> RXA00715 (1-795, translated) 265 residues
VVTVDWLSHN LDRDDVIVLC ATMEDDEIAR QAGIPGAFLA DLEGDFSDPH SELPHTAPPN
LVGLLESYGI STDSTVVVYD LHGLMVAPRV WWLLRVAGLS SIGVLDGGLP AWVDAGLPTE
PLSLPTSGGR ISAEPQPDLL VGASGVERAI ARSSKAVIDA RNASRFAGVE EEPRPGLRKG
SIPGSVNIPF TDISDEHGFV RPAEELKELI FSRTNGAQSL VFSCGSGVTA CVDAYAAVIA
GYDDVVVYEG SWAEWGNPAN QKPIA

> RXA00744 (1-942, translated) 314 residues
MGNWAEITDE ISKIYQDNQY KIRQINDVDA VSDKRREALQ ALFEHTGRNV IVYYSAWLEN
GRRFSGQSTD FSVNDTDKNS FMTALHKLDQ SKGLDLILHT PGGDVAATES LVDYIHALFG
QDFRVIVPQL AMSAGTMIAL SSKEIVMGKH SSLGPIDPQF NGLPAHGLLE EFEQAKKEVS
ENPQTAHIWQ VILNKYNPTM LGEAKKAIQW SNSMVKQWLE KGMFLDEPDK EEKATRAIKE
LADHSVTLAH NRHISVSKAL ELGLNIKELE SDPKLQDLVL TLHHLSVIAA QRGPLIKFVV
NHDNRGTFLQ GHEN

> RXA00756 (1-996, translated) 332 residues
VNIDVQALKA IESEKGIPVP DLLRTIASAL LHSYMDNRET VASANLKPRV DIDSTTGTVN
VIVSEFDENG ELASEYDDTP SNFGRVSARA VRDAIVKSLR EAEASRAFDA YADYEGTVVS
GIVQADARAA ERGIIIVQLG TEADNQDGVL LPAEQIPGEK LKHGDRVKCF VVGVGKGNTD
IQINLSRTHP ELVRRLFELE IPEVADGSVE IVAISREAGH RSKVAVQAKV KNLNAKGACI
GPRGQRVSNI MRELGGEKID IIDYSEDPAT FVGNALAPSK VVNVEVTDLE AQTARVTVPD
YQLSLAIGKE GQNARLAARL TGWKIDIHSD ID

> RXA00772 (1-1506, translated) 502 residues
MSDRIASEKL RSKLMSADEA AQFVNHGDKV GFSGFTGAGY PKALPTAIAN RAKEAHGAGN
DYAIDLFTGA STAPDCDGVL AEADAIRWRM PYASDPIMRN KINSGSMGYS DIHLSHSGQQ
VEEGFFGQLN VAVIEITRIT EEGYIIPSSS VGNNVEWLNA AEKVILEVNS WQSEDLEGMH
DIWSVPALPN RIAVPINKPG DRIGKTYIEF DTDKVVAVVE TNTADRNAPF KPVDDISKKI
AGNFLDFLES EVAAGRLSYA GYIMQSGVGN VPNAVMAGLL ESKFENIQAY TEVIQDGMVD
LIDAGKMTVA SATSFSLSPE YAEKMNNEAK RYRESIILRP QQISNHPEVI RRVGLIATNG
LIEADIYGNV NSTNVSGSRV MNGIGGSGDF TRNGYISSFI TPSEAKGGAI SAIVPFASHI
DHTEHDVMVV ISEYGYADLR GLAPRERVAK MIGLAHPDYR PLLEEYYARA TSGDNKYMQT
PHDLATAFDF HINLAKNGSM KA

> RXA00773 (1-1143, translated) 381 residues
VTLKIGPFDL ASPVVLAPMA GVTNVAFRTL CREQEMQRTG TISGLYVCEM VTARALVERN
EKTMHMTTFA PDENPRSLQL YTVDPKYTYE AAKMIVDENL ADHIDMNFGC PVPKVTRRGG
GSAIPYKRRL FENIVSAAVK ATEGTDIPVT VKFRVGIDDE HHTHLDAGRI AVDAGAKSVA
LHARTAAQRY SGEADWNEIA RLKEHLADTG IPVLGNGDIF AASDATRMME QTGCDGVVVG
RGCLGRPWLF AELSAAVRGE EIPEEPTFGE VTQIILRHAE LLMQHDGETK GLRDLRKHMG
WYLRGFPVGG EFRSNLAKVS TYVELEDLLA PWADSTAKAE DAEGARGRQG APAKVALPDG
WLDDPEDATV PKGAEMENSG G

> RXA00778 (1-834, translated) 278 residues
RNNFAAAQVA FGGSDSAMKD DQAAEAEARC NGNEAWHLPF VIGPVAVAYN LPGVDTLNLD
TNIIAQIFKG EITKWNDEAI ASQNEGTDLP DQDISVLYRS EESGTSDNFQ KFLGASTDIW
ETEGQQFPTE VGSGAQGSNG VASEASNIEG AITYVEAGFA NQSGLGVANI DFGSGPVELN
AESVGVALGA LDFLTEGHNM VVDTDAMFAM NEAGAYPLIL TTYEIVCSAG YDETTRDQVK
DFLTVALDSQ DDQLEALGYI PVTGEHYDRL VAAVEAIQ

> RXA00787 (1-594, translated) 198 residues
VSQPLSKRLS IRKALASAFI VALAFSLSPV AKAQANETPT MIVLDNSGSM TAQDAGGQTR
IDAAKQASTQ LINDISDRTD VGLTYYGGNT GETEADVEMG CQDVTILGGP SRGNADTLID
TINSLQPRGF TPIGKALTDT AAELPEGGNI VLVSDGIANC TPPDVCEVAQ ELAQSGINLV
INTIGLNVDP AAREELEC

> RXA00791 (1-828, translated) 276 residues
LFLTDLPQES RFWKIPVEPG ETISVSANTV TDPTVLTMGQ GGIKLEAQLH TEEAPQYGLR
GRCTRVSFDN FKPGLGVRGI QNASVASKEV GTNNCDTDAI YLEISRSGDY LNGQDIPTEI
TIERFGKVDE STIGNVTEEH SSVDLTEAAA SEAHPVTPGQ WFTSAADLDP AGEKVSSIIV
PGETHFYALP VDYGQELRAA VETTFDQIDS SALGTHLYIQ AFSPNRAEIE LTNRDTSYAD
DNGLKTFGFF TPVSAANLFE KSSQGISLRS PWQGGT

> RXA00793 (1-1176, translated) 392 residues
MSENNPTTLH WFLPTYGDSR GITAGGHGFG FHSGSRTADL DYLSQIALAA ERNGFESVLT
PTGLWCEDAW ITTAALLSRT SKLKFLVAIR PGQVSPTIIA QQGAAFQKFS NNRLLINVVV
GGEDHEQRAF ADYSSKEERY HKADETLEII DHLWNSAEPL NFQGEFLSVE NAVLKEQPEV
SPPIYFGGSS QLGIEIAAQH SDVYLTWGEP AEKVEEKLAR VRAEADKRNR ELDYGIRLHV
IARPTEDEAW SVAQNLLDQL DQEEVARIQE GLARSQSEGQ RRMTELHGQG AAFTAGADAR
SLEIAPNLWA GVGLVRGGAG TALVGSYEQV AQAILRYRDI GLSHFIFSGY PHLEETYHVG
EGVVPELLKL GVPVNNHEEQ RNDVVATPFI SR

> RXA00797 (1-360, translated) 120 residues
MATAENTTQE NRKILFNAFD MNCVAHQSPG LWTHPKDKAR DYNTLDYWVH LAKTLEKGLF
DGLFIADVLG TYDVYGSSNE AALSSGAQVP VNDPILLVSA MAYATKNLGF GITAGTAYEH

> RXA00820 (1-363, translated) 121 residues
VNTFADATDD QQWIHTDPER AKDGPFGGAI AHGFLTLSMI IPFWGELLDV TGVTTKVNYG
LDKVRFTSPV KVGSRIRMGA VVREISEVKG NGLHLVADGT IEIEGQERPA VVATFLTRFY
A

> RXA00833 (1-369, translated) 123 residues
MAKTHFQGNE TATSGELPQV GDNLAEFNLV NTELGEVSSK DFQGRKLVLN IFPSVDTGVC
ATSVRKFNEA AASLENTTVL CISKDLPFAL GRFCSAEGIE NVTPVSAFRS TFGEDNGIVL
EGS

> RXA00844 (1-834, translated) 278 residues
MSSASFTTKA LSVLAALTAA SAPLVAASPA HALANARNVT GSSTTSDSIV RLHIGNTACT
GTMITPTWAI TARHCIPEGG IAGAAIGSST LSQFQQVSQA ILHPTADLAL VELPNQASSN
TVDLYGAHVQ PGENGQAAGW GGYSAFGQNV AQQADVQIQR RVVNVPSPDR TAVLLEGTVS
NGRLVPGDSG GPLYINGQLA GVLSMSTDVE NDALDGTVGW YIPVAEHAEW IAYYTGKHIA
PIAGAPAELV DATANPTFIP APQPFTGSSI GGWALGSS

> RXA00857 (1-1290, translated) 430 residues
AVGIEVPNSD REMVRLGDVL NARATVENKD SMLIGLGKDI EGDFVSYSVQ KMPHLLVAGS
TGSGKSAFVN SLLVSLLTRA KPEEVRLILV DPKMVELTPY EGIPHLITPI ITQPKKAAAA
LQWLVEEMEQ RYMDMKQTRV RHIKDFNRKI KSGEIETPPG SKREYRAYPY IVCVVDELAD
LMMTAPKEIE ESIVRITQKA RAAGIHLVLA TQRPSVDVVT GLIKTNVPSR LAFATSSLTD
SRVILDQGGA EKLIGMGDAL FIPQGAGKPQ RIQGAFVTDE EIQAVVDMAK AQRQPEYTDG
VTEDKASEAK KIDADIGNDL EDLLEAVELV VTSQMGSTSM LQRKLRIGFA KAGRLMDLME
TRGVVGPSEG SKAREVLVKP EELETILWML KGADPADAPK EETWDDEVAA EAEEAANTTV
VQADPSKGVC

> RXA00860 (1-894, translated) 298 residues
MTARRAADTS EERTGSAFRA VGSGIGTLFG ATASGLGKMT RSIGELGRRR NEDVLDDFDD
FEEEIATKPA TRKSRSKAVE PEPEFDEDFD EQSGNRTSAY VEEHADGIAL SLVGIAIVLG
AAVWLGIGGP IGTFIADIVH LAIGAGAWIL PVGLIGWAVA LMLRYTPERQ AQGRVMLGIG
VIIVCMLALI HLFAGNPAEW EGRKTAGGAI GAWIGTPLEL GFSVFLAVPI LLLLLFWGAL
KTTGISIREF IEFAGGFFGF AGFNRDEDEF DEEDDDLYGH VERELESRAS GRAPSRTP

> RXA00866 (1-945, translated) 315 residues
MNDSRNRGRK VTRKAGPPEA GQENHLDTPV FQAPDASSNQ SAVKAETAGN DNRDAAQGAQ
GSQDSQGSQN AQGSQNRESG NNNRNRSNNN RRGGRGRRGS GNANEGANNN SGNQNRQGGN
RGNRGGGRRN VVKSMQGADL TQRLPEPPKA PANGLRIYAL GGISEIGRNM TVFEYNNRLL
IVDCGVLFPS SGEPGVDLIL PDFGPIEDHL HRVDALVVTH GHEDHIGAIP WLLKLRNDIP
ILASRFTLAL IAAKCKEHRQ RPKLIEVNEQ SNEDRGPFNI RFWAVNHSIP DCLGLAIKTP
AGLVIHTGDI KLDQT

> RXA00877 (1-1065, translated) 355 residues
AAAVGTEGYV VPLELPTVQS EQAVLTESAS RAKLYEASQK RGASLNKDVL LETVRLRAER
ATLLGYDTHA DYVIEEETAD DVAAVRALLY DLAPAASANA KAEYKLSAEE AEEHGQKVGA
ADWSFWEAKV RARDYALDET ELRNYFPLNQ VLRDGVFFAA NRLYGITVEP RPDLRGYAEG
VDVWEVLDSD GSGIGLILTD YYGRPSKRGG AWMSSFVDQS ELLGTKPVVV NVMGITKPTT
GEALLSLDEV TTIFHEFGHG LHGLLSKVRY PSFSGTSVPR DYVEFPSQIN ENWAFDPAVV
RNYARHVDTG DIIPDSLLEA VEACGISDRV VEHVSTCPHL LSTCPVSPCP QRMPH

> RXA00888 (1-1017, translated) 339 residues
VTAPRKTRTE VITTVLNLER TLAQTVLGIN DENLRVLDNQ IDCDIHVRGT HVELTGPAHE
VSRASKIFEE LQAIARRGHV ISPETVKNVI SMINVETPQT VSEILTGDIL ARRGKVIRPK
TLGQKHYVDA IDTNTIVFGL GPAGSGKTYL AMAKAVQALQ SKQVSRIILT RPAVEAGEKL
GFLPGTLNEK IDPYLRPLHD ALRDMVEPEV IPKLMEAGIV EVAPLAYMRG RTLNDAFVIL
DEAQNTTPAQ MKMFLTRLGF GSKMVVTGDI TQVDLPGGQK SGLRLVRHIL RGVDDVHFSE
LTSSDVVRHQ LVGHIVDAYE DYEEREAREL KRKRQETRP

> RXA00892 (1-894, translated) 298 residues
MSATSSVTVE CPAGTITGEP HYFRSIPYAK ARPFADAEKL EPLRIDATGK HEGLYLTLAT
PEARFGADAP VIVYIHGGGY DGGTRFDART EPTFFREQGF VVVSIDYRVG LEGFARFHDD

EANRYRGIDD CVLALEWVQK NIEHFGGDPT NVTLIGQSAG AGIALWLTRL DHYKGAFRRL
VALSPSFPRQ PFAARKGALR RALGKPVTRA SLAGIKPARL DKGYRRFARR YFTDLALGPT
PYDPNELADI DLIISSTRDE MYGHRAGLWF DQRGFGAKLA ARLFGLENSD TNIKEAPR

> RXA00905 (1-693, translated) 231 residues
DPNLLEDYAG AKEWVKETLT NAGLTVSEFA AEDGTTNFIG TRKGSEGAPK VLLYSHFDVV
PSGPLDLWDT NPFELTERDA GHGTRWYGRG AADCKGNLVM HLAALRAVEA SGDTTLNLTY
VVEGSEEMGG GALSALIKDK PELFDADVIL IADSGNASVG TPTLTTTLRG GGQVTVTVDT
LEGAVHSGQN GGAAPDAVAA LVRVLDTLRD EHGRTVIDGC QHHRKLEGRA L

> RXA00903 (1-633, translated) 211 residues
MGNPLAVIAD ADDLSAEQMA RIARWTNLSE TTFLLKPTQE GADYRVRIFT PTGELPFAGH
PTLGTAHVFR ELHGEQGTQL VQECVAGLVA VRAIDGPASG LAFQAPPTLK DGPLDASDLD
AACEALGISP DFIRAHQWVD NGPGWAVVEL PSAQHVLDLE PDFSAHPTLK LGVIGAYPEG
APHAFEVRAF AQGIGEDPVT GSLNAFIAQW L

> RXA00906 (1-504, translated) 168 residues
MNTDAPLSTA VNTTANWKGE PYDPETFRSD AGILDGVDIM GDGDNPASML WSRPAISITG
FTSTPVAEAL NAVPATASAK LNLRVPAGLE ANDVAEKLKQ HLINHTPWGA KITVEIDDIN
QPFSTDITGP AMSTLASCLS AAYEGKDLVT EGSGGSIPLC TELIEVNP

> RXA00907 (1-123, translated) 41 residues
LALYGVEEPL TVIHSANESV DPNEIRDIAT AEALFLLNYT K

> RXA00912 (1-273, translated) 91 residues
MDNTLYTAGL TIAAAFFMLS FIFTIYRIIV GPNSIDRLLG LDGTVSMIQC SMATYICWTL
DTTVTNFMMV IALLGFISSV SVARFRKRDG A

> RXA00944 (1-972, translated) 324 residues
VDFWTILDTM TSLLTPIAIR GLEIPNRMWL APMCQYQANN LDGVPLDWHL VHYGARAVGG
FGLLIAESTG ISPEGRISSR CTGLWNEAQV EAWERITNFV HAQGGLIGVQ LNHAGRKAST
YPALPNFPTG TQSVDEGGWE TFGPSAVAQP GLADPTELTR EGIEKVIQDF AAAAERAVRA
GFDAVEVHGA HGYLLHQFLT PLANKRTDIY GGSFENRTRL FREVAQAIRA VIPGSMPLIA
RISATDWIDD EPSWDDDQTV SLVSGSEKAG CGCSRYFHRR CSTRDNPCGA ELSSEICSSC
EARGGYPYLR GWINYSCGSG AGAS

> RXA00961 (1-432, translated) 144 residues
LENWRIGRML LLGDAAHAPL QYLASGAVMA MEDAEAVALF AADAARAGNL DWEEVLAEVE
AERRPRCSRI QTVGRFWGEL WHVEGTARLI RNEVFRQADR NGWFIYADWL WGYDASKRAH
IANPELGEMP QALKEWRYAL LEQK

> RXA00964 (1-1125, translated) 375 residues
MGAPGKNDYA TEHVKQEVPP ATPEEQAELD TMYKRMDDLH LKPLWTQIGG LMPNHPEPRA
VAHKWDWAEL LKLAQRSGEL VPVGRGGERR AIGLANPGLD GNTYISPTLW AAIQYLAPGE
NAPEHRHSQN AFRFVIEGEG VWTVVNGDPV PMRRGDFLLT PGWNYHGHHN IATEPMAWLD
GLDIPFAYQM DTGFFEYGTE KLTDESTPDL SRSERLWAHP GLRPVSFPGK TSYSPIGRYA
WEHTDAALND QLALEEAGHP GTVAPGHAAI RFSNPTTGGD VMTTIRAEFH RLRPGASTAP
IHEVGNRCFQ VFEGSATINV GDKTFEANHG DVINVPSWQK WNIVAGSDGV DLFCFSDTPI
FEALNLARTF TPEGI

> RXA00977 (1-1014, translated) 338 residues
MPTAAAQENI RWEECPPQVD IASAQCGSID VPMHYSDPSL GDISVGFVKV PAQGEKHGTI
FGNSGGPGGD AYSFFGSQSM NWPEAMYQNY DLVAVQPRGM VGSTPVNCDN IAPGYDFLSL
LTREGAFVKE SCEIGTPGYT SSLTTDNTAN DWERVRQALG DDKISIFGLS YGTYLGSVYA
TRYPQHTDKV VLDSAMAPSL AWNGIMASQE QGYKNSLNDF FTWVAENNDT YGLGTTPLAV
YQNWSNKIVA ETGTNPTVAP PPAQVGDVPP AFAWAGQAGA DMMTATNPTS VQLQGLATQL
LNPGSNQSLS PLLNVTRAYI PQPSTWPMLA GAISGQTP

> RXA00982 (1-246, translated) 82 residues
SQLAVQPLLL QGTSDPQTPY WTHNELADAM NAHVVTVNGP GHGQSIGGTN QAINDIVVDY
LRTGHTDATW VEGNTPTPIT AG

> RXA00983 (1-1197, translated) 399 residues
VTAGETTTMN VTLTNPFDNA IFDRAVSLER PEGWQAEDVR VSIPSGESVT IPVQVTAPLV
ADNGELPVEV SILDGADRYT GRLNLTVQGG QEPAPTSVKV SIPNLKDTYV AGEKISINFA
VNNPFDVTVN SVPSLGEGEN WMPANLRGFD PEQGTPNCRY KNLGANKSYD CTTTTYEVSD
LDVERGYVDI PTVWTFTNSA GETVWSKNVD VPRVELNGTQ DAVTDAIVTV DPINPVHSNG
QSQTVEVQAN VTSEGDLPAG SKVAFYLDSS PIDTAAVDAE GHASISIDVD NIASEQPERT
FEVRARLVVP EDAPRSIARD ALARFTVLSE QVQQNSLVIM NHPDVFSDGQ TKTIVIAAKA
TAHDGSPAAI GTLIAFRVNG IERDVVPTNA QGTAKLQLD

> RXA00984 (1-417, translated) 139 residues
QRGTPVLLGE TPWMKTKIVE LSDGTLMNNS RSSGADTYRK VSYSTDGGVT WTEPTLDTQL
PDPRNNASLI RVFPTAPEGS AQAKVLLFSN TATTSGRTNG TVRMSCDDGQ TWPVSKVFEP
GAIQYTSMAT LPNGDIGML

> RXA01014 (1-1578, translated) 526 residues
DDLWLNESFA TWSAAISQAE ETEYNTAWVT FANVEKSWAY QQDQLPSTHP VFSDGYDIET
VDQNFDGITY AKGASVLKQL QAYVGREEFL AGVRRHFANH AWGNASFDDL LGALEQSSGR
DLSDWANQWL KTTGINTLGA KFTTDNGKYT SFSVTQTGAA PGAGELRTHR IAVGLYKLVD
GSLNRYARVE LDCSGASTSV EEIVGLEQAD FVLVNDDDLT YALLDLDDDS RNFVIDNIDK
FSDPMPRTLV WSAAWEMTRA GQMKARDFIA LVARGAAAET EIAVLERILA QATSALKSYA
DPAWAEATGN DLLADAFLEG ARSAEPDSDT QLAFIQALAK ATLNDAAADY FRDILAGNVE
GLTVDPDLRW WALTALIARG DIEAVEDAIA AELSRDNSSA SFLASLRAGA AVNTEEVKAA
AYKHVPAVDS GLSNLELRHK IEGLTFTGSF ELLQAYNEQY FEILDDVWAN FSGEMAQQIV
LGLFPSWNVS EEGLKRTDEF LDGEHVAGIK RIVSESLDRT ARALRN

> RXA01018 (1-864, translated) 288 residues
LTSTNLTRQE ASDRSRLLSV ENYDIALDLN NGDEFFSSST VVSFTVRKAG DTFIDLRAAS
VEEVRLDNVS IKDEALTLGK NGYDETFGIA LKGLTPGAHT LRVTASIPYS RTGEGLHRMV
DPADNEVYLY TQFETADAKR MFACFDQPDL KATYDLNIKT PKGWKIISNS EQQVSTQHTD
YDTHISRVDY PLSTYLIAVC AGRYHEVCDV WKGTLTHHAE TPADQPTELT VPLALYCRSS
LAKDLDAVRL FTETKQGFDW YHRNFGVAYP FGKYDQIFVP EFNAGAME

> RXA01022 (1-804, translated) 268 residues
HFSDGSLYAT ADVIFPVLHG RFGEDGTVQG LFALSDIPVV GPGVLASAAG MDKEYTKKLM
AAEGLPVGRE VILRDRTELT EAEKNLLGLP VFVKPARGGS SIGISRVTAW EDFNKAVGLA
RAHDEKVIVE SEIVGSEVEC GVLQYPDGRI VASVPALLSG TESGAGGFYD FDTKYLDNVV
TAEIPAPLDE KTTELIQSLA VESFQALACE GLARVDFFVT ANGPVLNEIN TMPGFTPISM
YPQMFTASGV AYEELLDVLV QQALHRDN

> RXA01055 (1-102, translated) 34 residues
MWGVVLGPAT GKYLAELMAT GNTNPIIKPF DPLR

> RXA01056 (1-900, translated) 300 residues
MSSSGKVIVV GAGIVGLATA WHLQEHGFEV SVLDRDGVAA GSSWGNAGWL APAKTIPLSE
PGLWTYGPKE LFNPVSPMHM PLRVDPKLWL FLAQFMAQAF QRKWDSTMAD LTEIDKVALE
AFDELSIGGV EGLTHEGPFV IGFEEERQSA GFRKEIDGVS RHGQKVEMSR LENPQELAPM
LNEQIQVAYR LEGQRFIEPG PYVQSLADAV VKRGGVIRAG AEVVHVAKGD RPAVILADGS
REEADKVVVA TGAWLPGLTR EYGVKTLVQA GRGYSFSVAT DIPAKHSVYL PHHRHGLHAV

> RXA01057 (1-1503, translated) 501 residues
LPEGQSGTIV LVSDGIATCT PPPVCEVAAE LADQGVDLVI NTVGFNVDES ARAELECIAQ
AGNGTYADAS DADSLVAELK RAATRTAVGY ESDLEQIDGN SSQTSLTPIP DDVELFKADL
PALDNKDGEV TQYWSIPVED YERVQVTTSY VAPVTFGLGN DYLSIRNELL FGDEQDQTCH
RSISNDQILD NYGARPLVAS VESDVIGDKC DTDELVLAIT RSQPFNWEEE LPVEIVVKRL
NHADTSGLPL GDQQREIPDL DVAAVQTWAP TTGGSWFTNA TELTPGEGVE AEIVPGENHV
YRLPMATGQQ LHGFVEVVEN TAPDDPGVTD KLGVAVYSPT RQDAGVDMWT DIAPREGTSE
YFAAPVALTY LNMFPAEGGF GTTSKATSTF TFEGDYYLVV HYDDLSGSTI RDASNQQSFP
LRYRLAADAF GDAEPGPVFE KVSATTSESS SPSTQPDEPA QNTATEESST GISPLIVGAI
VALILAFAAF ASWLVLKGRK K

> RXA01059 (1-609, translated) 203 residues
MTTVTQDLLA LDEDAQNLLF REARTANAFT DEPISDEQIE AIFDLVKWAP TAMNSQPLRV
VIVRSEEAKA RLVPLMAEGN QAKVAAAPAV ALLAADIDFH EEMPKLFPPF PGARDMFEAD
EASRASSAEL NAGLQIGYAI IGIRAAGLAA GPMTGMDADA ISKEFFPDGR HRVLVAINMG
KPADNAWYDR LPRLEQDEVV ETL

> RXA01073 (1-831, translated) 277 residues
MTNTQTEIIN ELKVSPAIDV AKEVEFRVQF LVDYLRASHT KGFVLGISGG QDSTLAGRLT
QLAVERIRAE ENSTDYVFYA VRLPYAIQAD EDDAQVALEF IAPDKSVTVN VKDATDATEA
TVAAALELPE LTDFNRGNIK ARQRMVAQYA IAGQLGLLVI GTDHAAENVT GFFTKFGDGA
ADLLPLAGLS KRQGAAILEH LGAPSSTWTK VPTADLEEDR PALPDEEALG VSYADIDNYL
ENKPDVSEKA QQRIEHLWKV GQHKRHLPAT PQENWWR

> RXA01082 (1-660, translated) 220 residues
LTQWGNSNVV EDYLTALFRA EEWDEEPTTG KLAEVIGVTA STVSATLKKL NPEGFVNYRP
YGDIELTPAG RDIAINVIRR RRIIETYLSE KLGLGAHELH GEADLLEHAV SPLVLEKMFQ
AVGYPTLDPH GDPIPTESGE MTINDGLMLL GLKAGASATV TRVRDGNPSV VRYLTGVGIT
VGTTVTVVEA LSDIATLRLQ IGEMFQDIPL AVANAVRVSR

> RXA01090 (1-312, translated) 104 residues
MALPLPSKSA RALVTGASQG IGLAIAKDLA RYGHNLILVA RREDVLKEIA ADLEKKHGVI
VEVRPVDLSD EPARKVLIDE IKTREINIII NSAGIGKLWA VQGP

> RXA01113 (1-237, translated) 79 residues
GDIWERPGLD HTQRRLLTIA ILTAVGNDGE LDMHIRAALR AGVDQETIGE VILHTAVYAG
VPNSNHGFKL LNNAVSDLQ

> RXA01117 (1-741, translated) 247 residues
MINKSISSTA EAVADIPDGA SIAVGGFGLV GIPTALILAL REQGAGDLTI ISNNLGTDGF
GLGLLLLDKK ISKSIGSYLG SNKEYARQYL EGELTVEFTP QGTLAERLRA GGAGIPAFYT
TAGVGTQVAE GGLPQRYNTD GTVAVVSQPK ETREFNGQLY VMEEGIRADY ALVHAHKADR
FGNLVFRKTA QNFNPDAAMS GKITIAQVEH EVDELHPDEI DLPGIYVNRV VHVGPQETGI
ENRTVSN

> RXA01120 (1-1278, translated) 426 residues
MARMQESADL LKCSFCGKSQ KQVKKLIAGG AVYICDECIE LCNEIIEEEL GQAQHDEQER
NELPKPSEIS AFLDTYVIGQ DPAKRILSVA VYNHYKRLRA SETIGRRRND EPETELVKSN
ILMLGPTGSG KTFLAQTLAK LLDVPFAIAD ATSLTEAGYV GEDVENILLK LLQAADFDVE
RAQRGIIYID EVDKISRKSE NPSITRDVSG EGVQQALLKI LEGTVAAIPP QGGRKHPNQD
FIQLDTTNIL FIVAGAFSGL EKVIADRNGK KGLGFGVEVS SKKEEANIVD IFKDVLPEDL
VKFGLIPEFI GRLPVVATVS NLDQKSLVKV LTEPRNSLVK QYRRLFEMDD AVLTFTDDAL
EEIANQALER KTGARGLRAI MEEILVPIMY DLPDRKDVGE VIINGAVARG EAEPEMLEAV
AEEKTA

> RXA01224 (1-1023, translated) 341 residues
MSILDTLKTP VIVAPMAGGP STPALVNAAA EAGSLGFLAG GVMPLEQLKQ ELSEVKGVFG
VNLFRPQTDA PKPSDIDELA GLLSSAFRQF GLDEPTVPTP DLSNGWEAKF EAVLAAKPAV
FSCTFGIFSA EEFARIKATG IEAWVTVTNP EDALAAQKAG ANALVVQGPE AGGHRSTWSI
EVEPDERDLK TLLAAVKQAG VYLPLIAAGG LSTSADVAAI LEAGASAASC GSAFLLSDEA
GTSSLNREIL DAAPALGLES VSSRAFSGRY ARGVETRFTR SNEGLPPLYP YLNPMITSLR
KVAGSAGNWD YAYCLVGVGL ESIAKGSAKQ ILESLTPSAL G

> RXA01126 (1-564, translated) 188 residues
SAESLPPTLF LKPPTAVTGP ESPIRIPSFA TKVEFEGELA VVIGKPCKNV KADDWKSVVL
GFTIINDVSS RDLQFADGQW ARAKGIDTFG PIGPWIETDI NSIDLDNLPI KARLTHDGET
QLKQDSNSNQ MIMKMGEIIE FITASMTLLP GDVIATGSPA GTEAMVDGDY IEIEIPGIGK
LGNPVVDA

> RXA01147 (1-1260, translated) 420 residues
MHVTDDFLSF IALSPSSYHA AAAVERRLLH EGFIRQEDTD EWDARPGGHV TVRGGAVVAW

WVPEDASPDS GFRIIGSHTD SPGFKLKPRG DLSSHGWQQA GVEVYGGPIL PSWLDRELAL
AGRIVLADGS VKLVNTGPIL RIPHVAIHLD RTVNSQLTLN PQRHLQPVFA VGEPDVSILD
VIAGAAVVDP ADIVSHDLIT VATQDAEVFG AHGDFLASGR LDNLSSVHPS MTALIAASQS
DDTGSDILVL AAFDHEEVGS NSTSGAGGPL LEDVLNRTAR ALGADEDERR RMFNRSTMVS
ADAAHSIHPN FPEKHDQANY PIIGKGPVLK VNANQRYTSD AVTSGMWIRA CQIAGVPHQV
FAGNNDVPCG STIGPISATR LGIDSVDVGI PLLSMHSARE MAGVKDLMWF EQALEAYLVN

> RXA01151 (1-858, translated) 286 residues
MSSPTDSSPS NSFSDFNREE QSRLSDEVRQ LKRTNSDLGA RNAKLAEMLK SSRDKLSVLF
SQLEDMAQPP SVYGTFLETA KDGSNAEIFA GGRRMRVAVS PMLCAADLMP GVQVRLGEGN
QVLEACDFEQ TGELATLMEM IGRDRALVSD RSGEERVVKL AGPLMDRTAK LPRPGDTLLV
DRKAGYAFEA IAKTEISRLA LEEAPDVSYQ DIGGLDDQIE LIQDAVELPF LHPEMYRAYN
LHPPKGVLLY GPPGCGKTLI AKAVANSLAN RIGETGTSYF INVKGP

> RXA01161 (1-1137, translated) 379 residues
MSDPSTNNFP TSVYAQRLAD AQEGARKAGL NGLIIGTGAE LAYLTGSWIS THERLTALVI
PSEGTATIVL PAVDRGDLAL SAIPGLDINV AGWVDGDNAH ELAVDALGVS EFEALGIGSS
ITADHLIPIQ NLVGSTCRME LAVQVLKELF VSKDEAEIEQ LRGAGAAIDR VHAKVPELLQ
DGRTEAEVAA QLNDLILEEH SEVDFVIVGS AENGANPHHG FSDRVLRNGD IVVVDIGGTF
GPGYHSDCTR TYIVGGNPDD ADPEFAKFYQ VLYEAQLAAV AHVRPGVTAE SVDAVARDHI
AAAGYGEYFI HRTGHGIGLS THEEPFIMAG NSLVLEAGMA FSIEPGIYIE GIHGARIEDI
VVVNEDGCET LNNQPKELR

> RXA01181 (1-957, translated) 319 residues
SVLLARDLVN TPSSHLYPES YSVIASNEAS KHGLQTTILD EKQLADQGFG GILAVGNGSS
RKPRLLRIDW KPRKAKKSIA LVGKGITFDT GGISIKPGAS MENMISDMGG SASVLATIIA
AARLNLSINV FAFLPMAENM PSGDAFRPGD VITHFGGITS EILNTDAEGR LILADAIAYA
SEDKPDYLID AATLTGAQLV ALGLRTSGVM GTDEFRDSVA KTGREVGEQA WAMPLPEELD
EQVKSPVADL RNVTNSRFAG MSAAGRYLQE FVGADIEWAH VDIAGPAYNT AGEFGYTPKR
ATGQPVRTFV QVLKDLSES

> RXA01182 (1-393, translated) 131 residues
VFNLFGRKTP RSNLRPPRGP GDTVRPEDLK FLMQWVQDKP FVEAFVEPET LVNEMSVVLV
DAHGVFVRRR IGGPKGIDVI AKKLGVPVYD VEETGYPQRM RERIEYERIL RKREEQKARR
AKFERGENPD L

> RXA01189 (1-609, translated) 203 residues
MISISIADDE ALIASSLATL LSLEPDLDVR PTAGSGEELI ETWADPSNRT DVCVLDLQLG
GIDGIDTATR LMETTPDLAV LIVTSHARPR QLKRALAAGV LGFLPKTSTA DEFATAIRTV
HAGRRYIDPE LAAMTISAGE SPLTNREEEV LELAGQGLSA EEIAVAAHLA PGTTRNYLSQ
AMTKVGAQNR FEAFTRAREL GWL

> RXA01192 (1-573, translated) 191 residues
VAARYADTYL TWGETPDQVA QKINWINELA AQRGRELRHG IRFHVITRDT SEEAWVVAEK
LISGVTPEQV AKAQAGFATS KSEGQRRMAE LHSKGRAFTS GSTARDLEVY PNVWAGVGLL
RGGAGTALVG SHEEVADRIE EYAALGLDQF VLSGYPNLEE AFHFGEGVIP KLLRRGVDIK
NQESRVLEPV G

> RXA01214 (1-1491, translated) 497 residues
VLAATVVGAQ VLVACSSDDV RGYGGEPRTL PIPPADLGTR EGSSVHFALE AQTGESQILP
DVTTKTWGFN GTHLGPTLVV KKGDDVHVDV INNLDEMTTV HWHGMKLPAI ADGGPHSPIG
PGQTWSPTWT VANDAATLWY HPHTHGLTGL HAYRGLAGMI IVEDEATDKL DLPREYGVDD
IPLVLMDHRF LEDGSLDEED LPDLGLLGDT PTANGITNAH FDATTRRVRF RVLNGSNMRF
YNLAFSDTRT FQVIASDSGL LDEPQDRTTL AIGPGERWEI VVELEPGEDV TLESVGFEDN
YGVPDDEFVP DFGMSDSFQL LTITGPSDDA AQAPALPGVL VKSTEPDVID ATERTFIMNT
FSINDLQMDM QRVDVVIDHD QPEVWIVTND NSDWPHNFHV HDARFKVLKF EGTDVELFND
GWKDTVGLPP GATATLAVEF GHYPDPQWPY MYHCHMLYHE DQGMMGQFVI VEPGDEPAAV
LGSGTGSSID SAGGHAH

> RXA01224 (1-1023, translated) 341 residues
MSILDTLKTP VIVAPMAGGP STPALVNAAA EAGSLGFLAG GVMPLEQLKQ ELSEVKGVFG

VNLFRPQTDA PKPSDIDELA GLLSSAFRQF GLDEPTVPTP DLSNGWEAKF EAVLAAKPAV
FSCTFGIFSA EEFARIKATG IEAWVTVTNP EDALAAQKAG ANALVVQGPE AGGHRSTWSI
EVEPDERDLK TLLAAVKQAG VYLPLIAAGG LSTSADVAAI LEAGASAASC GSAFLLSDEA
GTSSLNREIL DAAPALGLES VSSRAFSGRY ARGVETRFTR SNEGLPPLYP YLNPMITSLR
KVAGSAGNWD YAYCLVGVGL ESIAKGSAKQ ILESLTPSAL G

> RXA01232 (1-687, translated) 229 residues
MSRQXXTYTD KDISQFHWTN GLPPTDDESP EWIAARDNEW EGYTITLGDD PNGTEKTITL
DDLRELPQTS YVAVXXXXQX LGQXXPXXPX GAGYRDVLCH DLVHTLDLHH RHSPRLLTIE
IIPKPLPPET RCKIIDFDLF APNSPSIEEF CSRLKISRRS FYNIRNRYQQ DASAALHPRS
SAQITSRRTY DESITSIXVG HXAHRLKAQG XGIRSDLYPI XKASXTXGN

> RXA01236 (1-945, translated) 315 residues
VLVATALIAG CSSAEDGTVD SGSSTEVTTT QSKEGFPVTV TFAPEAPVTI EDQPERIVSL
SPAITETLFA VGAGDHVVAV DEYSNYPEDA PLVQGLSGFT PNVESILDYD PDLVVLMSAD
DSILTGLDAA GVDTLVIPAA ENLDETYSQI EQVGRATGFE DQATTVVDQM KTAIDAAVAT
VPEEVKEQGL TYFHELGSDL FTVSEQTYIG QIYDMFGLTS IADGGDAYSQ LSNEAIIAAN
PDLIFLSDAK AENLTAEDIA ARPGWDTIDA VANGRIYILD DDIASRWGPR VSQLVEEIAA
QLNQLASSEA VPAAA

> RXA01250 (1-588, translated) 196 residues
LDIGGIEAKT WGYVSDTGDA AIEATAGDVL QVDITNDLPE STSIHWHGIA LHNAADGVPG
MTQDPIEPGE SFSYVFEVPH GGTYFYHSHT GLQLDRGLHA PLIIRDPQDA EDQDVEWTIV
LDDWVDGIQG TPDDELDKLT GMGSGDHNGR MGMGGHGQMM HGTPDRVLGG DVGDVMYPHY
LINGRIPRAH RTFEAR

> RXA01254 (1-1269, translated) 423 residues
MKLSLPAPLR RLRSAAAIIS AKVATSASKA TGRGSGGMIG GLVASKVDPD IMSNLINNRP
TVLVTGTNGK STTTRMLAAA MRSTYTVATN EGGDNMDAGI ISALLAGRNA SHVVLEVDEL
HVPAAIERLK PDALVLLNLS RDQLDRVGEI NKIERVLRDA VRSRPEMTVI ANCDDVLVTS
VAFDAENVIW VGAGTGWQGE SATCPRTESR ILHDGRHWSA EKTLLDGRTF ARPTPSWEVD
GDTIHSPSGD LTLDLNLPGQ ANRGNAAQAI AASTVFNVPV SSALPAVNSV NNVAGRYSTI
TVGEHKVHLL LAKNPAGWQE ALSMVDRTAD GLVIVVNGQV ADGEDLSWLW DVRFEDFENL
SVKASGERGT DLAVRLTYAE IDHELISNPV DAIAACPPGR IEVLANYTAF RDLKKALEKG
TEQ

> RXA01257 (1-846, translated) 282 residues
MHVAELSLPT GIIIAATPLG NIGDASPRLV HALANATVVA AEDTRRTASL AAALGVEIKG
QLVSNFDHNE QARVGKLIEA ARTGTVLVVS DAGMPVVSDP GFALIDAAHD ANIPVTCFPG
PSAVPTALAL SGLHVGRFAF DGFAPRKQGA RTTWLESLKT EKRAVCFFES PHRIAETLAH
AAEVLGERRV AVCRELSKTY EQVKRGTLPE LAEWAQDGVR GEITVVIEGA GDIAADVDSL
IDAAQQRVDS GERLKAVCAD LAKIHGVSKN ELYDAVISAR EN

> RXA01270 (1-1155, translated) 385 residues
MTNERIFLSS PDVTQLEEDA LVRAIRSGWI APLGPEVDAF EQELAEYCGR KYVVALSSGT
AALHLGLLAL GVGEGDLVLT SSMTFAATTN AIVYTGAEPI FVDCDESGNM DPDLLEKAFA
ELKSEGKEVK AVVPVDLLGK VVQHEKIKKI ADEYGAVVLS DAAESLGAIR NGKSAAAYGV
AAAVSFNGNK IMTTSGGGAL LTDDKDIADN VRYLATQARQ PVVHYEHTDV GYNYRLSNIL
AALGRAQLSR LDKMIERRRQ HRAFYRELFA GVSGVEIFGE PSGVDGGDTI DNFWLTSILI
DKEVAGFSSE DLRSVLNQAN IESRPLWKPM HLQPVFKKYR SFTNEEGQRL FDSGLSLPSG
SVLDNASMNR VETTIGQFLE SQHAI

> RXA01277 (1-1689, translated) 563 residues
MTDYTFLEDI DTPEALAWAE KWSGESVEKL KSPAKDALEA RLLAALDTDD RIAYVSRRGE
KLYNFWRDAQ HPRGVWRTTT LESYESDQPE WDVLIDVDAL AEDEGENWVW KGAVVRSPEF
DRALVKFSRG GADATVIREF DLATAAFVDD SPFELKEAKS DVTWVDLDTL LVGTDTGEGS
LTDSGYPARV LTWKRGTPLE QAELFFEGSR QDVATHAWRD STPGFERTFV SRSLDFYNSE
TSLETEGGLV KLDVPTDCDV IVKKQWIFVS PRTDFAGIPA GGLGVLLLKE FLEGGRDFQP
VFTPTESTSL QGLATTKNFL VLTLLNNVST EIVTVPLNDP TTEHEHIDLP EHVTAHVVAT
SPLDGDEIWV QAASFTEAPT LLRAELPGAL EAVKKAPLQF ENAGQETRQH WATSADGTKI
PYFITGAFEE EPQNTLVHAY GGFEVSLTPS HSPTRGIAWL EKGYYFVEAN LRGGGEFGPE

WHSQATKLNR MKVWEDHRAV LADLVERGYA TPEQIAIRGG SNGGLLTSGA LTQYPEAFGA
AVVQVPLADM LRYHTWSAGT SWM

> RXA01288 (1-375, translated) 125 residues
MNGIGGSGDF TRNAFASTFI SPSAAKVDAI SAIVPFASHI DHTEHDAMVV ITEYGYADLR
GLSPKQRVPK MIAIAHPDYR PLLEAYFDRA LNSADSYQHT LHDLRTAFDF HNRLNSQGTM
KIEKA

> RXA01302 (1-366, translated) 122 residues
MTTTTSSGKS SEKINPLFKL GSFLRKGTVG SEGQQIFLQG GRQADVFYRN RWAFDKVVRS
THGVNCTGSC SWKVYVKDGV ITWESQAVDY PTTGADMPDN EPRGCPRGAS FSWYTYSPTG
IR

> RXA01303 (1-1335, translated) 445 residues
VTQLNTKGVV LQGWDPEDPE HWDSKIAWRT LWITTFSMII GFCVWYLVSA IAPLLNRIGF
DLSAGQLYWL ASIPGLAGGL IRLIYMFLPP ILGTRKLVGI SSGLFLIPMF GWFLAVQDSS
TPYWWLLTLA ALTGIGGGVF SGYMPSTGYF FPKAKSGTAL GIQAGIGNLG VSIIQFMGPW
VMGFGLLGIG FLTPQRTIEG TTVFVHNAAI VLVPWTILAA VLSFLFLKDV PVTANFRQQI
DIFGNKNTWI LSIIYLMTFG AFAGFAAQFG LIINNNFGIA SPMAETYPAE MLHAGATFAF
LGPLIGALVR AAWGPLCDRF GGAIWTFVGG IGMTIATAAA AIFLSRAETP DDFWPFLWSM
LALFFFTGLG NAGTFKQMPM ILPKRQAGGV IGWTGAIGAF GPFIVGVLLS FTPTVAFFWG
CVVFFIIATA LTWIYYARPN APFPG

> RXA01307 (1-681, translated) 227 residues
VLAWRDIVET PEKRKAYVSQ RGKGGLIRVQ YEEAMEIAAA AHVYTIRQYG PDRIHGFTVI
PAMSQVSYGA GTRFLQMIGG VALSFYDWYA DLPPASPQTF GDQTDVPESG DWYNSSYLMM
WGSNIPVTRT PDSHFMVEAR YKGTKVVVVS PDFADSTKFA DEWARIHPGT DGALAFAMGH
VILKEFHVDK KTPYFMDYMR KYTDSPFLVE LDEHGDGTYT PGKFLTA

> RXA01308 (1-1206, translated) 402 residues
AATPNATHRL LVLQKDGSVV DPGGTVADRW GEEGMGKWNL RLDGVDPVMT IADVQTDTET
AEVLFPRFDL PATATQEGPI GAGTISRGVP TITLNGRKYT TVFDVLLAHY GVNREELNLP
GEWPKDFQDP VMGTPAWQEE LTGVPANQAI RLGREFAQNA DDSKGRSQII MGAGVNHYFH
ADSIYRTFLA LTSMCGTQGV NGGGWAHYVG QEKLRPMNGW AQYAFATDWQ RPPRQMITTG
FYYLTTDQWR YDNTRANRLA SPLANRGTVG DKMTADTLVE SMKRGWMPSF PQFNRNPLIL
SQEAEEKGVS VSDHIVQQLT DGDLQFACED PDAPENWPRI LLNWRTNLMG SSAKGTEFFL
RHMLGVDSDA SAEKNAPEDR PSSIVWRDEA SEGKLDLMLT TD

> RXA01309 (1-669, translated) 223 residues
IADHEGTHIN WDMVKERSAE VITSPEWTGS KKDGRRYTAF SINIEYDKPW HTLSGRMHYY
LDHDWFIDYG EQLPIFRPPL DKIHINGEVG PGQSVTGTDG EPEVTVRYLT THNKWSIHSQ
YYDNLHVLSI SRGGQVIWMS NKDAEKLGIA DNDWIEAYNR NGVVSARAIV SHRIPEGTVF
MNHAQEPTAG TPLNEKSGRR GGTHNSLTRI MIKTVHVAGG YGT

> RXA01324 (1-300, translated) 100 residues
MSNSECHTHG YIEEKQRYLA RLKRIEGQTR GIHRMIDEEQ YCIDILTQIS AVNSALKNVA
FGLLDDHLAH CVKEAADLGG DELDAKLKEV SDAIARFSKA

> RXA01340 (1-990, translated) 330 residues
VGPVLAITPW NFPIAMATRK IAPALAAGCP VLVKPASETP LTMVKVGEII ASVFDTFNIP
QGLVSIITTT RDAELSAELM ADPRLAKVTF TGSTNVGRIL VRQSADRLLR TSMELGGNAA
FVIDEAADLD EAVSGAIAAK LRNAGQVCIA ANRFLVHESR AAEFTSKLAT AMQNTPIGPV
ISARQRDRIA ALVDEAITDG ARLIIGGEVP DGSGFFYPAT ILADVPAQSR IVHEEIFGPV
ATIATFTDLA EGVAQANSTE FGLAAYGFSN NVKATQYMAE HLEAGMVGIN RGAISDPAAP
FGGIGQSGFG REGGTEGIEE YLSVRYLALP

> RXA01354 (1-936, translated) 312 residues
MKISRRAFLG TLLGATTLAV TACAQSSQNQ NSSASSSSSS SAESSTSSSS SDEQRIVALN
TGQLDNLLLL GITPVGVAAA KNSDLIPQFL KDRFGADMDL DSIADCGLRQ SPDIEAIANL
NPTLICANSR ADEEVLNKLR TIAPVVTGEG GGENWKQDLL TIAEAAGQKE KAETLLKSYE
DSAAEIAANQ PANPPTVSFL RTKDQEFQMY GAQSMAGTVA ADCGYARPEN QQFTDTAGQD

LSAELIAQAD ADWLFYGIKE GNINPEDTPL WTSLKAVQSN QAIPVDGDSW YLNASLVSAE
IILQGLKDNV TV

> RXA01358 (1-1521, translated) 507 residues
MALGRTISTA QLGVQAKIVR VEANVGPGLP GTYIVGLADT AISESRDRIK TAVQNSGLMW
PKTKVIINLS PASMRKQGSQ CDLAMTVAVL VAHGSNPKAK FHAQNTLFLG EVALDGTLLP
VTGVLPALLA AKEEGIGKIV IPEGNAQEAG LVEDPSVFLA HSIDQVLRWL DGEEALPQPG
LFNDENSLKL PDMRDVVGQP EARFAAEVAA AGGHHMLMIG PPGSGKSMIA ERIPSLLPEL
SPQQMIEATA VHSVVGRTFS GPVSRAPFIS PHHNVSKAAL LGGGSGSPLP GAISLAHHGV
LFLDEVSEIP ASILDSLRTP LEYGSIRIIR SRHDVTFPAQ FQLILAANPC RCGAEQPQEC
VCSGSARATY LNNLSGPLRD RLDMVVATHS KGAVLRSDDV EASAPIADRV AQARERAAFR
WRRSGLGNLV NAHVDPHFLR RNFAATEDAM VYLGAFLAEG TISQRGCDRA IKLGWTLCDL
DGEQQPNLDH IARAMELRGT TYSEVAA

> RXA01385 (1-1881, translated) 627 residues
MQFHYEGYAT GDPMEMRAEG SGINRPDDLP EVMDVLIVGA GPAGTIAAAQ LSRFPNVTTR
LVERSDRRLE LANADGVHSR TIETFQAFGF AHEILAEAHE ITDMAFWKPD PQNPREIIRD
NSTRELPQHI SEFPMALLTQ TRIIDHFNRF MKNSPTRMKP DYGYEFVDFE VEEDAEYPVI
VTLRRTSGEQ TGELVTVRTK YLVGADGARS QVRKSLGYRL QGKQANHAWG VMDIHANTEF
PDVRKKCTIK SDSGRTILLI PREGGFLFRL YVDLGEVPDD GSKAVRDTPL QDVIDTANQI
MAPFTLDVKN VVWNSIYEVG HRVADHFDDR VSEKTSSEHP RIFIAGDACH THSAKAGQGM
NVSMQDGFNL GWKLGHVASG NSPRELLQTY AEEREDIAYK LIEYDKNWST LMAKPSSEMG
SAQDLEDFYR ANSEFNAGYM THYPPSSITM DGSNQDLAKG YPIGRRFKSA MVGRVCDFTE
THLGHQATAD GRMRAYVFAG SDALNGEGSE LDRWAEWAEA NLDPTLVDAK VIYQSPYTEL
DTRQVPSVFK PAVGIFELTN VENSFGITTD SDIFDSREIS RDGVVVVVRP DQYVSGIFPL
TDTQGLGEFL TGYFPKMKGA HQLINAN

> RXA01412 (1-204, translated) 68 residues
MALKNYTVEG MTCAHCVASV TEEVSEVNGV SAVDVTLESG NVAVSGEGFS DAEIQAAVEE
AGYKIVAS

> RXA01426 (1-627, translated) 209 residues
MTTPPAAAEI FGDNLEKAIA YHESLATDGS VRGFIGPREV PRLWDRHILN CGVIGEAMDE
GISVADIGSG AGLPGIPLAI ARPDLNITLI EPLLKRSVYL NEVKEALNLD NVTVVRGRAE
EKVVRKQVGL VDIVTSRAVA PLGKLATWSL PLVKIGGRMV AMKGSSVEEE IERDAKEIRK
AGGTDIKVYT VGEALLSEPT TLISIRREK

> RXA01427 (1-921, translated) 307 residues
MEDTTWEDTP IAAAARRAAQ VMTPNSLTLP KPKEPRLITI ANQKGGVGKT TSTVNLAASL
AIHGLKVLVV DLDPQGNAST ALGVEHRSGT LSSYELLIGE CTADEAMQPS TANENLFCIP
ATLDLAGAEI ELVSLVRREY RLADALGREF IDKHDFDYMI IDCPPSLGLL TINAMTAVNE
VLIPIQCEYY ALEGVGQLLN NITMLRQHLN RQLHISAILL TMYDARTNLA EQVATEVNDH
FGDVVLGNKI PRSVKVSEAP GYGQTVIEYD PGSRGAMAYL DAAKELATRG DYLPSDESGP
IGLKPAK

> RXA01428 (1-1137, translated) 379 residues
MAQNKGSDKS QTEKRKGGLG RGLAALIPSG PSNSPGLGGG AADIILGGTV GARTAAAPKR
ESTPAAPAPE APAQAAPQHT EATKPEVVPE PAAPAPTQSA QQEAPQAQPA QQSEFGASYL
EIPIEQIRPN PQQPRHEFDP QALDELVHSI SEFGLMQPIV VRRSEDGYEL IMGERRWRAS
KRAGLEVIPA IVRETEDSAM LRDALLENIH RVQLNPLEEA AAYQQLLEEF GVTQAELADK
LGRSRPVITN MIRLLGLPVN VQTKVAAGVL SAGHARALLG LKAGEDAQDT LATRIIAEGL
SVRATEELVL LHNRGDQDEE KKPREKAATP EVFTRAAESL ADNLDTKVSV MMGKKKGKLV
VEFGDKDDFE RIMSLIQGQ

> RXA01430 (1-1188, translated) 396 residues
VSKVLRVGDR SPRVAEVRTT LARLGVIEGY SREMSAKTES QKFHEEETLF DEELSLSIKS
FQQARGVVPS GLIDDPTLRA IREASYTLGT RVLAYQPGNQ LVGDDVVEIQ SHLQELGFYA
DRVDGHFGEL THKAVMNYQL NYGMQVDGIC GPDTIRALSR LGLRIKGGSA QAIRERERMR
NAGPRLAGKR VVIDPALGGS NKGQIVKGPY GEISEEEILW DLATRLEGRM IATGMETILS
RPHMDDPSSR DRASIANAFG ADLMLSLHCD SYPNEKANGV ASFYFGSENG TNSLTGETLS
AYIQKEIVAR TPLNNCGSHA RTWDLLRLTR MPMVEVVTGY LTNPDDLAVL TDPQMRDHIA

EAIVVAVKRL YLLDEEAQPK TGTFKFSELL QSEQAG

> RXA01435 (1-870, translated) 290 residues
PLDLGFTTEA RQWLETLEGR IGDDWRHKWF SGITYLLLDD YATAQVFFNH VLTILPGEAA
PKLALAAVDE LILQQIGAES TAYLTPDIVS ATATLSKDFE DLDASAFESL SDTWSHISSD
PHVVRFHSLR LYALVWATNP TTVSSAFGLA RQLMAENQIE LAVQALDKLP QSSTHYRMAT
LTTILLLVSS NLSESRIRRA ARRLTEIPTN EPRFNQIKIA IMSAGLSWLR ERKLKASASA
NPLFEYPFSQ KGLRTGISEA LRIQARSAPF PHHRYALVDM ANAVRPLSWF

> RXA01437 (1-1383, translated) 461 residues
MSDTPTSALI TTVNRSFDGF DLEEVAADLG VRLTYLPDEE LEVSKVLAAD LLAEGPALII
GVGNTFFDAQ VAAALGVPVL LLVDKQGKHV ALARTQVNNA GAVVAAAFTA EQEPMPDKLR
KAVRNHSNLE PVMSAELFEN WLLKRARAEH SHIVLPEGDD DRILMAAHQL LDQDICDITI
LGDPVKIKER ATELGLHLNT AYLVNPLTDP RLEEFAEQFA ELRKSKSVTI DEAREIMKDI
SYFGTMMVHN GDADGMVSGA ANTTAHTIKP SFQIIKTVPE ASVVSSIFLM VLRGRLWAFG
DCAVNPNPTA EQLGEIAVVS AKTAAQFGID PRVAILSYST GNSGGGSDVD RAIDALAEAR
RLNPELCVDG PLQFDAAVDP GVARKKMPDS DVAGQANVFI FPDLEAGNIG YKTAQRTGHA
LAVGPILQGL NKPVNDLSRG ATVPDIVNTV AITAIQAGGR S

> RXA01458 (1-1050, translated) 350 residues
VNRRIKTLTW GAIPLVLLAS LVSIDHIPGT NINLSVPYAA EGPGPTINTL GQVDGEDVVS
ISSADLDETE GNLNMTTVSV RSGMTLSQVI SRWLFTDDTI VPIEQVFPPG QSTEEVEESN
RTAFISSESS ATIAAMNYLN IPVEVEVAEV LTDSAATGIF EPGDKLLSID GTAISTPGDA
QTIVRSKAPG DEITISYERN DAESQATITL REHPDDSSVA LLGISMLSVP SSAIEVDYNL
EDIGGPSAGM MFSLAVVDKL SPGALNGGKF VAGTGTIAED GSVGPIGGIA HKVRAAEDAG
AEVFLSPADN CAEAMSAKPQ DMTILKVDSL SQAIDQMAAY NEGSDFQTCG

> RXA01461 (1-459, translated) 153 residues
MIDTGKNGEF RYEQSNIIDQ NEAEFGITPS QTVGPYVHIG LTLEGAEHLV EPGSEGAVSF
TVSATDGNGD PIADAMFELW QADPEGIHNS DLDPNRTAPA TADGFRGLGR AMANAQGEAT
FTTLVPGAFA DEAPHFKVGV FARGMLERLY TRA

> RXA01462 (1-690, translated) 230 residues
MDIPHFAPTG GEYSPLHFPE YRTTIKRNPS NDLIMVPSRL GESTGPVFGD RDLGDIDNDM
TKVNGGEAIG QRIFVHGRVL GFDGKPVPHT LVEAWQANAA GRYRHKNDSW PAPLDPHFNG
VARTLTDKDG QYHFWTVMPG NYPWGNHHNA WRPAHIHFSL YGRQFTERLV TQMYFPNDPL
FFQDPIYNAV PKGARERMIA TFDYDETREN FALGYKFDIV LRGRNATPFE

> RXA01464 (1-291, translated) 97 residues
MLFLARMDVV FPDSMDADVM ADFQAKEKAY SGDLQSRGIM KAIWRVVGEY ANYSIFDVDD
HDELHAILSG FPMFKYMNVK ITPLAKHPNA LEYYLKG

> RXA01465 (1-1161, translated) 387 residues
VAGLFPLNQK AIEKLSDLTI QKVESRILDV PLIRPHGFAT TTSTEQHILL VSVHLENGVI
GYGEGVVPGG PWWGGESVET MKALVDGYLA PVLIGRAVSE LAGIMADLER VVARARYAKA
AVDVAMHDAW ARSLNVPVRD LLGGTVRDKV DVTWALGVLP LDVAVAEIEE RIEEFGNRSF
KLKMGAGDPA EDTRRVAELA REVGDRVSLR IDINARWDRR TALHYLPILA EAGVELFEQP
TPADDLETLR EITRRTNVSV MADESVWTPA EALAVVKAQA ADVIALKTTK HGGLLESKKI
AAIAEAGGLA CHGATSLEGP IGTAASLQFA ASTKAISYGT ELFGPQLLKD TYIVQEFEYK
DGQVAIPQGP GLGVDVDMDK VNFYTRK

> RXA01466 (1-822, translated) 274 residues
MTPNGRRQLL LERGAAFSKN RTPGLKHVDR HTIVDSDGLS IHTYMVGHAE NATATVVFIH
GFTLAAEVYY MQVDYLQTFY PNIKSVLIDA RGHGATGQIR PELCTIEGTA NDVLAAIHEH
APTGPLILVG HSLGGLTALN LVKRADHSLR KRIVGMVLVA TSIESLSTQG LPQVLASPLA
DNIKNAVEAA PNDAQKFRQY ATTFLAPTLA TAVFQRDTND EVIDFHAAMI HETPLDTFVG
FFDDLQEHDE LDAAPTLEGL KGYVLAGELD DVTP

> RXA01477 (1-1548, translated) 516 residues
MPQLSRRQFL QTTAVTAGLA TFAGTPARAE ERQFQHGVAS GDPTATSAIL WTRLTPIPDA
TPGSGLGPDS PVTWEVSPTP DFASITRSGT VITSAASDHT VHAHATGLSP STRYFYRFIS

STGEVSPVGR TQTTSLVDAP LPHLRFALAS CANWEAGFFA AYGDIARRAD AGELEMLIFL
GDYIYEYATG MFAGKDGVVR PHQPLHETIT LEHYRTRYGH YRSDNHLQAA HAALPWIVMW
DDHESANNSN REGAQNHSAD EGSWVDRQNA ARQVFLEWMP IRQEDTLYRS FTFGDLATLS
LLDLRSFRDP APSQQQWLEG QRADTMMGSQ QFEWLKSNVE HTTTTWNIIG SSVMFAPMAI
TGQPLFQIPE PIPANLDQWD GYSRERDRLL AVLADFATPT LFLSGDIHSE WANAIRFNGR
EIGVEAVCSS ITSANVNDFA KLPEDNPVSL QAEQVIRANS SHVRHVDLDA HGYATVNLTQ
DGAHMVWHRV ADLSLPDSEV APAIALEWKP GVGFTT

> RXA01498 (1-1563, translated) 521 residues
MIKRLPLGPL PKELHQTLLD LTANAQDAAK VEVIAPFTGE TLGFGFDGDE QDVEHAFALS
RAAQKKWVHT TAVERKKIFL KVHDLVLKNR ELLMDIVQLE TGKNRASAAD EVLDVAITTR
FYANNAGKFL NDKKRPGALP IITKNTQQYV PKGVVGQITP WNYPLTLGVS DAVPALLAGN
AVVAKPDLAT PFSCLIMVHL LIEAGLPRDL MQVVTGPGDI VGGAIAAQCD FLMFTGSTAT
GRILGRTMGE RLVGFSAELG GKNPLIVAKD ADLDKVEAEL PQACFSNSGQ LCVSTERIYV
EEDVYEEVIA RFSKAAKAMS IGAGFEWKYE MGSLINHAQL DRVSTFVDQA KAAGATVLCG
GKSRPDIGPF FYEPTVLADV PEGTPLLTEE VFGPVVFIEK VATLEEAVDK ANGTPYGLNA
SVFGSSETGN LVAGQLEAGG IGINDGYAAT WASVSTPLGG MKQSGLGHRH GAEGITKYAE
IRNIAEQRWM SMRGPAKMPR KVYSDTVATA LKLGKIFKVL P

> RXA01499 (1-3822, translated) 1274 residues
LWDVLESVAS TYPEAAAIDD GQVLTYAELM EEVTALADSI HAQGIRRGDR IGIRMPSGTR
DLYIAILATL AAGAAYVPVD ADDPEERAEM VFGEAANINAL FDATGFHMLR PTAGGDTRRP
RLDDTAWIIF TSGSTGKPKG VAVSHRSAAA FVDAEAQMFL VDHPSGPLGP EDRVLAGLSV
AFDASCEEMW LAWGHGACLV PAPRSLVRSG MDLGPWLIRR DISVVSTVPT LAGLWPAEAL
SQVRLLIVGG EACSQELVER LSTPDREVWN TYGPTEATVV ACGTQLYAGQ PVGIGLPLAG
WDLVVVDDAG EPVGIGEVGE LVIGGVGLAR YLDPEKDREK YAPLKSVGWT RAYRSGDHVR
LEEDGLYFVG RVDDQVKIGG RRIELGEVDA NVAALSNVRS SAVVVQTTGA DQKVLVAYVS
LEDAAAGFDH NVATARLTET MPAALVPRIH VMDDLPVTTS GKVDKKSLPW PLPGTVVEAN
DLSATEAWIA QEWVDILGTS VSSKDADFFS LGGTSLAAAT LVGRVRAKVP TAAVRDLYDH
PRLEKFAERV EAIAADTGIS LEAPNQVEER VVKPVSFGTR VMQTLIQIPI MTLQAAQWIA
WLLLGNNIMA ALDFDWAVHV SWWLVIGMIL VFATPIGRLP IGGWGARIIT RGITPGSYPR
GGSTHLRIWS AERLADASGS RNISGATWVN YFARSLGVKM GKGVDLHSLP PITGLLTLGN
NVSIEQEVDL RGYWLDGDIL RVGTIEVHDN ARIGARSTLL PGTVVGTGAH LLPGSTVTGD
KTIKPGSRWA GSPAQKVGRA KHRFPTSHPP RRSRWVPVFG ATSIVLSLLP LQALAIGAAI
TLWLATISPL PLIWGVLVFA TVGALAAFFA YTVTIWVLVR LIQIGIKGGT APVRSRLGWQ
VWAVQRLMDD ARTYLFPLYA SQLTPLWFRS LGAKIGKDVE ISTAVMVPKL ADIREGAFLA
DDTLIGGYEL GNGWLLSGET RVGKRSFIGN SGIAGPERKL AKNSLVAVLS STPKKAKANS
NWWGSPPERM RRVTVEVDEG EAKTYSPGFG VKFARGAVET ARLLAPITSG VLAALSLLLM
QYLLTEFNMW ITWLLGGLIL MTVGVLAMGI TVVMKWVCVG KHKPSEHPLF SRFVWLNELQ
DAFVESVAGP WFLVPNLGTG ALNAGMSALG AHIGRGAWIE SYWLPETDLC YIGKGATVGP
GVVVQTHLFQ DRVMSLDTVT VADGATLADH SVALPASLID ASATIGPGSL VMRGDKVPAH
TRWQGNPIEP WSNS

> RXA01502 (1-1233, translated) 411 residues
MSTPQSIVII GGGLAGAKTA EALRVNGYEG SITLIAAEDY LPYERPPLSK EYMAGKVGFD
KAIVHPAEWY KENNVTLRQG VRATAIDAGS RQVTVDDGGN TETINYDKLV LATGSAVRKL
PIPGADASNV HYLRTVEDSD AIKATFGEGK KLVLIGGGWI GLEVASAARG AGTDVTVLEG
GKLPLLKVLG ETVAQVFADL HVANGVDLRT EVKITDIVTE DGRAVGVRLD DGEVVPADAV
VIGIGVTPVI DLAETAGLEI DNGVLVDAAL RTSDPDIYAV GDIANHDHPV LGHRIRVEHW
ATALNQPAAA VKSLLGKDAE FTNLPYFFTD QFDLGCEYVG HATGSQEKVF IRGNLETREF
VAFWVDTENR ILAAMNVNVW DVPDQIKPLI ASGKSVDTEK LVDPEVPYSE L

> RXA01509 (1-474, translated) 158 residues
MSIEVTVEIP KGSRNKYEID HETGKVYLDR YLFTPMAYPL DYGYIDHTLG EDGDPLDALV
ILPESVFPAV VVKSRIIGVF KMTDEAGGDD KLLSVLDDPR YDHIQDISDV SDFLKDEIEH
FFVHYKDLEK GKHVDGSGWG DKAEAEKIHA EAIDRYKA

> RXA01510 (1-1281, translated) 427 residues
MKNAWWVGSS VGVLIAVGAV IGGGVWVNHS GFGLDHPEPM SVEMPEQLFS SAIDPDALEA
PDFATLEKDL TSQAADSRLG TFVGVARDVE SGEVVWEQNQ GTAVRPASAT KILTAAVALY
ELGREDTITT KVVEGEQPGT VVIKAGGDVT LSEEMLDDLA TQLEGQDIGT VLIDTSIWPD

EGFASTWDPV DVDAGYIADV EPAMIEAARI GGSEGDLPRS HTPALDVAQA LADRVGADTV
DEGSAPDKTV LASVESDTLD QRLARMMKDS DNVMAEGIAK EVAASKDLAT DSASTSKMTL
EILKDKGFDL SGVSIVDNSG LSFDNLITPR LLDDILTRAA TEPELSSLLT SLPIAHGTGT
LEDRYDGLSG AGWVRAKTGT LTDTSALAGV VTSESGRVFT FAFVSNGSAI VPAREALDEM
ASILRDF

> RXA01511 (1-942, translated) 314 residues
VASLIGNLEL PRVSPNFLEL RKAVRPYLKE HVHIGLSGGP DSLALVAAVL AEKSQVTAIC
IDHNLQTGSA EVTHNAAAMA RHMGAQAIVK SIEVAPGEGM EAAAREARYA AFAQLTDEIW
VAHTMDDQAE TYLLGGLRGN PAGMKDASRR PELSIIRPLL GARRAHTHGA CVELGLKPWH
DPQNFDDAFR RVAIRNQVIP LLAQVHGGDP VPGLALAARR AVEDAEVVEG DVEKRRLEWQ
DGFPVTLAGE PTGLRRRMLA DFLRGEGIAV TSRKLDAIDR LLTDWRGQGG VAVGKSDNGR
LEVVRQSGKL KITD

> RXA01513 (1-2559, translated) 853 residues
MKNKKYLQFG GIAAVILIVL FLVSLFSSDT RNFQEVDTSV AMAQLDAGNV AEAQIDDREQ
RVRLTLREPI TVDEREGVEE ILAQYPARTA PAIFEKVEAS NTDSYTTNVT QESFLMSMLS
FILPMVIIFG LLMFFLTRMQ GGGMFGIGGS KAKQLTKDMP TNTFADVAGA EEAVDELHEI
KDFLEDPTRY EALGAKIPRG VLLYGPPGTG KTLLARAVAG EAGVPFYSIS GSDFVEMFVG
VGASRVRDLF KQAKENSPCI IFVDEIDAVG RARGSGMGGG HDEREQTLNQ LLVEMDGFGD
RQGVILMAAT NRPDVLDPAL LRPGRFDRQI PVTNPDLRGR EQILEVHAKG KPFAPDADIK
ALAKRTAGMS GADLANVLNE AALLTARVGG NVITADALEE ATDRVVGGPR RSGKVISEKE
KKVTAYHEGG HTLSAWALED IERVYKVTIL ARGRTGGHAM TAQEDDKGMY NRNELFARLV
FAMGGRSAEE LVFGEPTTGA SADIEMATKI ARSMVTEYGM SPAVGMVKYG QEQGDPFSGR
GGGGNLDHSQ EVAATIDTEV QFLLDKAHEV SYSILAEYRD HLDRLAEKLL EKETLRRPDL
EALFDDIVPR KVAEVFPDES TRFPRQENRE PVKTPVELAL ERGEEPPKKF SILEASRATR
ERRRKELEAQ GKLPVQPASS AGVAPAAGAA AGSYGTPPPA DWSVPGSAGK HRSRAEEQPA
EQGFPAQTPA QAPEQSPDSS GGRPNPYATP TASGEHPGMK AYGFGDSELM DQSTGAEHTP
GNVSQESPTE MIGFRLPDHE RSDYPEKAQK ESVLDASETT EMPVVPDQPI DGDSGKSAEG
TQENPENEGD NRG

> RXA01571 (1-600, translated) 200 residues
VSISVKALQK SGPEAPFEVK IIERRDPRAD DVVIDIKAAG ICHSDIHTIR NEWGEAHFPL
TVGHEIAGVV SAVGSDVTKW KVGDRVGVGC LVNSCGECEQ CVAGFENNCL RGNVGTYNSN
DVDGTITQGG YAEKVVVNER FLCSIPEELN FDVAAPLLCA GITTYSPIAR WNVKEGDKVA
VMGLGGTRTH GCPDRCSQGC

> RXA01589 (1-837, translated) 279 residues
YAELGVKKIR ITGGEPLMRR DLDVLIAKLN QIDGIEDIGL TTNGLLLKKH GQKLYDAGLR
RINVSLDAID DTLFQSINNR NIKATTILEQ IDYATSIGLN VKVNVVIQKG INDDQIIPML
EYFKDKHIEI RFIEFMDVGN DNGWDFSKVV TKDEMLTMIE QHFEIDPVEP KYFGEVAKYY
RHKDNGVQFG LITSVSQSFC STCTRARLSS DGKFYGCLFA TVDGFNVKAF IRSGVTDEEL
KEQFKALWQI RDDRYSDERT AQTVANRQRK KINMNYIGG

> RXA01603 (1-621, translated) 207 residues
VSDAGKKDSS KVEIGLTGRP LRELPEPSPL EKHGPATIIA MANQKGGVGK TTSTINLGAC
LAEAGRKVLL VDLDPQGALT AGLGIHYDDV DITVYDLMVD NNSTIDQAIH HTGLPDLDVV
PANIDLSAAE IQLVNEVGRE QTLARALRPV MKDYDFIILD CQPSLGLLTV NALACAHGVI
IPMECEYFSL RGLALLTDTV EKVADRL

> RXA01607 (1-630, translated) 210 residues
VIRILLADDH PVVRAGLASL LVSEDDFEIV DMVGTPDDAV ARAAEGGVDV VLMDLRFGDQ
PGIEVAGGVE ATRRIRALDN PPQVLVVTNY STDGDVVGAV SAGAVGYLLK DSSPEDLIAG
VRDAARGESV LSKQVASKIM GRMNNPMTAL SAREIEVLSL VAQGQSNREI GKKLFLTEAT
VKSHMGHVFN KLDVTSRTAA VAEARQRGII

> RXA01608 (1-1839, translated) 613 residues
MALCMTVAFA GGSLTACTPR PDTADPIAEE FLQAWASQDF DTIADITDQA DLATEMLSTS
FDGLQADSVE LTLDSVDSRD TIATANFSVV WKLPRDREVS YDSSMTLTKM RNEWTVRWEP
SLVHPKLGAN QHLELRAIEA QRANVISSDG APVLAPGSIY RVLVDPSAGD ADVVVKRVAD
YLNEAHATDE NVNTLDVEDI MSNLGDSTYS LTTVDANLGA RMEQDLAGIP GLTFNEEASM

VATDPGFAPD IVSRVARIVE DELEGSNGWR ASIVTSNGAV IDDIAYDAPE LAPSVRISLD
HNVQRAAEEA VDLRAEMKAM MVVMRPSTGE ILAVAQTDEA DKDGDVALMG QYPPGSTFKI
ITAAAGLAHE GLTPDSIVPC PGTMNIYGRI VTNYNSFSLG NTSLDDAFAN SCNTTFADIF
HHLEPGQLKN VAKQFGLGID YQIPGLDTMT GSVPEGDIVL DRTESGYGQG LDLASPFGMA
LVASTAATGS VPTPTLISGH ETVASEEVLA LDPEVLANVQ RMMKSVVNDG TARGMRQTGG
QIYAKTGEAE INEGSHAWFT GYREDDIAFA TLVVLGGGSE AAAAVTDQFF VKLDELRAGG
EVAVSEAEEQ PVG

> RXA01609 (1-873, translated) 291 residues
MSKMRAPLVP GIPTPIREVP AHIERPEYVW KDEVQEAIGE PFVQAPEVIE KMRETSRIAA
NSLKIAGEAV KPGVTTDELD RIVHEYTCDM GAYPSDLGYR GFTKSSCISL NEIVCHGIPD
STVIEEGDIV NIDVTAFKHG VHGDCNATFL AGDVSEEHRL LVERTEEAMM RSIRAAKPGR
EINVIGRVIE SYAKRFGYNV VRDFTGHGIG PTFHNGLVVL HYDNTQYRDL LVPGMTLTIE
PMINLGSLDY EIWEDDWTVQ NVDRKFSAQF EHTIVITEDG NEILTLPDDS V

> RXA01620 (1-948, translated) 316 residues
MQSIRTTFRS LSRSAVIVGT VLALGIAGCS TASDEATSTS DDVAVGGRLF STADSATAAL
GSDAEPGQFP RTVVHSRGET TLEQQPQRVV VLDSGEIDQV LSLGVTPVGI ASPKDASSQP
AYLENQLADV QTVGTTSELN FEAIAALKPD LILGSKLRVD ESYDQLSQIA PTVLSIRPGF
PWKENFLLTA DALGLEGKAV EVLNEYQTHV DAVRETIDGS PEISLVRFMP GRTRLYGNLS
FIGAILKDLG LSRPEIQNID DLAVEISPEN ITDANGDWIF YSTYGKPEAT EQDNILSNEL
WHNLPRRPRR SCPGGQ

> RXA01640 (1-3318, translated) 1106 residues
MFAPPEGDDT DEVRRTYLRH LGALRAKATD HAAMQRRHEW HRHPDPATLW STLGTRRMWE
RTQDDQDCLE IRFGLGVTRL DPAINVSDSG APEDLDPVCA VSLRHTIRDV GSVQSMPVSV
QLQAFRFIGL NGAGAHDLAR ALVVQLLYHH GPEVVGIKAI GESGWEWLKW VPHTRDPEKA
AFRILLVDSV LTNGTESFID DPQWTTIINV GAQTSTALGQ LAEDEGLLLH VDKRLHVATA
HGAEELGTPD AVSAELAEVF GRRLTAFRRT TTAHAASSGE LLSLLGIDDV EHLTPETLWM
NKRTQPKTRL AVPLGLNASG RPMVLDLKES AHGGMGPHGL CIGATGSGKS ELLRTLVLGL
TITHSPEELN LVLVDFKGGA TFLGFEQLPH TSAVITNLEE EPVLVERMHD AISGEMNRRQ
EALRQAGGCA NVDEYNQRDG VKPMPALLIE SDEFSELLGQ HPDFADLFVA VGRLGRSLHI
HLLLASQRLE EGRLRGLDSH LSYRIGLKTF SASESRQVLG ITDAYQLPSQ PGAGFLKSDV
DTVTRFQASY VSGPIMRRHH LAPTQSRVRL FTSWEEPKEE VIVEQSTETL IDAVVARAIS
AAKLRGLSAH RIWLPPLPAE VSIGALADDV GELSAVIGMI DRPYQQRQDP LLIDFSLTGG
SGHWAICGGP QTGKSTALRS IVISMAATHS TENIRFYVLD LSGTSLENLS RLPHVAGVAG
RKDPEKVRRV VDEVRGLINH PEQRHTFLIV DGWHTITQEF DELFDAFVDI AANGLASRVH
LVLSTQRWSS IRPAVRDLVT GRIELKLGEA MDSVIDRKAQ LRIPSKPGRG LNLDKEHILI
AHASGQDIAQ VCVMADGQGW QQVPQLSVLP AHILLHELEL SATPGIPIAR GGAELSTLTW
DPESSRHLLA FGSQGCGKSS LIRTIVTGLT IVGREKARLV FFDLRRTHLG LVPEDMLAAY
CATSTAVHNT IKDMVATLSA RLPGPDITAQ ELRDRSWWQG PDIYLVIDDY DLLPAGTLHP
LREIIPHARD VGLHIVLTRK AGGASRALYD PVMSEIKDQS PHVVLFDADR DEGAILGIKP
TAQPPGRATM SIRGENIGVA QMAPHR

> RXA01653 (1-939, translated) 313 residues
GSDLQASRGL LEDDAVQNNT ETSVFTDSSK VHAINHHGKY FDVPGIAITE PSVQRTPVIY
QAGASPRGLK FAGENAEAVF INSSTVEAIT KTVAKIRAAA VAAGRDPHAV KIFAMQTIIT
GETEADAQAK LEEYSRYIDP VGGLTLMSGW TGADLSQYDL DEPITNIESN AIQSTAATIS
NGTGEGAWTV RKLGEATGIG GFGPVLVGSG ANVAAELARI QDLSDVDGFN LAYAITPGTF
EDVVDFVVPE LQKLSRYKTE YAPGSLRNKL LGKGDRLDDT HRGASYRLGA RNSTATIDLS
SISAQLVSQG AHS

> RXA01654 (1-996, translated) 332 residues
MSPSANAAEA PASEWVNTTA IVDQANAQLS QFGVSLDRSA AELFDDQANS QIDAALSPYA
DKVPTSGGQV VEQSLQVVEQ EVQKALPNYE IRTDLQSQVM GATLGEVLHR VPGSWFDAPA
VPEESRIVEE QGKSLYGPGT PIYLNGNSMC TLAVTGTDAD GRKIGITAGH CGKSGDAVRS
ADSFWVGDTG TVVYNAPNAD YSVIEFGSNA ELSNTYNGVT ANAVGGGVTN GQEVCKNGVA
TGYTCGLVWT ADERMTMSQV CAGRGDSGAP LIADGRVVGL VSGGVIPDYN LACATPLQGP
FFMPTLSVNM DTVLTDLDSQ DLPGRGFQPT AG

> RXA01664 (1-822, translated) 274 residues

MTVLISPSTL AESIHAGKKQ TVLAAFWAPI EGAGRTVFCS EHIPTSIFCD PALELSGVPS
SEDGRNPLPP LNVLARSFRT WGLNTDREIV FYDQGRGLFA ARAWWILRWA GMPNVRILDG
GFQKWEDHEL GHAGGPGNFP HFCNVRPNPG QLSVATIEDV KAHQGILIDS RDEQRFAGRS
EKLDLKAGHI PGAININAKS LLEDDFTFKS PEEIRQIFAD KGVTSGENVI VYSGSGNHSS
QLLAGMEHAG LTGASHYFAG WSQWSANPEN PIEA

> RXA01668 (1-1716, translated) 572 residues
MSSFNPTTKT NEAMQAALQQ ASSAGNPDIR PAHLLAAILE QTDGVAAPVL MATGVDPKEI
LAEAKKLVAS YPKASGANMA NPNFNRDALN AFTAAQELAG ELGDEYVSTE VLLAGIARGK
SDAADLLTNK GATYDAIKEA FPSVRGSQRV TTQDPEGQFQ ALEKYSTDLT KLAREGKIDP
VIGRDQEIRR VVQVLSRRTK NNPVLIGEPG VGKTAIVEGL ARRIVAGDVP ESLKGKTLIS
LDLGSMVAGA KYRGEFEERL KAVLDEIKGA NGEVVTFIDE LHTIVGAGAS GESAMDAGNM
IKPLLARGEL RLVGATTLNE YRKYIEKDAA LERRFQQVYV GEPTVEDAIG ILRGLKERYE
VHHGVRIQDS ALVAAAELSN RYITSRFLPD KAIDLVDEAA SRLRMEIDSS PQEIDELERI
VRRLEIEEMA LSKESDAASK ERLEKLRSEL ADEREKLSEL KARWQNEKTA IDDVREMKEE
LEALRSESDI AKRDGNYCRV AKLRYGRIPE LEKQIEDAES KVEVNENAML TEEVTPDTIA
DVVSAWTGIP AGKMMQGETE KLLNMERVLG NP

> RXA01691 (1-567, translated) 189 residues
MASQQIRYPF SAVVGQDELR LALILTAISP RIGGVVIRGE KGTAKTTTVR AFAGLLGDAP
LVNLPLGSTE DRVVGSLNME TVLTTGRAEY QPGLLAQADG GVLYVDEVNL LADHLVDALL
DAAASGRVSI ERDGISHSSP ANFVLVGTMN PEEGELRPQL LDRFGLAVDV AASTNPEVRV
EIIRRRLDF

> RXA01728 (1-975, translated) 325 residues
MADAVEREVF GYPPDATGLN DALTGFYERR YGFGPNPESV FAIPDVVRGL KLAIEHFTKP
GSAIIVPLPA YPPFIELPKV TGRQAIYIDA HEYDLKEIEK AFADGAGSLL FCNPHNPLGT
VFSEEYIREL TDIAAKYDAR IIVDEIHAPL VYEGTHVVAA GVSENAANTC ITITATSKAW
NTAGLKCAQI FFSNEADVKA WKNLSDITRD GVSILGLIAA ETVYNEGEEF LDESIQILKD
NRDFAAAELE KLGVKVYAPD STYLMWLDFA GTKIEEAPSK ILREEGKVML NDGAAFGGFT
TCARLNFACS RETLEEGLRR IASVL

> RXA01795 (1-435, translated) 145 residues
VLIVGIRRDT GFDFKHPAPT HGPRGDMPYK TAGEALKGVK DVPTNNNHMK IMPRTVEVLK
RIPEGENFTA IPKDDPYYVK GMISHVYRRL HRDEPSKTLI AGGGGGTWGY HYEKNRALTN
RERARIQSFP DDFEFLGSNT QVRRQ

> RXA01802 (1-831, translated) 277 residues
MGDQDIIGKE SKQMDFRLVA TDMDGTLLNT HHEVPEKFWD ILEQMRAKGI AFAPASGRQL
ATLQKQFGHA GEPISYIAEN GTVVVHDGEI ISLTTIDSDT VHSIIDAVRA SDIDMGVVVC
RPERAYVERN DEAFRAEGLK YYVSIEEVQD LHEAVNNEVI KVAIFTFQDA EKDCAPIIRA
ASPNANVVVS GQHWVDVMDP SANKGQALAA LRDALGLEES QTLVFGDYLN DTELIKAAGK
SYAMSNAHPD ILELADEIAP SNIEEGVIVV LEKLLNG

> RXA01828 (1-1422, translated) 474 residues
VNRSIRITSL FSLLLILVLV ANLTWIQAFR DDDLAQNPLN ARGFLEAKST PRGQISTGGQ
VLAESSQDDQ GFYQRSYITN PTAYAPVVGY LSDVYGAAGL ELGYNSILNG SDSSLFTSQW
LDVISGSPTH GANIELTLDP NAQQTAYEQL SQSGYEGAVV ALRPSTGEVL AMASSPSYDP
NQIVDPATAE DAWAEYTSTE GAPLLNHATQ ESLPPGSIFK IITTAAALEN GYSADSTVTA
EAAVTLPGTN TTLTNYGGQT CAGGGTTTLL TAFQLSCNTA FVETGIDVGA DALRASAEDF
GVGQTYSLGL DNVPGGLGEI PDDAALGQSS IGQRDVQMNV LQAAVMAGTV SNGGVRMEPY
LVSRVTGQDL SELSTHKPKS VGGVEPEIAE QLKTLMEASE RNTSGYTGIQ IASKTGTAEH
GDENTPPHTW YVAFNNDIAV AVLVKDGGGF GTSATGGQVA APIGRAVLQA AGGF

> RXA01829 (1-1323, translated) 441 residues
MNTLERLKLR RTEMWLLILA TLVVSIMFIS LELAMGNELG THILMLMGGY IGIFIVAHLA
MAWVAPFADQ IMLPVVAVLN GIGLVMIYRL DEATGYSTVN SQLMWTVVGV TLMVAVLLLL
RDYKSLSRYS YLLGVVGIVL LALPLVWPQP GGVEARIWIW LGPFSIQPGE FSKILLLLFF
AQLLATKRAL FTVAGYRFLG MDFPRLRDLA PILVVWALAI LIMAGANDFG PALLLFTTVL
AMVYLATGRG SWLLIGAVLV AVGAFTVYQV SSKIQERVQN FVDPVAHYDT TGYQLSQSLF
GMSWGGITGT GIGQGYPNMI PVVHSDFILA AIGEELGLIG LAAIIVLFGV FVTRGMRTAT

LARDSYGKLV ASGLSMTIMI QIFVVVAGIS SLMPMTGLTT PFMSQGGSSL MANYILMAII
LRISDSARRP VMSKQASEVA A

> RXA01838 (1-819, translated) 273 residues
QHLSGGRVDL MMGRGNTGPV YPWFGKDIHQ GIPLAIENYH LLRRLWREDV VNWQGKFRTP
LQGYTSTPAP LDGVAPFVWH GSIRSTEIAE QAAFYGDGFF HNNIFWNKEH TAQMVNLYRQ
RFEHYGHGQA DQAIVGLGGQ VFIGDSEEEA KKTFRPYFDN APVYGHGPSL EDFSRLTPLT
VGTAEQVIER TMEFADWVGD YQRQLFLIDH AGLPLEMVLD QIERLGHDVV PEVRRRMEER
RPDHVPSNPP THQSLKANRN SPYFQINPGQ PTE

> RXA01848 (1-744, translated) 248 residues
MGEEDSTPGR RSKAYSRQGA DVRPMKGGHG INLVGTLMAA TERGANIVEG VVDFRPTDLR
GSLRRGREAN LIVFVVDTSG SMAARSRVRA VTGTITSMLN DAYQRRDKVA VIAVNGNKPT
LVLNPTNSVE QAQQKLKDMP MGGRTPLAEG LLMAKDLMAR ELRKEPGRRA ILMVMTDGQD
TSDAGEAGIA TAAETVVKSR LSGNVVIDCE GRLKVRKERA GVLAEMLGGV CVRLRDLNSE
HIKMVINA

> RXA01849 (1-450, translated) 150 residues
LPGVELPDLI LSQIAWLCAR IEVDGMRADL VITRTALAHA AWAGRTVVTE EDVEIAARLA
LPHRRRRNPF DAPEMEERKL QETLQEARDF FKDNEDKGPA AKITDEETGA EAFTDTDNPT
EEDGLQGTAQ AKAQTTGKVG TAGSGDPFRS

> RXA01868 (1-1611, translated) 537 residues
VEKDSSSNES VAYVIQSGLG LPDEAYYREE AHAETLAAYK EHVERMLGYL DNSRLFGLSA
ASAAARIVAL ETEIAAGHWD VVKTRDAVAT YNPTELGALP PKVRTLLSSA GLPDQRLVSM
MPSYLDHLNG LLVDDRLPDW QLWATWHILR SRAGLLTEEI SQANFDFYGT KLSGATEQKD
RWKRAVGLAE RMVGEEIGQR FVERHFPASS KEHMLELVDY LVAAYRDRIS NLEWMTPATR
ERALEKLGKF NAKIGYPDKW RSYEGLEFGS DLVDNSRKGS AFLHDYELGK IGKPADRDEW
VTTPQTVNAF YNPVVNDITF PAAILRAPFF DPEAEAAENF GAIGAVIGHE IGHGFDDQGS
QYDGDGNLNS WWTDEDRSAF EQLTSRLVTQ FSGLVPAVLT SEGIDTDGVN GEFTLGENIG
DLGGLGIAVV AYEKYLADRG QTFETSPVQK FEAEGAEEGL AEQEFNGLQR LFLSWARVWR
TKIRPQMAVQ YLAIDPHSPA EFRCNVIAGN VAEFYEAFDV PEDAPVYIKP EERLAIW

> RXA01869 (1-303, translated) 101 residues
MKDLYRFVNG LWLDTHIIPD DRAVDGTFHK LRDDAEEDVH EIVKEDTGRA GTLYASFMDT
DAINAAGVAP LDADLNRLSV ANSSFSQLLS ANWTVKALAR Q

> RXA01885 (1-801, translated) 267 residues
MTTKPIIPES THSAERAGGH WILARLGKKV LRPGGRETTQ FLLENLSLTG ATVVEFAPGL
GVTARDILGK GPARYIGVDS DADACANVRA ILPAGPHEVR NTNATDTGLE SDSFDVVIGE
AMLTMQTDKH KLELMREAAR ILKPGGLYGI HELSLVPDNV STAVKEDIAK ALARSIKVNA
RPITVPEWAA LAREAGFDVI NIRQADMALL SLKRNLKDEG LKGVFTIVRN VISQPDLRKR
VLGMRKTFTE HKDHLGAVGI ILQKRAQ

> RXA01914 (1-426, translated) 142 residues
MAKNAYSTTA PTKVSKDATL PVRGTVAELK LEKKLPKKID AIIVAIFEGE DSIELAGGEI
LDFIFSTEQQ ADILTQLEAV GAKATANSIT RVPGTDVAPV IAVGLGKADL LDDETLRRAS
GTAARSLGGF ENVATTIGDL GL

> RXA01918 (1-414, translated) 138 residues
MTPDLAAFLD KLYAEGQEFD AEQPDRLDRR RNLESESAAL LRSLIYGISP KSVLELGTSN
GYSTIWMADV VNLTTVDNDP ERSLDAAANL RAAGVEEKVQ RIVADGATVL ADSADEQWDF
IFLDAEQSLY VNWWPDLQ

> RXA01932 (1-897, translated) 299 residues
MLLHPDAQFY IDTLPTLSAE EQVSFGKDAP VSEADATHVA TDQDIAGVPV RVYTPLSGAG
DLPCLVYFHG GGWSGGTLNM IDATVHSLVV GLPIIAISVD YRLAPAHPFP AAIDDAFAVV
SAVLDGVSGL SIDTSRVAIG GDSAGGNIAA VTAQQLRERA VGSTPVLAHQ VLIFPVTDVS
TTSTPSYLTF GKDCYLTKDA MERYIEQYAD GHDRTDPRLS PLLASDLSDL PPTTIVYGEC
DVLAHEVRAY GQALLEAGNS VTMTEFKGQI HAFINLGGIS SDARAARRLI RAELEAALC

> RXA01933 (1-603, translated) 201 residues
MSKTRTFLFD LYGVLIKEHG AAQFERVARA VGEPSKNDKL HEVYESLRLD LDAGRVSEVN
YWNQIKLLVG LEFLDIQEVI AADYRGLYER DQDMVDYVLS LKAKGHRIGI LSNIPEGLAK
LLKEHNSEWL DQLDAVTLSC DIGAAKPEPK SFHVALEALG EKAEDVTFID DRVRNIEAAR
EEGLSTIHFT GLDSLKESIQ E

> RXA01934 (1-558, translated) 186 residues
MTPQPLILPF GDKVPRIHES AWIAPNATII GDVEIGPDAS IFYGVVLRGD VNKITIGART
NVQDNCVLHV DGDAPCTLGD DVTVGHMALV HGATVGNGTL VGMKSALLSG SHVGAGALIA
AGAVVLEGHE IPAKALAAGV PAKVRRLLDD AQSQSFIPHA GRYVETSKAQ ASIAEALSLD
EVRVRE

> RXA01967 (1-1143, translated) 381 residues
MRIQSPMEIS WSEAVREGGE HSARRCGDMA VSALAKPNPI IDDDPEGNPD VCMYTWIVEC
PGATAVLLWI NGVFDHERIE ESEMTRLEGS DLWILSLRMP SDWRASYTVN AWSGDGVAPW
REAGDRMHIR KAAMSGGRPD SRAMGHIMDS SLVEGPDALP DCWVAASTSV KVVEETVAGE
HFWFYEAPVK APLLVLFDGQ HWNNSMNLPA QVDAAIAIGL LPPVSLLMID SVNTERRWDS
VGVPGGQVDV LIDALLPHVR ETYNVSARGE DTIVTGASFG GLASLWALAL SDGEVGHAIA
QSPSLWRFNV ADALSAAEQW SSIHLQAGKY EGEMLRLSHQ LAEDLSGDIR EVRVRGVHGG
HDWAWWRVHM LTELTRLLKT L

> RXA01971 (1-831, translated) 277 residues
MSKKKPRPIP VPAQFIPGLI DAHTHLASCG GDLAGLVERA KEAGVEKLCT VGDGLAEAEL
ALEAAQQFGN VFAACAIHPT KADQLDGAAR ARLTQMAADP NCVAIGETGL DSYWIKHDPE
DTAALDVQEE ALRWHIDLAI SADKPLMIHN READADLMRV LADAPPPKDT ILHCFSSPLD
VAKEALDRGY VLSFAGNVTF KRNEELREAA RIAPISQILI ETDAPYMTPE PFRGSRNEPS
LIGHTALCIA EVRGMAVEDV AAALNENFDR VYGVTNL

> RXA01993 (1-366, translated) 122 residues
AGTGAQDGDR SQGVNGYVMN TITPDSDRFS HYFWAFMRNY RLESQTITTQ LRDGVSGVFK
EDEDMLTAQQ DAIDANTDYE FYSLNIDAGG MWVRRILEEA LSKEGRLDIP TTFPRATPKP
EA

> RXA01994 (1-975, translated) 325 residues
MNSQWQDAHV VSSEIIAADI RRIELSPKFA IPVKPGEHLK IMVPLKTGQE KRSYSIVDAR
HDGSTLALSV LKTRNSRGGS EFMHTLRAGD TVTVSRPSQD FPLRVGAPEY VLVAGGIGIT
AIRSMASLLK KLGANYRIHF AARSLDAMAY KDELVAEHGD KLHLHLDSEG TTIDVPALIE
TLNPHTELYM CGPIRLMDAI RRAWNTRGLD PTNLRFETFG NSGWFSPEVF HIQVPELGLH
ATVNKDESML EALQKAGANM MFDCRKGECG LCQVRVLEVD GQVDHRDVFF SDRQKESDAK
ACACVSRVVS SPSSSPTSTI TVALS

> RXA01997 (1-390, translated) 130 residues
MTINEKIASA FNNQVTAELE ASMVYLQLSY VLDDLGLTGM RDWMKAQSKE ELEHAQKFAQ
HLLDRDYTPQ IGDIAPPKLD VTSAIEAFEA SLAHEQKISG LIRELAAIQD AEKDYDSRAL
IDWFLNEQIE

> RXA02000 (1-504, translated) 168 residues
MKVTQSTFLK SVAAFTVAAL TLTISSCSSG EDTSASSTDT ENSSTQAAAS PPLAPCELPA
DASAEEEVEG THTGEDISVA PEIGTGYREG MTPVQTQGYA VATANPIASE AACAVLREGG
TAADALVTAQ FVLGLTEPQS SGLGGGGYIL YYDAEANAVT AIDGRETA

> RXA02010 (1-447, translated) 149 residues
MVFTLADSVS QVALGPSWLD PMELLSGSGP FGSFILPAML AIVFIESGLL FPLLPGDSLL
FTGGLLANQA DPFAPLWLVL ILCPIAAILG DQVGYWIGHK FHPRLVNRPD GRIFKQEYLK
QTEDFFEKHG PVTIILCRFV PIVRTYAPL

> RXA02012 (1-669, translated) 223 residues
FTMTLSERKL TTTAKILPHP LNAWYVAAWD YEVTSKKPMA RTIANKPLAL YRTKDGRAVA
LADACWHRLA PLSKGKLVGT DGIQCPYHGL EYNSAGRCMK MPAQETLNPS AAVNSYPVVE
AHRFVWVWLG DPTLADPTQV PDMHQMSHPE WAGDGRTISA DCNYQLVLDN LMDLTHQEFV
HSSSIGQDEL SESEFVVTHT EDSVTVTRWM HDIDAPPFWQ KNM

> RXA02016 (1-777, translated) 259 residues
MSNFETFLWV AYPWLCIAAY IIGISWRWRA DQFGWTTHSS QIYESKLLRI ASPLFHWGMV
FVVIGHLMGL AIPKSWTQAV GISDAAYHLI ATIPGTIAGI AAVLGLIGLI IRRVINKTVF
LSTSRSDKVM YVLLGAAILS GFIATVSTQV FGGAHGYDYR ETISPWVRQL LIFNAQPELM
ADVPWEFKVH IVAGFTLIAL WPFTRLVHAF SAPVGYVTRP YVVYRTRDTT SEPARQNVAW
EPIRSVKNQL DNDSKWHGA

> RXA02017 (1-684, translated) 228 residues
MRTHTGKIPD HFVPRISMTE EQRRVVFMLN SLLLDYPEEG FVDKLNAVEA QLDVLPLPVA
AHVVEFLDAA RVAGLRAMQE AYVETFDQRR RCSLFLTYYA VGDTRQRGTA ILTFRQTLQQ
LGFESERDEL PDHLCVVLEA AALADSSLFD AATQVLSAHR DGIEVLRAAL DNLDSPYRYL
IMSLCQALPE IDEETANSYM ELIRSGPPAE MVGIGTPLPF PTSQPDIH

> RXA02018 (1-1050, translated) 350 residues
RICEHCLNPT CVSSCPSGAM YKRAEDGIVL VDQDQCRGWR MCVSGCPYKK VYFNHKSGKA
EKCTLCYPRL EVGQPTVCSE TCVGRLRYLG VLLYDADRVA EVAATPDEKD LFEAQKTLFL
DPHDPQVIAD AQRNGIPHSW LEAAQNSPIY DLIFKYEVAL PLHPEYRTLP MVWYIPPLSP
IVDEVTASGN DGEDHKILLT ALSTMRIPLE YLAGLFTAGD TRPVEKSLRR LAAMRSYMRD
ISLGREPQEE IAEAVGMTGK VVQEMYRILA IAKYDDRYVI PTASPETPRG ISSLDPFGDV
DPARATEQLN IGLGEGAPEA CGTGAPSGKV SLTSWNVGER PAAMFPPRKD

> RXA02048 (1-1374, translated) 458 residues
MRRLRSTPVP GTRDSYTGID FNLGFHIRRY ELDLTYRVAP NLLMGTATLH MDNYRALDAL
TLDLGGSLRV EKVTAKGTAG THIQVARFRH AGRKLRITFR NQIPVDQEFS LTIRYRGNPR
PLRSEWGMIG WEELDNGALV AAQPNGAPSW FPCDDTPDEK ALFDVHFHTD NGYAAIITGD
LISKHVSGSM TTWHYQSREP MATYLAAVHV GEYDTVSLGV SESGVVVEAY VPVGDAALRA
RILEDFAKQV DMLDAYEKLF GPYPFRSYRV VITEDELEIP LEAQGLSSFG ANHATGEGTW
ERLIAHELSH QWFGNSLGLA QWNDIWLNEG FACYAEWLWF EAAGVKSAAE SALEFYRGLE
ALPKDILLAN PGAKDMFDDR VYKRGALTVH ALRELLGDDA FFKAVRSYVA EGRHGLVEPR
DLKRHLYAVS TDHAALDAVW QSWLRDLELP EFPSGGLD

> RXA02052 (1-792, translated) 264 residues
MGTTEIPETP TRVVVIDSPH LDALLALGIT PVGATESGSE NGFPAYLADE LKDTESVGLT
SEPNLEKIAA LDPDLIIGAK VRHEAIYDQL SDIAPTVMSE GSGTNWNEQA EITAAAVNKS
DEMDKLISDL DTRATELGEE IGADGQTASM VRFRTDNFRL YGPETFSGSV LEQVGFDLGE
RDWNEYSMME LSSENFGQID GDLIFYTIPG SPEATTYPKI SELWVDSPAV RQGRTYEFED
ETWMVGIGVL GANEILDDLE ETLS

> RXA02064 (1-639, translated) 213 residues
VSNAFEYLRT YVESTTETDA AVARAREDAA EFGLPAPDEM TGQLLTTLAA TTNGNGSTGA
IAITPAAGLV GLYILNGLAD NTTLTCIDPE SEHQRQAKAL FREAGYSPSR VRFLLSRPLD
VMSRLANDSY QLVFGQVSPM DLKALVDAAW PLLRRGGALV LADALLDGTI ADQTRKDRDT
QAARDADEYI RSIEGAHVAR LPLGAGLTVV TKA

> RXA02083 (1-1410, translated) 470 residues
MEMVMKNKRV AIIGAGPSGI AQLRAFESAE KQGHEIPELV CFEKQDTWGG QWNYSWRTGT
DSYGEPVHSS MYRNLWSNGP KEVLEFAEYS FDEHFGKPIS SYPPREVLWD YIAGRAKKSN
VEKYIKFAHV VRWVSFDEAT KLFTVTVENL RTGETSSDTY DNVIVGAGHF SFPNVPHFDG
VETFPGQIMH AHEFRGAEAV ADKDILLIGA SYSAEDIGTQ AYKMGARSVT FSYRSNPMGY
EWPEEMTELP LVERFDGSEV HFVNGEKRKV DIVVFCTGYL HHYPFMPSEL TLSSPNNLYP
DTLYRGVVSE ANNQLFWLGA QDQWLTFNMF DAQAWYVRDV ILGRVALPSK EAQRNHMDKW
LSRFEGLKSE NDQIDFQCDY VEDLIDQTDY PSFDLKEVAN ILKGWVKSKE EDILNYRDYT
YTSVMTGTTS VEHHTPWMIE LDDSLERYLS EPQEDEARQV YRGKKVRDKA

> RXA02092 (1-1638, translated) 546 residues
MANSAAGSVL ADEMVVPTST GFVKGVKGPG LKTWRGIPYG RNTGGKYRFR APRPAKKWDG
VRDCSMFGEV ASQPTYSWTD KIRGSEDCLN LDVVRPDSEE KLPVVVYLHG GSFIMGSSSE
KALRGYNLVT NMNVVYVSVN FRLGALGYLD LRSVGEDCVA NPALHDQLLA LQWVSRNIKA
FGGDPDNVTL MGESAGAAAV VALMCVPAAG GLFHRAIAQS APVISVHSST QAKFWARELI
YRMALPRETT LDELRQESAD DLVRAGQSMM WRSGELLQLN SCYGPTVDGS LLPEHPLTMF

EQGRQHRIPF MIGTNNGETS FSKAFYLRSS ARRRSALRML SVYDPHNAER VVSAYGGGEA
RTDFSELLAD ALFWAPSVRL AQSHASQDED TWMYRFDYAP QSMRKLGLGA IHSFELNAVF
GDHESSRSMN LAKIAGGMDH LDKVTELVQE HWKQFIYFGR PGEEWKAYRG RSDTEPGRAT
FVIDINSRIA WDPRQDKRTA WENYDMLEWG TGRPDLANEL DFIEPEETEE EQQLKWLSLM
QFFGSR

> RXA02098 (1-1746, translated) 582 residues
MDATFWIIGL VVLVVLAIII VLIVGNQRGK SKTVSFEKPE ENKKELTQQE KSGNYQAQGG
FNFAPAKQTE EPVLREGQDL GAPKAETTPI VPPVVIPPAA PEEEKAPEQS TETFAAQKPA
EEAPATPEPE TSDDVVEEPE VKEPEVKEVV AVEPEVETEE PAVVEEPAVA EEPAIVEEPA
VAEEPAVAEE PAVAEEPAIV EEPAVAEEPA VVEEPAVAEV PETIEEPAVE ELAAVAEVTE
AAEAAQVAVE SAEAALEETP VPDVEPEPAA EPIDEIVPAA GRIGKLRGRL SRSQSVFGKS
VLGILSAGDL DEDAWEDIEA MLIKADLGAK ITARVVDELR DKIAEHGVGS EAEARAMLRA
SLIDACRPDL DRSIKAMPYE GKPPVVLVVG VNGTGKTTTT GKLARVLVSM GHKVILGAAD
TFRAAAADQL ETWGRRVGAE TVRGAEGADP ASIAFDAVAK GVERQADVVL VDTAGRLHTS
TGLMDQLGKV KRVVEKKAVV DEVLLVLDAT VGQNGMQQAR IFREVVDITG VVLTKLDGTA
KGGIVFQVQE ELGVPVKLVG LGEGADDLAP FEVEGFVDAL LG

> RXA02101 (1-1263, translated) 421 residues
MSRISELLNN HGVDLSWQEA AYQDFHEHPE LSGFESETAD RIQKYLERFD CEVIPNVGGY
GILAVFRNGS TDPGAPVALM RADFDGLPVK EITGVPFAST RMRPHDGANV HVMHACGHDV
HVTALLGACA ILDERRDAWE GTFIALFQPS EENSQGANKM VAGGLVDLIP RPDVCFGQHV
VPGAAGTVMS MPGGALAACD SIEIRIQGRS AHGSMPHNSI DPTYVAAMIV VRLQGIVGRE
VSPEDFAVIS VGTLQSGNTN NTIPASARLV LNCRFYNDKV KHKVYRAIER VVRGECLASG
IEEEPVIEYF AHGDLTNNTP VVFDTVRPVF DDVFGEDSID AYRWTASEDF PSIPKAFNSP
YLYWTIGVTP RDQWTEAVER DRVASDVPAN HMGDFLPDYA PTMSAATRAA AAALLTYLGT
N

> RXA02105 (1-291, translated) 97 residues
MVGTISTYIA FNGNTTEALK HWQEVFGGEL NLLTYGQLTL EGMPFDPPAD ALAHGVLTLD
NGGLISGSDS FEGEMLVKDT AYSMLYNAES VEDGRAR

> RXA02111 (1-1284, translated) 428 residues
MTTSITPSVN LALKNANSCN SELKDGPWFL DQPGMPDVYG PGASQNDPIP AHAPRQQVLP
EEYQRASDDE LHRRIREAKD TLGDKVVILG HFYQRDEVIQ HADFVGDSFQ LARAAKTRPE
AEAIVFCGVH FMAETADLLS TDEQSVILPN LAAGCSMADM ADLDSVEDCW EQLTSIYGDD
TLIPVTYMNS SAALKGFVGE HGGIVCTSSN ARSVLEWAFE RGQRVLFFPD QHLGRNTAKA
MGIGIDQMPL WNPNKPLGGN TVSELENAKV LLWHGFCSVH KRFTVEQINK ARAEYPDVHV
IVHPESPMPV VDAADSSGST DFIVKAIQAA PAGSTFAIGT EINLVQRLAA QYPQHTIFCL
DPVICPCSTM YRIHPGYLAW ALEELVAGNV INQISVSESV AAPARVALER MLSVVPAAPV
TPSSSKDA

> RXA02118 (1-342, translated) 114 residues
MSDQLAPCPE CSSEYTYENG GVLVCPMCAH EWVEGEVAEE TATVIKDSVG NILNDGDSVS
IVKSLKVKGG GAIKIGTKVS GIRLLEEPVD GHDIDAKVPG FGQMRLKSSV VKKA

> RXA02120 (1-762, translated) 254 residues
MSDLKSLATK FASDHESGKL LVLPTVWDTW SAGLVEEAGF SGLTIGSHPV ADATGSSDGE
NMNFADYMAV VKKITSAVSI PVSVDVESGY GLSPADLIAQ ILEAGAVGIN VEDVVHSEGK
RVREAQEHAD YIAAARQAAD VAGVDVVING RTDAVKLGAD VFEDPMVEAI KRIKLMEQAG
ARSVYPVGLS TAEQVERLVD AVSVPVNITA HPVDGHGAGD LATLAGLGVR RVTFGPLWQK
WLAATSAQQL KGWA

> RXA02126 (1-321, translated) 107 residues
MGQKVTAGRD ILGEFAPKSA ELNDDVLFGQ VWSRESELSP RDRSIVIVTM LMASGVLDSA
FESHVQRAKD NGVTAEEIAE IITHVAFYAG WPKAWAAFRI AKDIYTK

> RXA02192 (1-522, translated) 174 residues
IPDIGFGVFQ TPPDETRNSV NAALEAGYRH IDTAAAYGNE REVGEAIAAS GIGRDEITIE
TKIWVTDYGF EETLHAFDKA TGKLGVDTLD ILILHQAVPS SFDRTIAAYK ALEKLLFDGA
VRAIGVSNFM PEHLDKLLLE TSIVPALNQI ECHPYFQQRD VLARNEQLGI LTQA

> RXA02214 (1-609, translated) 203 residues
MSPTVLPATQ ADFPKIVDVL VEAFANDPAF LRWIPQPDPG SAKLRALFEL QIEKQYAVAG
NIDVARDSEG EIVGVALWDR PDGNHSAKDQ AAMLPRLVSI FGIKAAHVAW TDLSSARFHP
KFPHWYLYTV ATSSSARGTD VGSALLNHGI ARAADEAIYL EATPTRAAQL YNRLGFVPLG
YIPSDDDGTP ELAMWKPPAM PTV

> RXA02215 (1-867, translated) 289 residues
AQELLVKLLP HSGNALRIGI TGVPGVGKST FIEAFGLHLI EQGHKVAVVA IDPSSTKTRG
SILGDKTRMS KLSNAENAFI RPSPSAGTLG GVAKATREAM VVFEAAGYDI IIVETVGVGQ
SEVAVSHMVD IFTFLALSGA GDQLQGIKKG VLEMAELVAI NKADGPNEKP AKRAARDLAS
ALRMVRSPDE LWHPPTITMS AVEGTGVDTF WHHVQNHHKT MVEAGEFDRR RRDQQVGWTW
SMVHETIRMR LENDPGVQVV SQDMERALRK GSTTPTLAAQ NILEAFDKA

> RXA02264 (1-120, translated) 40 residues
MIPGEYILSS ESLTGNVGRE AKTIEIINTG DRPVQIGSHF

> RXA02265 (1-300, translated) 100 residues
LHITPREQEK LMIVVAADLA RRRKDRGLKL NHPEAVALIT YELIEGARDG RTVADLMSWG
STILTRDDVL EGIPEMIPDI QVEATFDDGT KLVTVHNPIR

> RXA02274 (1-1602, translated) 534 residues
YAAIGEEVAF GGGKVIRDGM GQNGTLVRDV DIPDTVITNV IVLDYTGVYK ADVALRDGKI
FRIGKAGNPN VMENVDIVIG VATDIIAGEG KILTAGGIDT HVHFLGTDQV NTALASGITT
MIGGGTGPSQ ASMATTVTPG QWNTYNMLSA FEGMPMNFGI LGKGHGSSKS PLAEQVRAGA
IGLKIHEDWG ATPSSINTAL EVADDMDIQV ALHSDTLNEA GFVEDTIEAI AGRVIHTFHT
EGAGGGHAPD LIRVAALPNV LPASTNPTLP YTRNTVEEHL DMVMVAHHLN PDIPEDVAFA
DSRIRAETIA AEDVLHDMGI FSITSSDSQA MGRVGETITR TWQVADHMKR TRGSLTGDAP
YNDNNRLRRF IAKYTINPAI AHGVDYVVRS VEEGKFADLV LWDPKFFGVK PDLVIKGGLM
VNSLMGDSNG SIPTPQPRTL RNTWGAFGQA VSRSSITFLS QDAIDANVPD LLNLRKQIRG
VRGVRNLTKR DMKLNAEMPD IRVDPETYQV FVNGELITSK PAETVPMARR YFLF

> RXA02275 (1-471, translated) 157 residues
MIITAIDTNI YDEPEFVEGR DVIGVRFEDL VLDKRIQRVA LPGGEELGLR LNHGHPILRE
GDVLKADDKT VFVVEIIPTD VLVITPSDIH QMGFVAHSLG NRHLPAQFSK PGELTEKAAM
IVQYDHTVVS FLDEHGIEYQ RTELVPPIPF RHSGHTH

> RXA02276 (1-678, translated) 226 residues
MDLDADFLLL HLSDSALPTG AFAHSFGFET YMDAERITNA EEFQDWLKVL LKVQLTSSDA
LAMRMFYATP TVSELKRLDE RLFAGTPARE IREANARMGI RMAEIVAETY SVPLIVEYLE
LIQHRELSGH PALALALATH SAGIDVDRAI HAHLTATVSS LIQNAVRGIP LGQMAGQRVM
FAMREHIGAA VKRSANLDEI DFCSGDPGLD ISQMVHETQR ARLFMS

> RXA02277 (1-615, translated) 205 residues
MGPIRIGVGG PVGAGKTQLV ERITRALIDE VSMAAITNDI YTIEDAKILA ANGVLPEERI
VGIETGGCPH TAIREDTSMN DAAIKDLVER FPDLELIFVE SGGDNLSATF SPELVDFSIY
IIDVAQGEKI PRKAGQGMIK SDLFIINKTD LAPYVGANLD VMVEDAKAFR KNKPFCLTNL
RTDDGLDKVL EWIRHEVMMQ DLQEA

> RXA02278 (1-849, translated) 283 residues
MTQTQPVGTL RLTIDDQGPQ GQSRAVEQFH QGALRVIRPH YLDDSGQVCY TIIAIGGGYL
GGDVYEQQFT IKDNAKALIT TQSATKIYRT PQGPATQHTE INVGENAVLE YLADQTIAYR
EATYHQFTKV ALHPSATFVM SEQITPGWHP DGKHFAYDEM RLHTEITDST TGRLVLLDNL
LLRPDSREGS FGWTEQYTHS GQMIVMGEGV DKQLVAELNE QLAAHPDVYG AVNFLSAPGT
LLRGFIARTL SNRTEELINL HEHIASLLRG RWRGQEPVNL RKY

> RXA02316 (1-1014, translated) 338 residues
MSTPTVDEIL ERAHVVSLPM RVKFRGVTTR EALLIEGPAG WGEFAPFLEY DPQESASWLK
SGIEAAWEGF PAPLRDRVEV NATIPAVPAD QVAEVLDRFP GCRTIKVKVA EPGQTLADDI
ARVAAAREAR PGAIIRVDAN CGWSVEQAVE AAQALAPLDY LEQPCATVEE LAEVRMTVQR
RGLFVRVAAD ESIRKSDDPY RVADLRAADV AVVKVAPLGG VKRVLEVVQH LRARTMDITV

ASALDTVVGM NAGLAAVAAL PKLDDDDLID VPPAAAGLAT SQLFLEDVAT PHAITDGFME
TRVIAPEMDR LETLAASKDR RDWWFERVRE SYPYLETI

> RXA02317 (1-612, translated) 204 residues
MAHMRLLLTS FGHDHIRDFV RGTVAYIPDA TRLFADSPEA APFMETERNM LREHGLSIRE
LPISTSTPEE VDRVLGEVDG VYVAGGETFD LMWLLRSTGN DEVLIKHVRA GLPYIGTSAG
AVIAGPSIEP ISFLDSPDVA PNLSDYSGLG LCEHVVVPHA GGTIPQFPID VFAETVRTYG
AEFPLVLLKD GQALLIDDHG VHLI

> RXA02334 (1-354, translated) 118 residues
GVLPDWMSTA TQPSNTGVLR GEHIPGAINL DWSDAVLPNG NFRTRAELDK LYADLNPADD
TVVYCQVGDR AAHTWFVLKY LLGFNNVRNY DGSWAEWGNM VRMPIETGEN TKNNVSVS

> RXA02351 (1-939, translated) 313 residues
VEGSVEKLGL ISWWEELART AERGKLDAVF LADGQAINPV GLENGPGWFL EPVTALTAMA
RATNNIGLIS TISSTFWQPF HAARMIASLD HISGGRAGIN VVTSMTDAEA RNHGMDALPG
HDVRYARAAE FIETITALWD SWPAESLVMD RAGKFADSSL IKSIDHDGEF FQVAGPLNIP
SPPQGRPVLF QAGSSPQGRE IAAKYAEAIY SVAWDLEQAQ DYRSDIHARA TAQGREPMPV
LPGLVTFVGT TVEEARAKQQ ALNALLPVKD SLNQLSFFVG QDCSTWDLDA PPPPLPPLEE
FSGPKGRYET VLR

> RXA02410 (1-666, translated) 222 residues
MDMGPGVLAA VQEIQDPADA HVIFSHLHTD HCADFASLMV WRRFHPTLAA KSRNLLFGPE
DTPNRLGRLS SDEPDGVDDM SDTFAFDAWE ERKPELIDNF TVTPFRVVHP IETYALRVEE
HRTGASITYS GDSAYTEALI DAARNVDIFL CEATWGTSCD DKAPGMHMCG QDAGRIAAAA
GVKKLIITHV PPWIDAEATV AAAAEHFDGP IELARSGMVI EF

> RXA02411 (1-849, translated) 283 residues
MATVTDFSGS MIERPVPGAD APIGIFDSGV GGLTVARTII DQLPHESVIY IGDTANGPYG
PLPIAKVREH AIRIADELVE RGCKMIVIAC NTASAAFLRD ARERYSVPVV EVILPAVRRA
VASTRNGKVG VIGTVGTINS GAYQDLFSAS PSIVVNAVAC PRFVDFVERG ITSGRQILNI
AQDYLEPLQA EGVDTLVLGC THYPLLSGVI QLAMGDHVSL VSSAEETAKD VLRILSQQDL
LADPDMHPEP SYSFESTGDP EIFAQLSRRF LGPIVSQVRQ NEG

> RXA02448 (1-1089, translated) 363 residues
VNNSLAFNHD TLPQKVMFGY GKSSAFLKQE VERRGSAKVM VIAGEREMSI AHKVASEIEV
AIWHDEVVMH VPIEVAERAR AVATDNEIDL LVCVGGGSTI GLAKAIAMTT ALPIVAIPTT
YAGSEATNVW GLTEAARKTT GVDLKVLPET VIYDSELTMS LPVEMSVASG LNGLAHCIDS
LWGPNADPIN AVLAAEGIRA LNQGLPKIVA NPHSIEGRDE ALYGAYLAAV SFASAGSGLH
HKICHTLGGT FNLPHAQTHA TVLPYVLAFN AGDAPEAERR AAAAFGTDTA LEGLQRLRLS
VNAPKRLSDY GFEASGIAEA VDVTLEKVPA NNPRPVTREN LSRLLEAALN GEDPAVLSAV
LSN

> RXA02449 (1-903, translated) 301 residues
MTTTTADHNI SAQQKAVEEN LVNRVLQSFD ACENPRLKQL MESLVVHLHD FIRDVRLTED
EWNYAIDFLT AVGHITDDKR QEFVLLSDTL GASMQTIAVN NEAYENSTEA TVFGPFFLDD
APEVELGGDI AGGAQGQAAW IEGTVTDTEG NPVPNARIEV WECDEDGLYD VQYADERMAG
RAYMHTDANG DYRFWGLTPV PYPIPHDGPV GNMLKAVGRS PVRCAHLHFM VTAPELRTLV
THIFVEGDPQ LEIGDSVFGV KDSLIKKFEE QAPGTPTPDG RDLGDQTWAR TRFDIVLAPG
A

> RXA02470 (1-981, translated) 327 residues
MFERFTDRAR RVIVLAQEEA RMLNHNYIGT EHILLGLIHE GEGVAAKALE SMGISLDAVR
QEVEEIIGQG SQPTTGHIPF TPRAKKVLEL SLREGLQMGH KYIGTEFLLL GLIREGEGVA
AQVLVKLGAD LPRVRQQVIQ LLSGYEGGQG GSPEGGQGAP TGGDAVGAGA APGGRPSSGS
PGERSTSLVL DQFGRNLTQA AKDGKLDPVV GRDKEIERIM QVLSRRTKNN PVLIGEPGVG
KTAVVEGLAL DIVNGKVPET LKDKQVYSLD LGSLVAGSRY RGDFEERLKK VLKEINQRGD
IILFIDEIHT LVGAGAARRR NRRCLPA

> RXA02471 (1-1833, translated) 611 residues
VQHEGAIDAA SLLKPKLARG ELQTIGATTL DEYRKHIEKD AALERRFQPV QVPEPSVDLT

VEILKGLRDR YEAHHRVSIT DGALTAAAQL ADRYINDRFL PDKAVDLIDE AGARMRIKRM
TAPSSLREVD ERIADVRREK EAAIDAQDFE KAAGLRDKER KLGEERSEKE KQWRSGDLED
IAEVGEEQIA EVLANWTGIP VFKLTEAESS RLLNMEEELH KRIIGQDEAV KAVSRAIRRT
RAGLKDPKRP SGSFIFAGPS GVGKTELSKA LAGFLFGDDD SLIQIDMGEF HDRFTASRLF
GAPPGYVGYE EGGQLTEKVR RKPFSVVLFD EIEKAHKEIY NTLLQVLEDG RLTDGQGRIV
DFKNTVLIFT SNLGTADISK AVGLGFSGSS ETDSDAQYDR MKNKVHDELK KHFRPEFLNR
IDEIVVFHQL TKDQIVQMVD LLIGRVSNAL AEKDMSIELT EKAKDLLANR GFDPVLGARP
LRRTIQREIE DQMSEKILFG EIGAGEIVTV DVEGWDGESK DTDRAKFTFT PRPKPMPEGK
FSEISVEAAE AIQDVDSAAD GDVPETDSLS DIDLETLEKF EEDVENGTDI DQVSGDYYGT
DDQGGTAPSK E

> RXA02477 (1-621, translated) 207 residues
MPLRNVDRTP PAVWEALLAG NERFISFNED RPNQDAPRRR ELRNGQTPAA VVISCSDSRV
PVEIIFDVGL GDLFVVRTAG EILDQAVLAS IEYATESIGV PLVIVMGHES CGAVAATAAA
LEGGALPGGY QRVLVEKVAP SILEAKAEGL SSIKEFEEHH VVATVNQLLS RSPEIHQKVE
TGELGIIGLR YRLSDGRTEP VISKNVG

> RXA02497 (1-927, translated) 309 residues
VRLGVLDVGS NTVHLVAVDA RPGGHPTPMS NWRTPLRLVE LLDDSGAISE KGINKLTSAV
GEAADLAKTL GCAELMPFAT SAVRSATNSE AVLDHVEKET GVRLSILSGE DEARQTFLAV
RRWYGWSAGR ITNLDIGGGS LELSSGTDES PDLAFSLDLG AGRLTHNWFD TDPPARKKIN
LLRDYIDAEL AEPARQMRTL GPARLAVGTS KTFRTLARLT GAAPSSAGPH VTRTLTAPGL
RQLIAFISRM TAADRAELEG ISSDRSHQIV AGALVAEAAM RALDIDKVEI CPWALREGVI
LTRIDKGLE

> RXA02513 (1-732, translated) 244 residues
MLPIWMGLPF KKAGALSRRK AVFSALGADA LMGAALPTIP TAQAQTPTGY GFDATASISE
EPEFSTQQLA DGGTLGFDCY RIPSLGVAPN GNVLASWDGR PNNCSDAPQP NSIVGKVSTD
NGATWGEQHD ISAGITAEPK TGYSDPSIVV DWERGDVFNF HVKSFDAGYF TSQPGTDPDD
RNVAHVAYAK SSDNGSTWVA DTVITDQVVA HDTWDSRFAT SGNGIQLQYG AYKGRLVQPS
VTRM

> RXA02526 (1-1206, translated) 402 residues
VITEDDAAQI NQAAVLSNID REKLWEDAKN VGYPILGLVR QIASHLPEGP NGRVHYGATT
QVIMDTGLVL QMTASLNALD KQIVRLGNAL AARAEEHKDT VMPGRTHAQQ AIPTTFGATL
ATFLDQIRRQ RERLEEALER VRVISLFGAG GNNAAQGEQA ATVRAEMARL LDLKDPVVSW
HVERDVLGDF GWVCSTLCGS MAKFGRNIVD LSRTEIGEVF EPYNSHRGAS SMMPQKVNPI
SSELMIGISV VAGALTSTLP RLQESGHERA AGEWQGEWLV IPTLANLAGA ALDEAIVVAE
GMRVDTDRMS SNLAFAGGLI MAEAQMIQLA PALGREKAHD LVYEASTKTR EEHTTLAEEL
PIIAVQHGVE DLLPKNFAQP ADYVGEAQSM VNAAVAAWNA QL

> RXA02530 (1-450, translated) 150 residues
MNRPDPKTPA GTLVAGYYGA YENEFSFAVV RPVKVSRVEP TSEDPSSPLR VSSDDGREWI
TRMVLNATGT WTNPYVPYIP GIDKFQGKQL HTVNYRKAED FKGKKVLVVG GGLSAVQFLL
ELEGLAETTW ATRRPRTYAA RVRRRLGHCG

> RXA02531 (1-711, translated) 237 residues
MKIPLYMAEE AAALNLLADG RLALGVSRGS PEPAEKGWEA FGYDGGDDPK AAGMAREKFL
RFLDAIDGRP MSIASENQYP RLYHPGTPLP IFPHDLDLGK SIWWGAGSHN TAEQAARDGV
NLMSSTLVAE ATGQSFGDLQ ADQIAFYRQA WKEAGHDWTP RVSVSRSIFP IVTDRDRELF
GLQGQGGDQV GILDDTRSTF GRSYAGSPDE LIDQLQGRQS CDGSRHLDAH RPQPNGC

> RXA02535 (1-1155, translated) 385 residues
VTPRPVSSVA RLVEDNAQDF LRAVQAKLLT LAPQARGHFP TADDATHISI AEMVSALLEG
TGEEGKVDDK TLEFFKEAAL DARRFGLTPE MHSALGEAVR SELLSLCEDL PFENVLFAER
AIAATTAVSV EAVREADEAH IPASYQAEIV EVEKRSRRFT VVRMQAETQL PYLPGQYLAA
TADFLPNTWR YLCPSIPTNE WGQVEFHIQS DADDIAGLLA TTRLGDKWRL GPGRGDFGQS
KISSGNDLLF IAHGTGLAPL RAYMFELMNQ AAPPRLHFFV GADYPGELYE LTGMWNFAAA
SPWLSVVPVS THDKDAWWVQ ATEASQPPRG LHLHQTGSMA KIVTEAGAWA DRDVLIAGPE
SWARDVRRAM IRRGTPAQQI EILGF

> RXA02548 (1-291, translated) 97 residues
PPIYFSHDRE VFERDGMWLT AGEWGGPKKG EEIVTKTVRY RTVGDMSCTG AVLSEARTID
DVIEEIATST LTERGATRAD DRLSESAMED RKKEGYF

> RXA02558 (1-975, translated) 325 residues
MSTIEERTPG AVATEPVGHE GARVSINEKN VWSLGAGPAA FALLAMIVLM IASGVFFAQS
INTLENDGGG TLAVTGLIAS IVVFTVALVV TITSVKVVSP GHTLTVQFFG RYIGTLRRTG
LSFVPPLSVT KKVSVRVRNF ETNEAKVNDY NGNPINIAAI IVWQVADTAQ ASFSVEDFEE
FLHQQAESAL RHVATQHPYD SPVDGRVSLR GATDEVSEEL ADEVAQRAAV AGLEIVEARI
SSLSYAPEIA QAMLQRQQAS AIVDAREKIV EGAVTMVETA LDQLEQREIV DLDPERRAAM
VSNLLVVLCS DTNAQPIVNA GSLYQ

> RXA02565 (1-342, translated) 114 residues
AALGDLADEV EIEHLISEEA TVSPTDSRLY NTLEKVLGDF FPDAPVVPII SSGGSDLRFG
RRLGGVGYGF AVHARERTLA EAMGQLHSHD EALYLEDLEL TVRGYDSVVR EFLG

> RXA02567 (1-738, translated) 246 residues
LIRNACVNDL TPDSGQEIRN AESLERFFEG TPNVKITKLE PHPGRTSIIV TVPGSDPDAE
PLTLLGHTDV VPVDLPKWTK DPFGAEISDG QIWGRGSVDM LFITATQAAV TRQVAREGGL
RGTLTFVGVA DEEARGGLGA KWLSEEHQNL FSWKNCLSES GGSHLPVHDG SDAVVINVGE
KGAAQRRIHV NGDAGHGSIP FDRDSAIVKI GEVARRIAAA DLKVAKDDIW QGFVQAHRFD
PETEQA

> RXA02574 (1-1008, translated) 336 residues
LARAQIPEQQ RDQVASLMMV GVANYDQALD ALNQGVGGIF IGSWTDENLL TEPGRNIEAL
REAVGRDFSV SIDFEGGRVQ RATNILGDFP SPRVMAQTMT PEQVEDLAEI LGTGLAAHGV
TVNFAPVVDV DAWGLPVVGD RSFSNDPAVA ATYATAFAKG LSKVGITPVF KHFPGHGRAS
GDSHTQDVVT PALDELKTYD LIPYGQALSE TDGAVMVGHM IVPGLGTDGV PSSIDPATYQ
LLRSGDYPGG VPFDGVIYTD DLSGMSAISA THSPAEAVLA SLKAGADQAL WIDYGSLGSA
IDRVDAAVSS GEYPQEQMLA SALRVQLLYI TRLEQK

> RXA02589 (1-765, translated) 255 residues
MSISDNSRDQ LGELPAGRPL QSDFDNDLDY PRLGSVTFRR GTLTENQQTM WDEKWPELGR
VLEDELIDVD AWFGREGAKT IVEIGSGTGT STAAMAPLEA DTNIVAVELY KPGLAKLMGS
VVRGEIDNVR MVRGDGIEVL NRMFADGSLD GIRVYFPDPW PKARHNKRRI IQSGPLNLFA
KKLKPGGVLH VATDHADYAE WINELVEVEP LLEYKGWPWE ECPQLTDRQV ITKFEGKGLE
KDHVINEYLW QKVQN

> RXA02592 (1-771, translated) 257 residues
MASFPELPAL RRLATLGRSW GLLSDFKYEQ TRPDIFYGNL ALDTSSLVAA LSEDISGAGL
NDLKVLDVGG GPGYFAEAFE TLGATYFSVE PDVGEMSAAG IDVHGSVRGS GLDLPFLPDS
FDVVYSSNVA EHVSAPWELG EEMLRVTRSG GLAILSYTIW LGPFGGHETG LWEHYVGGEF
ARDRYTKKHG HPPKNVFGES LFNVSCREGL EWGASVGNAE LVAAFPRYHP YWVWWMVKVP
VLREFAVSNL VLVFKKH

> RXA02603 (1-996, translated) 332 residues
VSEHAAEHHR DTQNFLTSEP HTTAIEDNKK RQPPKNLADG MIKALRPKQW VKNVLVLAAP
LAAGADAIFN QRTIIDVAIA FVVFCFGASA IYLVNDARDV EADREHPTKR FRPIAAGVLP
VGMAYGMAVA LIALSIGLSF LATDGVALAC VIGVYIALQL GYCFGWKHMP VIDIALVSSG
FMLRAMAGGV AAGIELSQWF LLVAAFGSLF MASGKRYAEI LLHERTGAKI RKSLESYTPT
YLRFVWTMAA TAVVMSYALW GFDLSQHSTD AGPWYQISMV PFTIAILRYA AGVDTGDGGA
PDEVALSDKV LQVLALAWVF CIVMAVYIMP MF

> RXA02630 (1-1323, translated) 441 residues
MTNQFPTNNG ENPDRASETP SETNSFEHVR SSYPQWGNTA SNQNPYPGAG FGSEQNTQQG
NEQQAPAWTS WDNQPLSTDV KPAKEKRKVG IGTALALMLV GSIATGSVVG VAATQLGSDS
STPVNALEQP SVQRTTNAEP GSAEQVAAAV LPSVVSIQAI TRTSASEGSG SIISSDGYVM
TNNHVVAGIE QSGVLEVSFS DGTTAQADFI AGDPSTDIAV IKIRDVSNLP VMSFGDSDAL
GVGQSVMAVG SPLGLSSTVT TGIVSAVNRP VRASGDGGES SLIDAIQTDA AINPGNSGGP
LVDMDGNLIG MNSVIASISS TSDSAGSIGL GFSIPSNFAK RVADQLISTG QVTQPMIGVQ
VGTDNSVTGA VIASVQDGGP AADAGLQPGD IVTKLNDRVI DSPDSLIAAV RSHDFGETVT

LTITQPDTSQ SREVEVTLTS E

> RXA02641 (1-2076, translated) 692 residues
MLAIILTAVL GASGLAAAGT QYLNTQGEGI GPVAVQNDSE SFNSGTNVVV EDAAVTAQGE
GGGARTVKEF QRDQQFSSFA LTWTGKKDIT AFVRAEQEDG TWSQWYDLEP MVNEDQGTNG
TELIWHGPTN KIQVSTLNVD LFGADAAAAD ENGQDIPAVD AAEAAPAAEP APAEAPVEEA
PAPVAEPAPA AEPIAEPVAD YSANDGLAPL PSNYGDIQPV ADVDDGLNAV FIDGNADAGV
GIANVADTDG MPKVISRAGW GADESLRCSN PTIDDGVSAI TIHHTAGSNN YTEAQAAAQV
RSAYSYHAKN LGWCDIGYQS LVDKYGNIYE GRAGGMTNAV QGAHAGGFNQ NTWAISMIGD
YSYNAPPQET INAVGELAGW RAKVAGFDPT GTDTHYSEGT SYAKYSYGTR VSLPNILAHR
NVGLTACPGD AGYAQMENIR QIVKAKYTSL QNGNTGGTTT TPATTPKETS TSNAPSTTTA
QLVTPAEPQQ YSESDALAAL LTGGSSGGTD LLNGANSEQL LTGLGSIAAV LIAASLADGG
LNGLISNVGS NNGVPVLGDI KITDVIPIVD TAINLTGDNK YSRGWNDLNN TLGPVLGAAT
GGETTVKYTS DQNSEVTFVP FENGIMVSSP EAGTHGLWGA IGDAWAQQGA DLGPLGLPTS
NEYTVGEQLR VDFQNGYITY DSATGQASIQ LN

> RXA02643 (1-1044, translated) 348 residues
MKNVSFGLDT FGDNAIDLQG NPVSPAQTLR NIIDEAKMAD KVGVDIIGIG EHHREEYSVS
APDIVMTAIL ASTERLKVTS SVTVLSSDDP VRLFERYSTM NALSNGRAEI TLGRGSFIES
FPLFGFDLQD YEQLFSERLD LFAKILEADS RGQGVTWHGE TRSALENQML YPPTENGIHA
WVAVGGSPES VVRAAKYRFP LMLAIIGGAP ERFRPYVDLY KRANEQFGQP QKPIGVHSPG
LIAATDEEAR ELALNDWLEL QRKIGAERGW APADAMQFER EIDHGSLYIG SPETVAKKIA
KTISVLDLDR FTLKYASGQT PHEYLLKSIE LYGTEVIPLV KDILTKQA

> RXA02644 (1-651, translated) 217 residues
MAHLTQYQLP QAGQVFEHEL EIKRSRFLTY ITRVQDQEQA REFIHSIKEL YPDARHHCSA
FIFHVDGSND VERSSDDGEP SGTAGKPMLE ALRGSGMKDI AAVVVRYFGG VKLGTGGLVN
AYTNAVTELL PEVLQVTRSV REIFKIDLPH SDAGRIEANL RGMGIIITDT EYGAEVTYTL
ALLPGEQAAV ESQLSSMMGA EIELKESGHM WVESPSD

> RXA02702 (1-1458, translated) 486 residues
VTTPHLDSAQ DIDLSRVHLI GIGGAGMSGV ARILLARGKT VTGSDAKDSR TLLPLRAVGA
TIAVGHAAEN LELSGELPTV VVTSFAAIPQ DNPELVRARE EGIPVIRRSD LLGELLEGST
QVLIAGTHGK TSTTSMSVVA MQAAGMDPSF AIGGQLNKAG TNAHHGTGEV FIAEADESDA
SLLRYKPNVA VVTNVEPDHL DFFKTPEAYF QVFDDFAGRI TPNGKLVVCL NDPHAAELGE
RSVRKGIKTV GYGTADAVQA HPEVPAMATI VDSQVVAEGT RATINIDGQE VSVILQIPGD
HMVLNGAAAL LAGYLVGGDV DKLVEGLSDF SGVRRRFEFH GAIEGGKFNG AAIYDDYAHH
PTEVTAVLSA ARTRVKAAGK GRVIVAFQPH LYSRTIEFQK EFAGALSLAD AAVVLEIYGA
REQPVDGVSS EIITDAMTIP VVYEPNFSAV PERIAEIAGP NDIVLTMGAG SVTMLAPEIL
DQLQNN

> RXA02703 (1-1089, translated) 363 residues
MANSPKPMRV VVAGGGTAGH IEPALAVAEA LRDKHGATVS ALGTARGLET TLVPDRGFEL
HLIEPVPVPR KPNMDLLKLP FRVAKALGQA RKALKDTDAQ AVIGFGGYVS APAYMAAKSL
GLPFFVHEAN ARAGMANKLG VKLGGVGLNA VAGSGMDGDV VGIPIRAVLS GARDESAADR
ARDTWGLDKD RQTIFVTGGS QGSVSINKAV EQAVDQLVEA GFQVLHAVGK KNELPAAKPG
YHPVPFIDDM QAAYTVADLI VCRSGAMTVA EVTAAGVPAI YVPLPHGNGE QALNAQAVIK
AGAARQIDDA DFTAQTLIDA TLDILLHPST HQSMSDAAKT STAGNASTVI ADMIAATINS
QHN

> RXA02704 (1-1689, translated) 563 residues
MTTGASKKPA RPNTGAKTRT GLGIRERISG AWNDLLARPL TDYIMILCIV VILSCLGVVM
VYSSSMTWSL REGGSVWGTA VRQGIMIVLG FFAMWVALMT RPQTIRNLSN LILIVSIVLL
LAVQIPGIGT GKEEVGSQSW IALGPIQFQP SEIAKVAIAV WGAHYLAGKG PVQHWFNNHL
MRFGGVGAFM AFLIFMEGDA GMAMSFVLVV LFMLFFAGIA MGWIAIAGVL IIAALAVLAL
GGGFRSSRFE VYFDALFGNF HDVRGIAFQS YQGFLSLADG SGLGVGLGQS RAKWFYLPEA
KNDFIFAIIG EELGLWGGAL VIALFAGLLY FGLRTAKKSH DPFLGLMAAT LTASVVSQAF
INIGYVVGLL PVTGIQLPMI SAGGTSAIIT LASMGLLISC ARHEPETVSA MASYGRPAID
RLLGLREPSS TLTTSNASLR SNKTKAAKQK PSPQKESRDR FGEPVTARRA QAPRSGRAGV
QSEAPRRSTG SVKGRSSGQD NGRSNEGTAR SQSTTGGRAA DRSVDRSRQS RPTERRSESR
AMIGVTTATA DKCEIRRTTN KDG

> RXA02705 (1-1416, translated) 472 residues
MGSLSHLPQA LQGRILVAGA GVSGLSIAKM LSELHCDVVV ADDNETARHM LIEVVDVADI
STAQAQEQLD SFSIVVTSPG WRPTSTLLVD AHRQGLEVIG DVELAWRLDQ AGVFGEPHTW
LAVTGTNGKT TTTSMLAAMM NEGGFTAKAV GNIGIPVSEA LVAKNRIDVL VAELSSFQLH
WSPTFTPDAG VVLNLAEDHI DWHGSMRDYA LAKMEVLKGK VAIIGADDPY LVQLTSEADL
SGLIGFTVNE PATGQLGVKA GELVDNAYGN NVVLASADGI NPAGPAGVLD ALAAAAVARS
QGVAPEAIAR ALDSFEVAGH RGQVVAEHDG VHFIDNSKAT NPHAADSALA GHDSVIWVVG
GQLKGADIAP LVKKHEQRIK AALVLGADRA EIVAALKEHA SQASVFVTDK TEPFEAMEEI
VTEAFSISEP GDTVLLAPAA ASLDMFKGMG QRGDLFAHNI IGTIKGLTEE KG

> RXA02706 (1-1098, translated) 366 residues
MQQIMVSGTV AFLVSIFLTP VLIRYFTNRQ LGQEIREEGL QSHLRKRGTP TMGGIAIIAG
IVVAYVFTNI LAMIQGVGGF TVSGLLVLGL TLGLGATGFA DDFIKLYMNR NLGLNKTAKL
VSQLAIALIF GFLVLQFPDE NGLTPASTHL SFIRDIDTID LGFGGSVFGI IVFLIFIYVV
VSAWSNAVNI TDGLDGLAAG TTAFVMGAYT LITFWQFRNS CDTAVEAGCY TVRDPLDLSV
LCAAGLGATL GFLWWNAAPA KIFMGDTGSL ALGGLVAGIS VVSRTELLMV IIGALFVIEI
ASVAIQIGVF KTRGKRVFKM APIHHHFEAL GWAETTVTIR FWLIAIMAVL AGVGVFYSDW
LHLAEV

> RXA02707 (1-345, translated) 115 residues
MGELGDDASE AHAELGAELA KYNVQELVAV GENPNCAALA ESAASLGVST HVVSDVDAAL
ELLAGHIKRD DVVLVKASNA DRLWRVAEAL HGMVPGLKNT GGSVNDDSRR NVEGQ

> RXA02708 (1-435, translated) 145 residues
MAPRTKARVV WFTTDAGQAK KSDYWATSIS LDAVARASFT LNTKDGSWPV TLQVFGEHQV
ANALAAAAIA MEAGVAPELV VAGLEAHSAA SAHRMDVKTR ADGVTIINDS YNANPDSMRA
GIAALAYTAS GRSEATKLGS AWPNG

> RXA02709 (1-729, translated) 243 residues
MTLGEIADIV GGRLTGGAQE DTLVSSSVEF DSRSLTPGGL FLALPGARVD GHDFAATAIE
KGAVAVLAAR EVDVPAIVVP PVKIQESNAD IYAHDPDGHG AAVVEALSRL ARHVVDICVA
GHQLNVVAIT GSAGKTSTKD FIATVLDQDG PTVAPPGSFN NELGLPHTAL RCTTDTKYLV
AEMSARGIGH IKHLTEIAPP RIAAVLNVGH AHLGEFGSRE NIAQAKGEII EALPSKKTAR
YQS

> RXA02710 (1-1563, translated) 521 residues
MATTLLDLTK LIDGILKGSA QGVPAHAVGE QAIAAIGLDS SSLPTSDAIF AAVPGTRTHG
AQFAGTDNAA KAVAILTDAA GLEVLNEAGE TRPVIVVDDV RAVLGAASSS IYGDPSKDFT
LIGVTGTSGK TTTSYLLEKG LMEAGHKVGL IGTTGTRIDG EEVPTKLTTP EAPTLQALFA
RMRDHGVTHV VMEVSSHALS LGRVAGSHFD VAAFTNLSQD HLDFHPTMDD YFDAKALFFR
ADSPLVADKQ VVCVDDSWGQ RMASVAADVQ TVSTLGQEAD FSATDINVSD SGAQSFKINA
PSNQSYQVEL ALPGAFNVAN ATLAFAAAAR VGVDGEAFAR GMSKVAVPGR MERIDEGQDF
LAVVDYAHKP AAVAAVLDTL RTQIDGRLGV VIGAGGDRDS TKRGPMGQLS AQRADLVIVT
DDNPRSEVPA TIRAAVTAGA QQGASESERP VEVLEIGDRA EAIRVLVEWA QPGDGIVVAG
KGHEVGQLVA GVTHHFDDRE EVRAALTEKL NNKLPLTTEE G

> RXA02711 (1-2112, translated) 704 residues
VTFPSNGRSR GERAGREDTS RRSAYQDESR RAARERELTR RSGKAKGVNQ EEGVTYRPKS
STQGGARKRR VNMVTAIALV IAGVLIIRLG WVQVVWGPEL SLNASEQRTR VYVDPARRGS
IVDREGNQMA YTMQARSLTV SPNIMREELK TGTDLALRLA AEETDPENVA SYVTIEEGNA
YVFASEEQRE TILSDKVEER IQSIADRIPE IIKSHDQDVT GISSEEILDK LNADSQYEVL
VRNVDPDVAS EITDEMPSVA ADHQDIRQYP NGAIGENIIG RISMDGEGQF GFEASNDSLL
AGNNGRSTQD MSILGQAIPG TLRDQIPAID GASVELTVDL DLQTYVQQAL EQAKANSGAE
NASAVVLDAK TAEVLAMANT DTINPNEDTG KQIEQGKSFD NPSVTHPFEP GSVAKVITAA
GVIQEGLTTP DEVLQVPGSI EMAGVSVGDA WDHGVVPYTT AGIFGKSSNV GTLMLAQRLG
EDKFADYLER FGVGQPTGIE LPSESQGLLP AREQWSGGTF ANLPIGQGMS ITTLQMAGIY
QALANDGERI QPRIIKSVTD SDGTVLEQPE PDKIQVVSAE AARTTVDMFR SVTQVDPTGV
QQGTAPDASI EGYQISGKTG TAQKVDPNTG AYSNSQYWIT FAGIAPADDP RFVVAIMLDE
PERGVHGGGG QTAAPLFKDI ATWLLNRDNI PLSAATEPII LQAQ

> RXA02713 (1-1011, translated) 337 residues
MEDFSLDGNH GHVPVMRDRM AALIAEHVEA LGENAVIVDA TLGAGGHAEF FLNTFPKARL
IGLDRDQNAL RDARARLAPF GERFIGVQTR FDGLREVLES VEGDIIDLAR EHGIAGALFD
LGVSSMQLDQ VERGFAYRTD APLDMRMDAT QGITAADILN TYSHGDIARI LKTYGDERFA
GKIASAVLKE REKEPFTTSA RLVELLYDAI PAATRRTGGH PAKRTFQALR VEVNNELDSL
KNVLPQITDA LNVGGRAVFM SYQSHEDKLV KKFFTDLTTS KTPPGLPVDL PGTAPQFKQV
TRGAETASEA EIEENPRAAP VKVRAIERIG NNSGDLS

> RXA02716 (1-561, translated) 187 residues
VSPIIRKLSI PEFTTNTPVL VDIYIAAMNY DKAIRDTRIE VWRRNSQNPG FTAVAALMDD
QVVGVAYGFN GSPDHWWQHQ LRRGLRQQGG PTEEEIHIIH NYFEVAEVHV QPGFQGHGIG
RKLMHELLKD KQNTFAILST PEVDDEANHA FSLYRSLGFT DLLRQFRFDG DQRPFAVLIT
ALPLHDS

> RXA02722 (1-1326, translated) 442 residues
MTSPNNYLAK IKVVGVGGGG VNAVNRMIEE GLKGVEFIAV NTDSQALMFS DADVKLDIGR
EATRGLGAGA NPEVGRASAE DHKNEIEETI KGADMVFVTA GEGGGTGTGA APVVAGIAKK
MGALTIGVVT KPFEFEGRRR TRQAEEGIAA LKEVCDTLIV IPNDRLLELG DANLSIMEAF
RAADEVLHNG VQGITNLITI PGVINVDFAD VRSVMSEAGS ALMGVGSARG DNRVVSATEQ
AINSPLLEAT MDGATGVLLS FAGGSDLGLM EVNAAASMVR ERSDEDVNLI FGTIIDDNLG
DEVRVTVIAT GFDAARASAA ENRRAGISAA PAAEPVQQQV PTTNATLPPE KESIFGGARE
ENDPYLSRSA GARHRIEETR SGGGLFTTGN DRDYRRDERR EDHRDERRDE RRDDRSYDRR
DDRRDDRRDD RGDDLDVPSF LQ

> RXA02723 (1-477, translated) 159 residues
DATAAGQNIV ELPWVKSVTV NRALPSTITV ELTEREPAVF IKRADGDHVI DTEGKEIIIG
TPPVGTVEVS GADEGNSEVL PAVIAVINAI KAQDAQMTES IQVVEAPDQF DILLKMNDGR
EIYWGSSENN HDKAVAMSTV LKREGQRWNI SSPSMVTVR

> RXA02745 (1-879, translated) 293 residues
AGISFEVPRG QVLALLGPNG AGKTTTIEMC EGFTAPTSGS IRVLGIDPAT EPDQVRRRIG
IMLQGGGSYS GIRVFEMLKL AASYNDNPHD PEWLLDLVGL REQRKTTYRR LSGGQQQRLS
LALALIGRPE IIFLDEPTAG MDAQSRNMVW ELVNDLRRDG VTIVLTTHLM DEAEALADHV
IIVANGQILA SGTPDELTAQ RDHLEINVSV ETTSPLDLDR LVDDLSSLNI GDVKARANRP
LHYSLRTQQA TPDSLAHIVQ AVARQNVMIR SLDTGHRSLE DVFLDITGKE LRS

> RXA02746 (1-267, translated) 89 residues
GVQGMTVTET QGFGQQKGHT EVYRGAEYAV DFVPKVKIEV IISDAQAEEV INIIVETART
GKVGDGKVWM TNIEELVRVR TGERGEAAL

> RXA02813 (1-642, translated) 214 residues
GALTGGWLVA VDNAARALEA LEFPVSYGGA SGNMTAVHPR GFEIQAKLAE ELGLFDPQWV
WHSDRTPITA IASALATAAG VVRKIAGDVV FYSQTEVGEL REKSPGGSSA MPHKANPAAA
IACDGYARRA PGLLATLFDA LDCRLQRGTG SWHAEWATLR ELAAVTHSAV SRAATSIDGI
TVNVDVMASR VNGPTGHAED LAERALEIYG KGRS

> RXA02820 (1-507, translated) 169 residues
ANSAEDLSHD PEAAAYFLDE NGDAKAPGTL LQNPDYAETI RLISEGGPDA FYTGEIAADI
VERATREVDG FTPSLMSTAD LAAYTPETRE ALCAPYRDKI VCGMPPSSSG GVTVMETLGI
LNNFDLAQYP PTEVGLDGGL PNAEAVHLIS EAERLAYADR DAYIGDPAF

> RXA02828 (1-558, translated) 186 residues
MKRRDFLSAL SAGTLSLGXF APQLLLAQGM NQPMRAPIHV GKSGLRARDA EALATWYQSH
VGLQEIGRDG ATIHMGAGGT VLLEITQYDG IVLAPMRVAG LYHNAFLLPA RADLARWVLD
ASARQLRIDG YADHLVSEAM YLTDPEGNGV EIYADRPASD WVWRNGQVEM DSLQIDFYSM
IATLDG

> RXA02834 (1-495, translated) 165 residues
DSKGRSVDFK NTIIIMTSNI GSQVLLENVK DAGEISDDTE KAVMDSLHAY FKPEILNRMD
DIVLFKPLSV NDMSMIVDKI LTQLNMRLLD QHISIEVTEE AKKWLGEEAY EPQFGARPLK
RFVQRQIETP IARMMIKESL PEGTIIKVDL NDNKELDFKV VKPTS

> RXA02839 (1-417, translated) 139 residues
CVVNDYADRK FDGHVKRTAN RPLPSGAVTE KEARALFVVL VLISFLLVLT LNTMTILLSI
AALALAWVYP FMKRYTHLPQ VVLGAAFGWS IPMAFAAVSE SVPLSCWLMF LANILWAVAY
DTQYAMVDRD DDVKIGIKS

> RXA02855 (1-1185, translated) 395 residues
VMEIGVQVAS WMDRHHDEVI KWRRHLHSHP ELSHMEYRTT EYLASVLKDH GMEPHLFPGT
GLMVDIGPEG DSRLAFRADI DALPLLESTG LEFSSTATGV AHACGHDVHT VIALALACAL
NTIELPIGIR VIFQPAEEVM TGGATDVIAH GGLDGVDAIY AIHVEPKLKV GRVGVRAGAI
TSASDVIEIR VKGEGGHSAR PHLSADVVYA LSKLVVDLPG LLSRRVDPRT GTVLVFGTIN
AGYAPNAIPD SGIVSGTLRT ADISTWRDMR PLISELVEQV LAPTGVTHEL IYNPGVPPVL
NDDVATALLA SAARDMDTQS VVQAPQSSGG EDFSWYLEHV PGSMARLGCW PGHGPKQDLH
QSDLVVDERA IGVGVRLFGS LVQQYSSRSE AFLNS

> RXA02859 (1-726, translated) 242 residues
QYTVDQLLHG LLLASGNDAA YLLAQELGGD QATLEKVNAL AKELGTQDTF VATYSGLDAP
GMSTSAYDMS LIYQHAWQNP VFESIISTDH IDFPGWGDNE GFQVWNDNAL FMNDPDGIGG
KTGYTDDANH TFVGGLDRGG RRLAAVLLDS TVSDIRPWEQ ARLLIDASLP ITPGSGVGQL
GSGSANDVAP ATPELPEPTD NLTSGEGGSQ NTLLKLVVPI GIIVLLLIAA LAWTFRSPKK
KN

> RXA02895 (1-666, translated) 222 residues
MAEQLRQFEG RVLPNQSEDL EDQGLGFDLG TVFSRRKVLG FIGVGGAGVA LAACSPSGSS
AASSTSSASS SAAATTSAAA ETLTEMKSET AGPYPGDGSN GPDVLEVSGV ERQDITKSID
SDTVAEGVPL TLTMTILDMN NNNQPMEGAA VYVWHCDAPG RYSMYDSELE DETYLRGVQI
TDKYGQVTFD TIFPGCYAGR WVHIHFEVFP DRDSITDSTN NI

>RXN00045 TRANSLATE of: rxn00045.seq check: 4044 from: 1 to: 909
MTDPTCTLALDIGATKIAYALVPDNTPTTTLSTGRLGTKEGDSPIEQIRLVLLAGLKAAE
EHGLSVARIGMGAPGVILGPEGTIVYNGETLTEWAGTDLRGLSREVLNVPFAAHNDVRVW
AYGEHHLGTGKDLTGRVLYVSLGTGVGGAIIEDGIMMSSPTGTAGEFAEVVCSDHAGLAV
RCENVASGTGLTRYYNEAAATQLDLPAIMERFHQGDGLAQQIITGNLRGFGQALGALVTV
LDLSAVVVGGGVAGIGAPVMDPITAGIFDRVLTPNKSVQVLSTSLGAQAAVIAAAKYARD
NAF

>RXN00073 TRANSLATE of: rxn00073.seq check: 5738 from: 1 to: 1683
MTTTTGSARPARAARKPKPEGQWKIDGTEPLNHAEEIKQEEPAFAVKQRVIDIYSKQGFS
SIAPDDIAPRFKWLGIYTQRKQDLGGELTGQLPDDELQDEYFMMRVRFDGGLASPERLRA
VGEISRDYARSTADFTDRQNIQLHWIRIEDVPAIWEKLETVGLSTMLGCGDVPRVILGSP
VSGVAAEELIDATPAIDAIRERYLDKEEFHNLPRKFKTAITGNQRQDVTHEIQDVSFVPS
IHPEFGPGFECFVGGGLSTNPMLAQPLGSWIPLDEVPEVWAGVAGIFRDYGFRRLRNRAR
LKFLVAQWGIEKFREVLETEYLERKLIDGPVVTTNPGYRDHIGIHPQKDGKFYLGVKPTV
GHTTGEQLIAIADVAEKHGITRIRTTAEKELLFLDIERKNLTTVARDLDEIGLYSSPSEF
RRGIISCTGLEFCKLAHATTKSRAIELVDELEERLGDLDVPIKIALNGCPNSCARTQVSD
IGFKGQTVTDADGNRVEGFQVHLGGSMNLDPNFGRKLKGHKVIADEVGEYVTRVVTHFKE
QRHEDEHFRDWVQRAAEEDLV

>RXN00136 TRANSLATE of: rxn00136.seq check: 222 from: 1 to: 1095
MSAVQIFNTVHVNGSSPYDVHIGSGLNELIVQRAAESGAEQVAILHQPSMDDIASELDAA
LVAAGLKVLHLNVPDAENGKSLEVAGQCWDELGGAAFGRRDIVIGLGGGAATDLAGFVAA
AWMRGVRVIQVPTTLLAMVDAAVGGKTGINTAAGKNLVGAFHEPDAVFIDTDRLATLPDA
EIIAGSAEIIKTGFIADPEILRLYETDPAACLKKEVEGSHLPELIWRSVTVKGSVVGQDL
KESSLREILNYGHTFAHAVELRENFRWRHGNAVAVGMMFIANLSHKLGLIDAPLLERHRS
ILAAIGLPTSYEGGAFDELYDGMTRDKKNRDGNIRFVALTAVGEVTRIEGPSKQDLQSAY
EAISH

>RXN00177 TRANSLATE of: rxn00177.seq check: 5596 from: 1 to: 1068
MSLQFDHETLGQRVLFGSGEAAQNLAAEISRLDAKNVMVVAGDFELPMARQVAADIDVKV

WHSNVVMHVPIETAEEARSVAKENDIDVVVCVGGGSTTGLAKAIAMTTALPIIAVPTTYA
GSEATNVWGLTEAARKTTGVDNKVLPVTVIYDSALTMSLPVEMSVASGLNGLAHCIDSLW
GPKADPINAAMAAEGIRALSAGLPKIVADAQDVDGRDEALYGAYLAAVSFASAGSGLHHK
ICHVLGGTFNLPHAQTHATVLPYVLAFNAPYAPQAEQRAAAAFGSATALEGLQQLRAQVG
APQRLSDYGFTAAGIPEAVEIILEKVPANNPRTVTEENLTALLTTALNGDDPATLN

>RXN00178 TRANSLATE of: rxn00178.seq check: 4972 from: 1 to: 885
MTISAQQQAVEEDLVERVLASFDSCENPRLKLVMKSLTVHLHDFIRDVRLTEEEWNYAID
FLTKVGHITDDKRQEFVLLSDTLGASMQTIAVNNEAYEDATEATVFGPFFVDDAPLVQNG
DDIAFGAVGQPAWVEGTVKDTEGNPIPNARIEVWECDEDGLYDVQYADERSAGRAHLYSD
ENGEYHFWGLTPVPYPIPHDGPVGQMLQAVGRSPVRCAHLHFMVTAPEKRTLVTHIFVEG
DPQLEIGDSVFGVKDSLIKKFVEQPAGTATPDGRDVGDQTWARTRFDIVLAPGNV

>RXN00249 TRANSLATE of: rxn00249.seq check: 3465 from: 1 to: 957
TGVSTSQVVVLLVDARHGVVEQTRRHLSVSALLGVRTVILAVNKIDLVDYSEEVFRNIEK
EFVGLASALDVTDTHVVPISALKGDNVAEPSTHMDWYTGPTVLEILENVEVSHGRAHDLG
FRFPIQYVIREHATDYRGYAGTINAGSVSVGDTVYLPEGRTTQVTHIDSADGSLQTASVG
EAVVLRLAQEIDLIRGELIAGEDRPESVRSFNATVVGLADRTIKPGAAVKVRYGTELVRG
RVAAIERVLDIDGVNDNEAPETYGLNDIAHVRIDVAGELEVEDYAARGAIGSFLLIDQSS
GDTLAAGLVGHRLRNNWSI

>RXN00250 TRANSLATE of: rxn00250.seq check: 5525 from: 1 to: 747
MVFTLADSVSQVALGPSWLDPMELLSGSGPFGSFILPAMLAIVFIESGLLFPLLPGDSLL
FTGGLLANQADPFAPLWLVLILCPIAAILGDQVGYWIGHKFHPRLVNRPDGRIFKQEYLK
QTEDFFEKHGPVTIILCRFVPIVRTYAPLVAGMAGMRYRTFIIYNMIGGILWGSGVVALG
AALGQFDFVRNNIDLIFLLIVFISVVPGLVGMARKLADGHKQANTEPQENPAVQTAPVKT
QEAQEAPQN

>RXN00299 TRANSLATE of: rxn00299.seq check: 5963 from: 1 to: 978
MSIPLSLIDFATIFEGERPGDSFKRSVALAQKAEGLGFKRIWYAEHHNMESISSAAPAVL
ISHIGANTKTIRLGAGGVMLPNHSPYVIAEQFGTLAELYPDRIDLGLGRAPGTDMNTLRA
LRRDPQSAENFPSDVVELNSYLTGRSRLPGVNAIPGKGTNVPLYILGSSLFGAQLAAQLG
MPYSFASHFAPTHLEHAVQTYRDNYQPSEQHPEPYVIAAVNVTASDSTEQAHDDFYKVAR
ARVKNMALRGRQVTDEQLDELMDSPAARQIVDMLHYTAIGTGSEVKEYLDGFVKTAQADE
LMISLQSPNTEATTRNMEILADAWIN

>RXN00343 TRANSLATE of: rxn00343.seq check: 7722 from: 1 to: 1113
MKHQYDVIVVGSGAGGLSAAVSAAYGGKKVAVIEKASVLGGATTWSGGWAWTPGTSLARK
DGVVESKEEFQTYLQAVVGEYYQEDNISAFLDAAPEMVDFFEKNTDLQWTPGAKINDIYG
NLPGAGTGHRSVGPKPFNGRKVPKSVLPKLRHQLYETSFLGMGIMAGPDLTKFLSASQFD
PRGWVHAARRVIVHMWDMVVHKRNMQMVNGAALTARLATSADKLGVDLLVNHSAVSLNYK
NDRVTGVKVQTPQGLVDFEATAGVVLATGGFPNNVDLRKELFPRTPSGQEHWTLAPAETT
GDGLSMAREIGAGFVNDLKSPAAWCPVSLVPYFNGKVGTFPHIMDRAKPGSIGVVSTGKR
FVNEANGYYDY

>RXN00393 TRANSLATE of: rxn00393.seq check: 4530 from: 1 to: 894
MSHTEPQPNSVTLSDWIQGARPRTWANAFAPVIAGSGVAAFHDGFVWWKALLALVVAWAL
IIGVNYANDYSDGIRGTDEDRTGPLRLTGSGLAEPKKVKAAAFISFGIAGVAGTALSLLS
AWWLILIGILCVLGAWFYTGGKNPYGYRGLGEIAVFIFFGLVAVMGTQFTQTGSVSWAGL
AAAVGVGSMSAGVNLANNIRDIPTDSKTGKITLAVRLGDAGARKLFLALISTPFIMSICL
AFVAWPALIAIIVFPLALKAAGPIRNNATGKDLIPVIGSTGRAMALWAVLTGLALAFS

>RXN00397 TRANSLATE of: rxn00397.seq check: 3065 from: 1 to: 801
LSLTEGEIIPIQTKLGHWRDVRDSEDLPFQVIASRTNVTIMENTLEWTNSRLERGEEFTE
LDIYAHYLEELEDYALQFTFDVEPYFTNLHSSNRMLFPGPPVDFPINAETRCIQLDAGVA
VKKDGVVLGTSDMARSLPRTAAGQEAYEYFFKVVREGIIGQLRPGVICADVHEATLDYLS
PQLPRMIDIGMLGADTDFNTIYRKRNVGHLMGKQESFANELRPGYKHILHHGSYGAAEIP
WRYNGVAIGTEDLWYIGADKTYILSQR

RXN00398 TRANSLATE of: rxn00398.seq check: 1161 from: 1 to: 750
MAKLFDSHFHIIDPQHPLIENNGYLPEPFTVEDYTARVEGLEVAAGAIVSGSFQAFDQGY
LKDALAVLGPGYVGVTQIPADTSDQEILDLDKAGVKAVRLNLKRGGSAGLDDLETLARRV
HDLAGWHTELYVDARELDELESTLASLPAVSIDHLGLHRDGLPALLRLVENGIKVKATGF
GRVELDPTEVIQAIMAVDPTALMIGTDLPSTRTKRPFEDADLDLIAETVGEDHVDNVFWN
NAAAFYLGDQ

>RXN00434 TRANSLATE of: rxn00434.seq check: 6086 from: 1 to: 867
VLVKVKPAGVNRADLLQTQGNYPVPAGASEILGLECAGVIVNAGDTGQTVGQEVACLLTG
GGYAQYVAVPEGQLMPIPEGYSFVEAASIVEVACTVWSNIGMLAGLQKEDTFLIHGGAGG
IGTFAIQMGKALGVTVAVTAGSTEKLKTCKNLGADILINYKEEDFAEVLKNKADVILDII
GAKYLSQNVKAMAKDAHMVVIGMQGGVKGELNLGHLLAKRGTISATALRGRDEADKARIV
SSTVENIWPLLQSKEITPHIDHTLPLAEAAAALQKIQDGTITGKLVLAV

>RXN00470 TRANSLATE of: rxn00470.seq check: 9539 from: 1 to: 1269
MGESPEKVAFRVFPDGLVSQGHDMIEDMSNTPAPYTPQPAGQAVPLYPTFTRSRDGRVVA
GVASGLAKHLNVSVFWVRALLIFAALLSGAGLFAYALIWIFTRIEKKGSGEASTSKRWVS
WCLVLLAIGGAAASVMLSTGFAVGTLVPIGVVGVGLLMVWLAYDRGVESGPNLLIIATGG
VLMLVAIVLIVMNWNTQDGFVMALVAVVLTLVGVAALGVPLWVRMWDQLGEERAEKAAAA
ERADIASRLHDSVLQTLALIQKRADDPAEVARLARGQERELRQWLFDSQDKTPQTTGTVF
TALERACGEVEDIYALRIVPVTVGTDEALTEKTQAAVMAVREALVNVAKHAGVETADVYA
EIMLGELNIFVRDRGAGFDPDNIPDGHHGLAESVQGRVERAGGKVRIKSEIGEGTEVAIT
MDV

>RXN00499 TRANSLATE of: rxn00499.seq check: 1415 from: 1 to: 1281
VVGVVSTPARNLGSMTKTLGSLQLEEITLTLPLTEDVADERTIDVFARIATRVGGEDLPY
LVFLQGGPGNEAPRPSLNPLNPNWLGVALEEYRVVMLDQRGTGRSTPVGNDILEKPTAEV
VEYLSHLRADGIVRDAEALRKHLGVNQWNLLGQSFGGFTTLHYLSRHADSLDNVFITGGL
SAIDRPAEDVYANCYNRMRRNSEEFYRRFPQLRETFRGLVNRARAGEIVLPTGEVVSETR
LRSLGHLLGSNDGWFDLYNLLELDPTSNAFVHDLAGLLPFGNRNPIYYVLHESSYADGVV
TNWAAERVLPEDFREDPTLLTGEHVFQEWTDTVPSLKPWKDVALALAQQEWPKLYDAKAL
ENSQAKGAAAVYANDVFVPVDYSLETAQHLPGVQLFITSQHEHNGLRASSGAVLKHLFDL
AHGREVR

>RXN00513 TRANSLATE of: rxn00513.seq check: 4398 from: 1 to: 921
MAGLFSSAVAPTERRKALRAALAAPEIARMPGAFSPLAARAIQEAGFEGVYVSGAVVAAD
LALPDIGLTTLTEVAHRSRQIARVTDLPVLVDADTGFGEPMSAARTVSELEDAGVAGCHL
EDQVNPKRCGHLDGKEVVGTDIMVRRIAAAVNERRDEQFVICARTDAAGVEGIDSAIERA
KAYADAGADMIFTEALYSPADFEKFRAAVDIPLLANMTEFGKTELLPAQLLEDIGYNAVI
YPVTLLRIAMGQVEQALGDIANTGIQTDWVDRMQHRSRLYELLRYNEYNAFDQQVFTYSA
DSYKPIF

>RXN00531 TRANSLATE of: rxn00531.seq check: 3085 from: 1 to: 495
MANYTVPGINENDAKQLIDGLQERLTDYNDLHLILKHVHWNVTGPNFIAVHEMLDPQVDL
VRGYADEVAERIFTLGGAPVGTPEGHVADRTPLQYERNAGNVQAHLTDLNRVYTQVLTGV
RESMASAGPVDPVTEDIYISQAAELEKFQWFIRAHIVDVDGNIQE

>RXN00549 TRANSLATE of: rxn00549.seq check: 5535 from: 1 to: 1674
MVFMGAYIMVDVPEPEELVSPQVSQIYASDGETELARIVPPEGNRQMVTIDQVPDTVKNA
VVAAEDREFYTNPGFSITGYARAALGVITGDSSAGGGSTITQQYVKKAVVGDERSLIRKA
KELVYSAKMANEWSKDEVLEAYLNTVYFGRNAYGVQAAAHAFFDKPVEELTAAEGAVLAA
SIQLPSQLDPWTNPVEAETRWNYVMDGLVEIGAISAEERAVATYPETTDPASNSAYTEAT
GTNGLIKNQVMAELSELGITEDDVQTCGLQVTTTIDPKTQEGAVEAVQNQLDLLSENNRA
AVVSIDPSNGAVRAYYGGENATGWDFANAPLQTGSTFKIFGLAAALQQGIPLSQPYSSAP
VTVGDAQIGNVGGSGCGSCSIEQALLHSYNTSFIRLQQDLENGSQDTADMAHALGIAKSL
PTIPETLTENGETPYEGIILGQYESRPLDMASAMATIANEGVWHRPHFVSKVETVSGEVL
YEFEDGDGERRVSEKVALNLLKAMGPIAAYSNGNALADGQVSASKTGTTQLGDTGANKDA
WMLGAAPQLATAVWVGTA

>RXN00550 TRANSLATE of: rxn00550.seq check: 1281 from: 1 to: 321
MYGSNSPATIWKQTMDNALENSPLETWDIAPALGYGNPPVPEYVWTPSPNIATNDPEGAT
EEAPVEDPNAVIDTPAVDPTAPAEETGNGQVEILPGLTIPGDLLGIG

>RXN00621 TRANSLATE of: rxn00621.seq check: 1431 from: 1 to: 783
MSERLNAPQAPIHPITRTHHGIDFVDNYEWLRDKESQETLDYLEAENAFTKQETEQLATL
RDNIYEEIKSRVKETDMSIPVRAGKHWYYSRTEEGKSYGYSCRIPVTEGSDAWTPPVIPE
GEPAQGETIIMDANELAEGHEFFSMGASSVTTSGRYLAYSTDVTGEERFTLRIKDLETGE
LLPDTLTGIFYGATWVGEEYLFYQRVDDAWRPDTVWRHKVGTPVEEDVLVYHEPDERYST
WVGTTRSEKVHPFWLRLQDHL

>RXN00622 TRANSLATE of: rxn00622.seq check: 2214 from: 1 to: 1416
MNVIPPGWAPLVQKKFILFGCASKITSEVRVLPFDQPEGTPEVLIPRAEGVEYDVDHAVV
DGSDIWLVTHNAEGPNFSVGWAGVDKLNSLDALAPLVAHKDDVRIEGVDTYRDFIILGYR
SGAIGQVAIMKLIDGTFGDFQQLEFDEEIYTVASGGNPEWDAPVIRLSYGSFTTPAQLFN
YWIESGERTLLKQQEVLGGYKPSDYVASRLWVTAKDGAQIPVSLVHRTDLDVSKPNPTLL
YGYGSYESSIDPGFSIARLSLMDRGMIFAIAHVRGGGEMGRGWYDNGKTTTKKNTFTDFI
DVADALIEQKISAPEMLVAEGGSAGGMLMGAIANMAGDRFKAIEANVPFVDPLTSMLMPE
LPLTVIEWDEWGDPLHDKDVYEYMASYAPYENIEAKNYPNILAVTSLNDTRVLYVEPAKW
VAQLRATATGGEFLLKTEMVAGHGGVSGRYEKWRETAFEYGWLINQATGVTE

>RXN00639 TRANSLATE of: rxn00639.seq check: 1844 from: 1 to: 855
MTSAEQIVDPTAHDSGNKATDKFKANRVSSDTSKERANAIYVDLLAAIAQVAHKHEVTYE
EYAVLKQWMIDVGEYGEWPLWLDVFVEHEIEEINYNRHDYTGTKGSIEGPYYVENSPKLP
WDAEMPMRDKDRACTPLIFEGQVTDLDGNGLDGAEVELWHADEDGYYSQFAPGIPEWNLR
GTIVTDEEGRYKIKTLQPAPYQIPHDGPTGWFIESYGGHPWRPAHLHLRVSHPGYRTITT
QLYFEGGEWVENDVATAVKPELVLHPETGEDGNHVHYPFVLDKED

>RXN00641 TRANSLATE of: rxn00641.seq check: 1023 from: 1 to: 1491
MSTPVSNLASVQKTLDHALEDRPEEGIVRVNRNIFTDPEIFELEMRHIFEGIWMDMAHES
QIPNGGDYFTTYIGCQRIMITRSKEGTLNGLINACSHRGAMLCRGKSDNRTSLTCPFHGW
PFCNGGALLKVKGEKEGAYPENFRTDGSHDVRRVPKLESYRGFLFGSLNDDVVSLEEHLG
DTRTVIDMLVDQSPEGLEVLRGSSTYTYDGNWKLQTENGADGYHVSSTHWNYAATTSRRG
TGESANETKAMDAGTWGKQGGGYFSYPYGHMLLWMWWGNPEDRPLFERRDEFKKEFGEEK
GEFMVGASRNLCLYPNVYLMDQFSSQIRHIRPISVDQTEVTIYCIAPKGESAEARANRIR
QYEDFFNATGMATPDDLEEFRSCQKTYQASAFPWNDMTRGLGHQVQGPNEVAKGLGMNEV
LSSGARTEDEGLYPIQHGFWHELMQEAVNKQSIKEKELADDTASSLATVAAAKIREEAKA
AAKSDAGEPRRRRRTRG

>RXN00658 TRANSLATE of: rxn00658.seq check: 6023 from: 1 to: 693
VRHDEHYPAAANLIAFDKGWSTLIAPQLEDPEAEEFTAGFLTEYQDNLITAGMEHQALAS
GFPVGRRFKSDIALRRCDAVTTHIGHEHSADGHWRIYVFAGQATPQDSESALNKWAQWME
ESEDSPLNRFTPEAGDRNAVFDIKATYQQHYHSFDLFDAPEVFFPRVGPYKLQNLENVWT
ALDSQDIFESRGISRDGAIVVVRPDQYVAAVLPLEDTAALAEFFNGNLLEP

>RXN00663 TRANSLATE of: rxn00663.seq check: 3662 from: 1 to: 1374
VTTTYPDFLGNSSLQTDTEHWEMEGGAQEVSVTYVLDTSVLLSDPLSLTRFAEHDVVLPI
VVITELEAKRHHPDLGFFARQALRMLDELREIHGDLSKPLPIGDEGGHIHVELNHQNTGS
LPVGFRLGDNDTRILAVAKNLQEEGHNVVLVSKDLPMRIKASASGIAAQEYRAALARDRG
YTGMTHANITDDQLSELYDTGEVRIEELEKLPVNHGFTLKSNSGSALGRMNSDKIIELVP
GDQQVFGISGRSAEQRVAIDLLNDDAVGIVSIGGPAGTGKSALALCAGLEAVMERRIQRK
IIVFRPLFAVGGQELGYLPGDQEEKMGPWAQAVFDTLSSMVSQNIIDEALSRGLIEVLPL
THIRGRSLHDAFVIVDEAQSLERNVLLTMLSRIGQNSRVVLTHDVAQRDNLRVGRYDGIV
SVVEALKDHELFGHITLQRSERSRIAELVTQVLDAPSL

>RXN00665 TRANSLATE of: rxn00665.seq check: 1137 from: 1 to: 501
MSSSTLLLASGQVTALAADYTLSHTPSDGILVVLGFAMILTFMTLIMLGRLTPMVAMLLV
PTIFGLIAGAGLGLGDMALDAIKDMAPTAALLMFAIMFFGIMIDVGLFDPLIRVITRVLH
DDPAKVVIGTAVLAGVVSLDGDGSTTFIITTFRDAAHLPAPWHEPCG

>RXN00675 TRANSLATE of: rxn00675.seq check: 9322 from: 1 to: 792
MGFRSKKKVIAAKTAAELDAMQAAGEIVGKALQAVRAEAKAGMSTWDLDQIAEQVIRDAG
AVPTFLGYQGFPASVCASVNEVIVHGIPSKETILEEGDLVSIDCGATFDGWVGDSAWSFG
IGELDEDVQGLNLATEWVLMEGMKAMVPGNRLTDVSHALEVATRKAESKFGVALGIVDGY
GGHGIGRHMHEEPYLANEGKAGKGPVIQEGSVLAIEPMLTLGTEDSAVLEDDWTVVTLDG
SWASHWEHTVAATKGGPRILTPRY

>RXN00689 TRANSLATE of: rxn00689.seq check: 7633 from: 1 to: 1491
MNAATRRASLQLPYTHVDDFYINGSWVKAEGTQRNPVVDPAVGQEWGSVPEATASELDSA
VGAARTALKSWSALTGAERTGYLLKIATEIESRSEALALTNTRENGSPISETRGAASNAA
GIFRYFATLAPWLDGEDIRPFPAGSAESIVDKDPIGVCALIAPWNFPINLVVIKLAPALL
AGCTVIIKPASPTPLSIRFIIEAIEAAGVPAGVVNLLTGSGRFGDALVRHPGVDKVAFTG
STPVGKKIAAACGELLRPVTLELGGKSSAIILPDADMSVLSTRLIRSCMRNTGQTCYIST
RIIAPSSRYAEVVQTVASTIAAGRQGDPYDEETVFGPVASASQYSTVMSYIDSAREEGAR
VVAGGTRSISLSEGLESGEFIQPTVFADVTPDMRISREEIFGPVISILKYDDTNGVSEAI
ALANNTKFGLGGLVFGADEEQALEVARQVDSGSVGINFFGSNHSAPFGGRHESGMGVEYG
IEGLSAYLTYKSIHRTI

>RXN00778 TRANSLATE of: rxn00778.seq check: 6349 from: 1 to: 1125
VNLTLKRSIALVGAVTAGSFALVACSDSNESDSTSSSAASTGSSDAASIEGLSGVTGQLV
AEGASSQQSAMDYFGIRYSEAVSGASLAYTPSGSGSGRTNFAAGQVAFGGSDSAMKDDQA
AEAEARCNGNEAWHLPFVIGPVAVAYNLPGVDTLNLDTNIIAQIFKGEITKWNDEAIASQ
NEGTDLPDQDISVLYRSEESGTSDNFQKFLGASTDIWETEGQQFPTEVGSGAQGSNGVAS
EASNIEGAITYVEAGFANQSGLGVANIDFGSGPVELNAESVGVALGALDFLTEGHNMVVD
TDAMFAMNEAGAYPLILTTYEIVCSAGYDETTRDQVKDFLTVALDSQDDQLEALGYIPVT
GEHYDRLVAAVEAIQ

>RXN00787 TRANSLATE of: rxn00787.seq check: 6866 from: 1 to: 1902
VSQPLSKRLSIRKALASAFIVALAFSLSPVAKAQANETPTMIVLDNSGSMTAQDAGGQTR
IDAAKQASTQLINDISDRTDVGLTYYGGNTGETEADVEMGCQDVTILGGPSRGNADTLID
TINSLQPRGFTPIGKALTDTAAELPEGGNIVLVSDGIANCTPPDVCEVAQELAQSGINLV
INTIGLNVDPAAREELECIAGVGGGTYADASDAQSLTDALTRAASRQYNSYTSDVTKIDG
ASEQSAAVEIDEDTELFLTDLPQESRFWKIPVEPGETISVSANTVTDPTVLTMGQGGIKL
EAQLHTEEAPQYGLRGRCTRVSFDNFKPGLGVRGIQNASVASKEVGTNNCDTDAIYLEIS
RSGDYLNGQDIPTEITIERFGKVDESTIGNVTEEHSSVDLTEAAASEAHPVTPGQWFTSA
ADLDPAGEKVSSIIVPGETHFYALPVDYGQELRAAVETTFDQIDSSALGTHLYIQAFSPN
RAEIELTNRDTSYADDNGLKTFGFFTPVSAANLFEKSSQGISLRSPWQGGTQYLAVTYLP
SGQDEDVSATDQLPTLEYELVAEAFGDPVDPPVFASLTGATPSTSTPPSDVAEDEQISEA
TEEDSSSFPIVWIGLGVIGLGIIIGLIFALRRKN

>RXN00818 TRANSLATE of: rxn00818.seq check: 6962 from: 1 to: 840
VKHPDPAQKVEGTTATTPTKVAAFFDLDKTIIAMSSTYAYGREFMNSGLISPVEALQLSL
AQATYMFAGHTSEQMDNTRDQLTAMIRGWEVQQVRSIAEETMHSVVTPTIYAEARELIEH
HQELGHDVIIISASVKELVEPIARELGVHKTVTTVLEAHDGMYTGEVLFYCKGDAKAQSI
LDLAEANNYDLSLSFAYSDSFTDLPMLEAVGNPAAVNPDRALKKIALEQGWKILSFKNPE
PLFQMPSTRDVGIGTGVVAGIAAVTAGSIWWMKRARRGSA

>RXN00820 TRANSLATE of: rxn00820.seq check: 6937 from: 1 to: 363
VNTLADATDDQQWIHTDPERAKDGPFGGAIAHGFLTLSMIIPFWGELLDVTGVTTKVNYG

LDKVRFTSPVKVGSRIRMGAVVREISEVKGNGLHLVADGTIEIEGQERPAVVATFLTRFY
A

>RXN00866 TRANSLATE of: rxn00866.seq check: 4209 from: 1 to: 966
MNDSRNRGRKVTRKAGPPEAGQENHLDTPVFQAPDASSNQSAVKAETAGNDNRDAAQGAQ
GSQDSQGSQNAQGSQNRESGNNNRNRSNNNRRGGRGRRGSGNANEGANNNSGNQNRQGGN
RGNRGGGRRNVVKSMQGADLTQRLPEPPKAPANGLRIYALGGISEIGRNMTVFEYNNRLL
IVDCGVLFPSSGEPGVDLILPDFGPIEDHLHRVDALVVTHGHEDHIGAIPWLLKLRNDIP
ILASRFTLALIAAKCKEHRQRPKLIEVNEQSNEDRGPFNIRFWAVNHSIPDCLGLAIKTP
AGLVIHTGDIKLDQTPPDGRPT

>RXN00877 TRANSLATE of: rxn00877.seq check: 565 from: 1 to: 1665
MTVEHLLKPSTLPYQLPDFAAIKVADFPPAFELALAEHDAEITAIATNEDAPTWENTIEA
LERAGLSLNRVAAVFFNLQGTDSSPEMDEIAATIAPKLSAHSDAIFHNAALFARIEAVEA
PADEESQRLLSHTKRAFRRRGAALNADGKARLSTINQRLSALSEQFGRNLLQDTRDLAVN
FEESELAGFSEARISAAADYAAAVGTEGYVVPLELPTVQSEQAVLTESASRAKLYEASQK
RGASLNKDVLLETVRLRAERATLLGYDTHADYVIEEETADDVAAVRALLYDLAPAASANA
KAEYKLSAEEAEEHGQKVGAADWSFWEAKVRARDYALDETELRNYFPLNQVLRDGVFFAA
NRLYGITVEPRPDLRGYAEGVDVWEVLDSDGSGIGLILTDYYGRPSKRGGAWMSSFVDQS
ELLGTKPVVVNVMGITKPTTGEALLSLDEVTTIFHEFGHGLHGLLSKVRYPSFSGTSVPR
DYVEFPSQINENWAFDPAVVRNYARHVDTGDIIPDSLLEAVEACGISDRVVEHVSTCPHL
LSTCPVSPCPQRMPH

>RXN00905 TRANSLATE of: rxn00905.seq check: 8965 from: 1 to: 801
MTQFENAQVLKENIENQREQIFTQLKEIVSFNSVHSDPNLLEDYAGAKEWVKETLTNAGL
TVSEFAAEDGTTNFIGTRKGSEGAPKVLLYSHFDVVPSGPLDLWDTNPFELTERDAGHGT
RWYGRGAADCKGNLVMHLAALRAVEASGDTTLNLTYVVEGSEEMGGGALSALIKDKPELF
DADVILIADSGNASVGTPTLTTTLRGGGQVTVTVDTLEGAVHSGQNGGAAPDAVAALVRV
LDTLRDEHGRTVIDGCQHHRKLEGRAL

>RXN00948 TRANSLATE of: rxn00948.seq check: 5347 from: 1 to: 1119
MANVVLVDRMEPLVSKLFTPIQIRDITIPNRVWMSPMCTYSAATGSGLPTDFHQAHYAAR
AAGGVGLVMVEATGVNPVAPISPVDLGLWSHDQIEPFSRVTAAIRAGGAVPAVQLAHAGR
KASTDAPWNGGGYVGPETNGWETVGPSPLAFPGLPAPRELTVSEIQEVVQQFAGAAVRAD
QAGFDVVEIHAAHGYLLHNFLSPISNKRTDSYGGSLENRARIVLEVIDAIRAVWPEEKPV
FMRISTTDWVEENPQDDRESWTLSQSRQLALWASEHGVDLIDASSGGLDIVPIPHDRDYQ
TAKAADLHASTGVTVAAVGRIDDAQTAHNLVDSGDVNAVFLGRPLLKDPSWANQAALALG
AEPRYVHQYDYVL

>RXN00982 TRANSLATE of: rxn00982.seq check: 8201 from: 1 to: 1506
MPTAAAQENIRWEECPPQVDIASAQCGSIDVPMHYSDPSLGDISVGFVKVPAQGEKHGTI
FGNSGGPGGDAYSFFGSQSMNWPEAMYQNYDLVAVQPRGMVGSTPVNCDNIAPGYDFLSL
LTREGAFVKESCEIGTPGYTSSLTTDNTANDWERVRQALGDDKISIFGLSYGTYLGSVYA
TRYPQHTDKVVLDSAMAPSLAWNGIMASQEQGYKNSLNDFFTWVAENNDTYGLGTTPLAV
YQNWSNKIVAETGTNPTVAPPPAQVGDVPPAFAWAGQAGADMMTATNPTSVQLQGLATQL
LNPGSNQSLSPLLNVTRAYIPQPSTWPMLAGAISGQTPIPDVTDTGDDPYVIESINASVN
MQRMVMCNENTVAPDPVAMARMAWTSMVTGDVFDIYSVKFSSGQACSGITPTSGRQPTDG
SQLAVQPLLLQGTSDPQTPYWTHNELADAMNAHVVTVNGPGHGQSIGGTNQAINDIVVDY
LRTGHTDATWVEGNTPTPITAG

>RXN00983 TRANSLATE of: rxn00983.seq check: 4228 from: 1 to: 1476
VTAGETTTMNVTLTNPFDNAIFDRAVSLERPEGWQAEDVRVSIPSGESVTIPVQVTAPLV
ADNGELPVEVSILDGADRYTGRLNLTVQGGQEPAPTSVKVSIPNLKDTYVAGEKISINFA
VNNPFDVTVNSVPSLGEGENWMPANLRGFDPEQGTPNCRYKNLGANKSYDCTTTTYEVSD
LDVERGYVDIPTVWTFTNSAGETVWSKNVDVPRVELNGTQDAVTDAIVTVDPINPVHSNG

QSQTVEVQANVTSEGDLPAGSKVAFYLDSSPIDTAAVDAEGHASISIDVDNIASEQPERT
FEVRARLVVPEDAPRSIARDALARFTVLSEQVQQNSLVIMNHPDVFSDGQTKTIVIAAKA
TAHDGSPVAIGTLIAFRVNGIERDVVPTNAQGTAKLQLDLKPVNTEDEEYEVTVEAELDE
LTAQTTFKVLAGEEEEEPTSTEEQPSETEQPSEPEEESTGVAGSSNGGSFVALLALLAALG
GIVGAVLGLLKL

>RXN01014 TRANSLATE of: rxn01014.seq check: 9151 from: 1 to: 2601
LTSTNLTRQEASDRSRLLSVENYDIALDLNNGDEFFSSSTVVSFTVRKAGDTFIDLRAAS
VEEVRLDNVSIKDEALTLGKNGYDETFGIALKGLTPGAHTLRVTASIPYSRTGEGLHRMV
DPADNEVYLYTQFETADAKRMFACFDQPDLKATYDLNIKTPKGWKIISNSEQQVSTQHTD
YDTHISRVDYPLSTYLIAVCAGRYHEVCDVWKGTLTHHAETPADQPTELTVPLALYCRSS
LAKDLDAVRLFTETKQGFDWYHRNFGVAYPFGKYDQIFVPEFNAGAMENAGAVTIRDEYV
FASKATRYRYERRAETILHELAHMWFGVLVTMQWWDDLWLNESFATWSAAISQAEETEYN
TAWVTFANVEKSWAYQQDQLPSTHPVFSDGYDIETVDQNFDGITYAKGASVLKQLQAYVG
REEFLAGVRRHFANHAWGNASFDDLLGALEQSSGRDLSDWANQWLKTTGINTLGAKFTTD
NGKYTSFSVTQTGAAPGAGELRTHRIAVGLYKLVDGSLNRYARVELDCSGASTSVEEIVG
LEQADFVLVNDDDLTYALLDLDDDSRNFVIDNIDKFSDPMPRTLVWSAAWEMTRAGQMKA
RDFIALVARGAAAETEIAVLERILAQATSALKSYADPAWAEATGNDLLADAFLEGARSAE
PDSDTQLAFIQALAKATLNDAAADYFRDILAGNVEGLTVDPDLRWWALTALIARGDIEAV
EDAIAAELSRDNSSASFLASLRAGAAVNTEEVKAAAYKHVTAVDSGLSNLELRHKIEGLT
FTGSSELLQAYNEQYFEILDDVWANFSGEMAQQIVLGLFPSWNVSEEGLKRTDEFLDGEH
VAGIKRIVSESLDRTARALRNRAADAA

>RXN01046 TRANSLATE of: rxn01046.seq check: 5893 from: 1 to: 1779
MIPFPGQPQQQSAPNDETRFIDLNERHKDDEPALFRDDVIDQTLAILISKNKPNALLVGP
AGTGKSRIAEDIARRLANDDVSIPDQLVGHRILDVSIAELVAGAGVVGQLKKRILDLIKY
ATDPSNKVIIFIDEIHQIAGDQSSHSGSQAKVAQILKPYLARGDLRVIGATTTQEARDFD
HDPALKRRFSRVNVDEFDRDQTLTILHAARDGYLKHFNNAVTVSDDVLGYVYTYSQQFNP
GNTAQPDAALTLFDKALASLTMEKQRLINNHVIAPSLKFPVSERHIHNTARKLAFGSQVP
ASINTDDARDKLETLFGQDHIIEPVLTAIKREQLGIFPRTKPLSWVFAGSSGVGKTEMAR
ILSRAINGGDPIIINGPEYISPESITGLIGSSDGYIGSNSKRAKPLDPLISNPRQVIVLD
EFEKSHPHFQQLFMAALDTGTMAMANGTTLNFSQAIIIATTNAARDKIGRDSFGFDSDNS
GVLGSAQAATDPRAQERLKSLMSKDFLLNCSTVSRISLPSTALMQAPTVRFWTISTSVAV
TPCCLATPHYAAQIPADIDSDTLDQLVETTFISDFGARPAARTIEDHIASLLM

>RXN01120 TRANSLATE of: rxn01120.seq check: 6283 from: 1 to: 1278
MARMQESADLLKCSFCGKSQKQVKKLIAGGAVYICDECIELCNEIIEEELGQAQHDEQER
NELPKPSEISAFLDTYVIGQDPAKRILSVAVYNHYKRLRASETIGRRRNDEPETELVKSN
ILMLGPTGSGKTFLAQTLAKLLDVPFAIADATSLTEAGYVGEDVENILLKLLQAADFDVE
RAQRGIIYIDEVDKISRKSENPSITRDVSGEGVQQALLKILEGTVAAIPPQGGRKHPNQD
FIQLDTTNILFIVAGAFSGLEKVIADRNGKKGLGFGVEVSSKKEEANIVDIFKDVLPEDL
VKFGLIPEFIGRLPVVATVSNLDQKSLVKVLTEPRNSLVKQYRRLFEMDDAVLTFTDDAL
EEIANQALERKTGARGLRAIMEEILVPIMYDLPDRKDVGEVIINGAVARGEAEPEMLEAV
AEEKTA

>RXN01145 TRANSLATE of: rxn01145.seq check: 748 from: 1 to: 1014
MAIELLYDADADLSLIQGRKVAIVGYGSQGHAHSQNLRDSGVEVVIGLREGSKSAEKAKE
AGFEVKTTAEAAAWADVIMLLAPDTSQAEIFTNDIEPNLNAGDALLFGHGLNIHFDLIKP
ADDIIVGMVAPKGPGHLVRRQFVDGKGVPCLIAVDQDPTGTAQALTLSYAAAIGGARAGV
IPTTFEAETVTDLFGEQAVLCGGTEELVKVGFEVLTEAGYEPEMAYFEVLHELKLIVDLM
FEGGISNMNYSVSDTAEFGGYLSGPRVIDADTKSRMKDILTDIQDGTFTKRLIANVENGN
TELEGLRASYNNHPIEETGAKLRDLMSWVKVDARAETA

>RXN01152 TRANSLATE of: rxn01152.seq check: 1196 from: 1 to: 834
MPYSGPFQAGDRVQLTDAKRRHFTIILEPGTTYHTHRGQIAHDDIIGADEGTVVHSTMGS
DYLCFRHLMVDHVLSMPRGAAVIYPKDSAQILVEGDIFPGARVLEAGAGSGALSMALLRA

VGEKGNVISYEIREDHLEYAVSNVEEYFGERPATWDPRLGDLKEVTVEDLGGPVDRIILD
MLEPWEMLETCKDLLIPGGVFMTYVATVPQLMKVMEGIREQKCFTEPRAWESLVRDWKVE
GLATRPEHRMNAHTAFLVLTRRLADGVEPPRPQRKARR

>RXN01166 TRANSLATE of: rxn01166.seq check: 5407 from: 1 to: 1305
MGYTNLNDTRVLRAGSCDAWWRTMSPLVQQGSEAVFRRIMGLSRRPDRKPGFDDVPHFGA
AVRVPGLKHGTLVNAAPLKVLGARGEPNPASSYRFEYITGDSAGRAITATGAVLFSTRPW
TTGPRPAIAMAPSTQGVAQHCDPSHTCAIGLNAFYDKPFDAIIAYELPVILWFLAHGLDV
VFIDYPRDPATGVQYYCDSIAAAKSLLDAVLASRQLGLSPEAPLGLWGFSQGGGATGWAA
QLQDYAPDVRPKAAVVGAPPVDLFRVLDTVDGGLLTGVIAYAIAGLAVNSSEMFEEIMSV
LNERGVSDVLKNITSCAGGSLLASGYSSSRGWTHQGTPLADILDDLPLVVAEFGKQKLGR
VAPEIPVLLWGSKNDDVIPIDPIRELRDSWADKGTPLTWHESQAPRVPGRTGLNHFGPYF
RNLEKYSGWLIDHLV

>RXN01181 TRANSLATE of: rxn01181.seq check: 3409 from: 1 to: 957
SVLLARDLVNTPSSHLYPESYSVIASNEASKHGLQTTILDEKQLADQGFGGILAVGNGSS
RKPRLLRIDWKPRKAKKSIALVGKGITFDTGGISIKPGASMENMISDMGGSASVLATIIA
AARLNLSINVFAFLPMAENMPSGDAFRPGDVITHFGGITSEILNTDAEGRLILADAIAYA
SEDKPDYLIDAATLTGAQLVALGLRTSGVMGTDEFRDSVAKTGREVGEQAWAMPLPEELD
EQVKSPVADLRNVTNSRFAGMSAAGRYLQEFVGADIEWAHVDIAGPAYNTAGEFGYTPKR
ATGQPVRTFVQVLKDLSES

>RXN01226 TRANSLATE of: rxn01226.seq check: 8697 from: 1 to: 540
MGDVNNSPLLVVGLGNPGPKYVGTRHNIGFEVAEELVSRSFGSFSVHKRSNTDIAQLPGL
IVAKPRSFMNLSGTPIRALCDFFKISPANVIVVHDELELDFGSVKLRQGGGDHGHNGLKS
TSKSLGTKDYWKLSMGIGRPPGRMDPASFVLKPFGKQELADIPIMAADAADLVEKHLQQG

>RXN01267 TRANSLATE of: rxn01267.seq check: 8891 from: 1 to: 1314
MYAEINGGFIPEGTVRVSGAKNSATRLLAAALLTDEVVHLGNFPTKLVDVEHKIRFIEEL
GGKVHVDHDEQILVVDAKDLAAREMTTDELNIPIRTTYLLAAAQIGRGEIARVPFPGGCA
IGGGPAGGRGYDLHLMVWEQLGCKILEKDDHIEVTAPQGFIGGVIDFPISTVGGTENALL
CASIASGDTKIANAYITPEITDLIELLRRMGAEITVYGTSRIHVKGRAGLLQGAYMDVMP
DRIEALTWIVYGIISGGRITVEGVPFSSMEVPFIHLEKAGVDLFRNSSSVYITPECLPSG
SVQPFELACGTHPGVISDMQALFVLLGLKGAGTSRVYDYRYPERIAFVEELTNLVSGDKL
SAEAGKITIQGDATFRPGYANSTDLRGSMAVVLAALCADGKSTINNVHMALRGYNELDKK
LRLLGADLTIREGEVPSP

>RXN01277 TRANSLATE of: rxn01277.seq check: 992 from: 1 to: 2004
MTDYTFLEDIDTPEALAWAEKWSGESVEKLKSPAKDALEARLLAALDTDDRIAYVSRRGE
KLYNFWRDAQHPRGVWRTTTLESYESDQPEWDVLIDVDALAEDEGENWVWKGAVVRSPEF
DRALVKFSRGGADATVIREFDLATAAFVDDSPFELKEAKSDVTWVDLDTLLVGTDTGEGS
LTDSGYPARVLTWKRGTPLEQAELFFEGSRQDVATHAWRDSTPGFERTFVSRSLDFYNSE
TSLETEGGLVKLDVPTDCDVIVKKQWIFVSPRTDFAGIPAGGLGVLLLKEFLEGGRDFQP
VFTPTESTSLQGLATTKNFLVLTLLNNVSTEIVTVPLNDPTTEHEHIDLPEHVTAHVVAT
SPLDGDEIWVQAASFTEAPTLLRAELPGALEAVKKAPLQFENAGQETRQHWATSADGTKI
PYFITGAFEEEPQNTLVHAYGGFEVSLTPSHSPTRGIAWLEKGYYFVEANLRGGGEFGPE
WHSQATKLNRMKVWEDHRAVLADLVERGYATPEQIAIRGGSNGGLLTSGALTQYPEAFGA
AVVQVPLADMLRYHTWSAGASWMAEYGNPDDPEERAVIEQYSPVQAVVGVEKRIYPPALV
TTSTRDDRVHPAHARLFAQALLDAGQAVDYYENTEGGHAGAADNKQTAFVESLIYTWIEK
TLDQQGSI

>RXN01302 TRANSLATE of: rxn01302.seq check: 612 from: 1 to: 453
MTTTTSSGKSSEKINPLFKLGSFLRKGTVGSEGQQIFLQGGRQADVFYRNRWAFDKVVRS
THGVNCTGSCSWKVYVKDGVITWESQAVDYPTTGADMPDNEPRGCPRGASFSWYTYSPTR

IRYPYIGGVLVDMSAKPRNAWAIRCWRGATL

>RXN01308 TRANSLATE of: rxn01308.seq check: 3036 from: 1 to: 2403
VLAWRDIVETPEKRKAYVSQRGKGGLIRVQYEEAMEIAAAAHVYTIRQYGPDRIHGFTVI
PAMSQVSYGAGTRFLQMIGGVALSFYDWYADLPPASPQTFGDQTDVPESGDWYNSSYLMM
WGSNIPVTRTPDSHFMVEARYKGTKVVVVSPDFADSTKFADEWARIHPGTDGALAFAMGH
VILKEFHVDKKTPYFMDYMRKYTDSPFLVELDEHGDGTYTPGKFLTADRAADISPALAAT
PNATHRLLVLQKDGSVVDPGGTVADRWGEEGMGKWNLRLDGVDPVMTIADVQTDTETAEV
LFPRFDLPATATQEGPIGAGTISRGVPTITLNGRKYTTVFDVLLAHYGVNREELNLPGEW
PKDFQDPVMGTPAWQEELTGVPANQAIRLGREFAQNADDSKGRSQIIMGAGVNHYFHADS
IYRTFLALTSMCGTQGVNGGGWAHYVGQEKLRPMNGWAQYAFATDWQRPPRQMITTGFYY
LTTDQWRYDNTRANRLASPLANRGTVGDKMTADTLVESMKRGWMPSFPQFNRNPLILSQE
AEEKGVSVSDHIVQQLTDGDLQFACEDPDAPENWPRILLNWRTNLMGSSAKGTEFFLRHM
LGVDSDASAEENAPEDRPSSIVWRDEAPEGKLDLMLTTDFRNTSTTLVSDIVLPAATWYE
KHDLSTTDMHPFIHSFNAAINPPWETRTDWEVFHDLTKEFSSQAATWLGTQTDVITAPIA
HDSPDELNMPGGIVPDIDEVGLIPGKTMAKIIPVERDYSKVYEKWTHLGPLTAKAGTGTH
GTAFNVTKQTEELALINGTSI

>RXN01309 TRANSLATE of: rxn01309.seq check: 2947 from: 1 to: 801
IADHEGTHINWDMVKERSAEVITSPEWTGSKKDGRRYTAFSINIEYDKPWHTLSGRMHYY
LDHDWFIDYGEQLPIFRPPLDKIHINGEVGPGQSVTGTDGEPEVTVRYLTTHNKWSIHSQ
YYDNLHVLSISRGGQVIWMSNKDAEKLGIADNDWIEAYNRNGVVSARAIVSHRIPEGTVF
MNHAQERTAGTPLNEKSGRRGGTHNSLTRIMIKPVHVAGGYGHLTYGFNYIGQPEITAMR
SPEFVAAPRRCSTNEGHGSDRNDHELG

>RXN01386 TRANSLATE of: rxn01386.seq check: 2161 from: 1 to: 930
MWEGHNARALLPLDIRTIDDRPMQASETNLHLPSMRMASVFGTSQFVERSESFISENPTG
VVAIFFATEGEAVFFHRGGHVALRPGQAIVYDADRPFLRGFNNRFRELVLTIPKQRYLEI
VGSKGPELPAIFEFGATGTANEQALARLVQESLHRIESGEPKHIDSSGPLGKPWSDIEHE
AHGLIRNVLGDATSSEEGLISAAQRFIDINISESDLQASRIAAAVGISERQLSRIFSDSG
QTIGRYVLNTRLDFAKEALSTPERDKVSVSEIGKRFGFASPSHFSRTFRERFEMTPLQWR
KESQRQSFQE

>RXN01461 TRANSLATE of: rxn01461.seq check: 3776 from: 1 to: 612
MIDTGKNGEFRYEQSNIIDQNEAEFGITPSQTVGPYVHIGLTLEGAEHLVEPGSEGAVSF
TVSATDGNGDPIADAMFELWQADPEGIHNSDLDPNRTAPATADGFRGLGRAMANAQGEAT
FTTLVPGAFADEAPHFKVGVFARGMLERLYTRAYLPDADLSTDPVLAVVPADRRDLLVAQ
KTDDGFRFDITVQAEDNETPFFGL

>RXN01466 TRANSLATE of: rxn01466.seq check: 3249 from: 1 to: 960
MTPNGRRQLLLERGAAFSKNRTPGLKHVDRHTIVDSDGLSIHTYMVGHAENATATVVFIH
GFTLAAEVYYMQVDYLQTFYPNIKSVLIDARGHGATGQIRPELCTIEGTANDVLAAIHEH
APTGPLILVGHSLGGLTALNLVKRADHSLRKRIVGMVLVATSIESLSTQGLPQVLASPLA
DNIKNAVEAAPNDAQKFRQYATTFLAPTLATAVFQRDTNDEVIDFHAAMIHETPLDTFVG
FFDDLQEHDELDAAPALEGLKGYVLAGELDDVTPISQADRICEVWPGARLQIAEGAGHML
PLEAPGILNNAIGNILDGLG

>RXN01499 TRANSLATE of: rxn01499.seq check: 1314 from: 1 to: 3822
LWDVLESVASTYPEAAAIDDGQVLTYAELMEEVTALADSIHAQGIRRGDRIGIRMPSGTR
DLYIAILATLAAGAAYVPVDADDPEERAEMVFGEANINALFDATGFHMLRPTAGGDTRRP
RLDDTAWIIFTSGSTGKPKGVAVSHRSAAAFVDAEAQMFLVDHPSGPLGPEDRVLAGLSV
AFDASCEEMWLAWGHGACLVPAPRSLVRSGMDLGPWLIRRDISVVSTVPTLAGLWPAEAL
SQVRLLIVGGEACSQELVERLSTPDREVWNTYGPTEATVVACGTQLYAGQPVGIGLPLAG
WDLVVVDDAGEPVGIGEVGELVIGGVGLARYLDPEKDREKYAPLKSVGWTRAYRSGDHVR
LEEDGLYFVGRVDDQVKIGGRRIELGEVDANVAALSNVRSSAVVVQTTGADQKVLVAYVS

LEDAAAGFDHNVATARLTETMPAALVPRIHVMDDLPVTTSGKVDKKSLPWPLPGTVVEAN
DLSATEAWIAQEWVDILGTSVSSKDADFFSLGGTSLAAATLVGRVRAKVPTAAVRDLYDH
PRLEKFAERVEAIAADTGISLEAPNQVEERVVKPVSFGTRVMQTLIQIPIMTLQAAQWIA
WLLLGNNIMAALDFDWAVHVSWWLVIGMILVFATPIGRLPIGGWGARIITRGITPGSYPR
GGSTHLRIWSAERLADASGSRNISGATWVNYFARSLGVKMGKGVDLHSLPPITGLLTLGN
NVSIEQEVDLRGYWLDGDILRVGTIEVHDNARIGARSTLLPGTVVGTGAHLLPGSTVTGD
KTIKPGSRWAGSPAQKVGRAKHRFPTSHPPRRSRWVPVFGATSIVLSLLPLQALAIGAAI
TLWLATISPLPLIWGVLVFATVGALAAFFAYTVTIWVLVRLIQIGIKGGTAPVRSRLGWQ
VWAVQRLMDDARTYLFPLYASQLTPLWFRSLGAKIGKDVEISTAVMVPKLADIREGAFLA
DDTLIGGYELGNGWLLSGETRVGKRSFIGNSGIAGPERKLAKNSLVAVLSSTPKKAKANS
NWWGSPPERMRRVTVEVDEGEAKTYSPGFGVKFARGAVETARLLAPITSGVLAALSLLLM
QYLLTEFNMWITWLLGGLILMTVGVLAMGITVVMKWVCVGKHKPSEHPLFSRFVWLNELQ
DAFVESVAGPWFLVPNLGTGALNAGMSALGAHIGRGAWIESYWLPETDLCYIGKGATVGP
GVVVQTHLFQDRVMSLDTVTVADGATLADHSVALPASLIDASATIGPGSLVMRGDKVPAH
TRWQGNPIEPWSNS

>RXN01555 TRANSLATE of: rxn01555.seq check: 3558 from: 1 to: 960
VNKGVVLVAGGFSQNPELRMKYMPEPTPQFSRTNESATGDTMALAAKVGARLGDDNGENA
LWFPSSIGTRADGSTAVYPHIWDRGRLGVIAVNAAGERFVDESVSYHRFVRAMYESNKTT
PTVSAWLIVDSHTLAKYGLGMITMPHLPKLALQKYIDSGYLHAGSSLDELARSIGVDARG
LEQTVKRYNTFAKTGIDEDFHKGELLFGQAAGDPDNKPNPNVGPIKKGPFYAIAVVPTPL
ATAFGISINPNGQVVSEDGEPIIGLYSAGNDAQSVMASEYPGAGSQVGSGMTFGWIAAQH
AVGKAGKSGGAKAGYAASSK

>RXN01608 TRANSLATE of: rxn01608.seq check: 9638 from: 1 to: 1839
MALCMTVAFAGGSLTACTPRPDTADPIAEEFLQAWASQDFDTIADITDQADLATEMLSTS
FDGLQADSVELTLDSVDSRDTIATANFSVVWKLPRDREVSYDSSMTLTKMRNEWTVRWEP
SLVHPKLGANQHLELRAIEAQRANVISSDGAPVLAPGSIYRVLVDPSAGDADVVVKRVAD
YLNEAHATDENVNTLDVEDIMSNLGDSTYSLTTVDANLGARMEQDLAGIPGLTFNEEASM
VATDPGFAPDIVSRVARIVEDELEGSNGWRASIVTSNGAVIDDIAYDAPELAPSVRISLD
HNVQRAAEEAVDLRAEMKAMMVVMRPSTGEILAVAQTDEADKDGDVALMGQYPPGSTFKI
ITAAAGLAHEGLTPDSIVPCPGTMNIYGRIVTNYNSFSLGNTSLDDAFANSCNTTFADIF
HHLEPGQLKNVAKQFGLGIDYQIPGLDTMTGSVPEGDIVLDRTESGYGQGLDLASPFGMA
LVASTAATGSVPTPTLISGHETVASEEVLALDPEVLANVQRMMKSVVNDGTARGMRQTGG
QIYAKTGEAEINEGSHAWFTGYREDDIAFATLVVLGGGSEAAAAVTDQFFVKLDELRAGG
EVAVSEAEEQPVG

>RXN01619 TRANSLATE of: rxn01619.seq check: 4967 from: 1 to: 975
MRAITHNTFGDPADVLQITEKEIPTPGPGQVRIQVTLATIHNHDLWTVKGSYGFVPDLPA
AAGTEAVGIVDALGEGVEGLQVGQRVASGTSFGIWAEYALVDASGLIPVPEQLSDESAAQ
LVAMPFSAISLLDFLDMKPGEWLIQNSANGAVGRMLAQLAESRGIHVVGLVRRDAGVQEL
AAQNISGVVSTETPGWEKQVEDITGGASIAVALDSVGGSSAADLVKLLGEGGTLVSFGAM
GNPIMEIPSGPVIFKHITVKGFWGSKVSREMPAEKKTQLFGELIARILDGTLTLPVDSTF
DAADIVSAVRASSEPGRAGKVLIRF

>RXN01653 TRANSLATE of: rxn01653.seq check: 1458 from: 1 to: 1461
MATAENTTQENRKILFNAFDMNCVAHQSPGLWTHPKDKARDYNTLDYWVHLAKTLEKGLF
DGLFIADVLGTYDVYGSSNEAALSSGAQVPVNDPILLVSAMAYATKNLGFGITAGTAYEH
PYPFARRLATLDHLTNGRVGWNVVTGYLPSAAQNMGDTDQLPHDERYDKADEYLEVIYKL
LEGSWEDDAVQNNTETSVFTDSSKVHAINHHGKYFDVPGIAITEPSVQRTPVIYQAGASP
RGLKFAGENAEAVFINSSTVEAITKTVAKIRAAAVAAGRDPHAVKIFAMQTIITGETEAD
AQAKLEEYSRYIDPVGGLTLMSGWTGADLSQYDLDEPITNIESNAIQSTAATISNGTGEG
AWTVRKLGEATGIGGFGPVLVGSGANVAAELARIQDLSDVDGFNLAYAITPGTFEDVVDF
VVPELQKLSRYKTEYAPGSLRNKLLGKGDRLDDTHRGASYRLGARNSTATIDLSSISAQL
VSQGAHS

>RXN01716 TRANSLATE of: rxn01716.seq check: 2732 from: 1 to: 486
EVTPEGFKEITRENTIVRLGKGVDATGQLDPEAIERTRVALENYVELMETHGVEAVRMVA
TSATRDASNRDEFFSMTRQLLSKIRPGYQAEVISGEEEALLSFRGAIVDLPEDQGPFCVI
DLGGGSTEFIVGTYDGEILGSHSTQMGCVRLTERIMRSDPPD

>RXN01842 TRANSLATE of: rxn01842.seq check: 4367 from: 1 to: 918
MSKVYVSNEYGGPENQELITRNTPQPGPGELGVKVHAAGVNPLDWKVRSGVAGTPRELPA
PLGEEASGIVTAVGDGVEGFAVGDPVLGLVAPGVGGYAEDTLLVAESTVLKPEEISFTDA
AAIPVAGASAYAGTHQVELEPGQSLLINGAGGGVGLMAAQIGRVHKFQVVGVDHEDKREL
IESTGAIFVATGDAVAEQVRALLPDGVDVVFDLVGGEALRVVAPLAKNPAHVISAADAAT
VGELGGQVLRRTPEMVGQITGVVQYGLVDPKVDTTYPLEQAGKALAHVEQGHARGKIVLE
LITSQD

>RXN01849 TRANSLATE of: rxn01849.seq check: 9896 from: 1 to: 1101
MASQQIRYPFSAVVGQDELRLALILTAISPRIGGVVIRGEKGTAKTTTVRAFAGLLGDAP
LVNLPLGSTEDRVVGSLNMETVLTTGRAEYQPGLLAQADGGVLYVDEVNLLADHLVDALL
DAAASGRVSIERDGISHSSPANFVLVGTMNPEEGELRPQLLDRFGLAVDVAASTNPEVRV
EIIRRRLDFENAPEQFMAKWAEQDADTSNRILAAKDLLPGVELPDLILSQIAWLCARIEV
DGMRADLVITRTALAHAAWAGRTVVTEEDVEIAARLALPHRRRRNPFDAPEMEERKLQET
LQEARDFFKDNEDKGPAAKITDEETGAEAFTDTDNPTEEDGLQGTAQAKAQTTGKVGTAG
SGDPFRS

>RXN01868 TRANSLATE of: rxn01868.seq check: 1336 from: 1 to: 1926
MKDLYRFVNGLWLDTHIIPDDRAVDGTFHKLRDDAEEDVHEIVKEDTGRAGTLYASFMDT
DAINAAGVAPLDADLNRLSVANSSFFAAALGELDREGVGAPVGFWVEKDSSSNESVAYVI
QSGLGLPDEAYYREEAHAETLAAYKEHVERMLGYLDNSRLFGLSAASAAARIVALETEIA
AGHWDVVKTRDAVATYNPTELGALPPKVRTLLSSAGLPDQRLVSMMPSYLDHLNGLLVDD
RLPDWQLWATWHILRSRAGLLTEEISQANFDFYGTKLSGATEQKDRWKRAVGLAERMVGE
EIGQRFVERHFPASSKEHMLELVDYLVAAYRDRISNLEWMTPATRERALEKLGKFNAKIG
YPDKWRSYEGLEFGSDLVDNSRKGSAFLHDYELGKIGKPADRDEWVTTPQTVNAFYNPVV
NDITFPAAILRAPFFDPEAEAAENFGAIGAVIGHEIGHGFDDQGSQYDGDGNLNSWWTDE
DRSAFEQLTSRLVTQFSGLVPAVLTSEGIDTDGVNGEFTLGENIGDLGGLGIAVVAYEKY
LADRGQTFETSPVQKFEAEGAEEGLAEQEFNGLQRLFLSWARVWRTKIRPQMAVQYLAID
PHSPAEFRCNVIAGNVAEFYEAFDVPEDAPVYIKPEERLAIW

>RXN01885 TRANSLATE of: rxn01885.seq check: 4597 from: 1 to: 801
MTTKPIIPESTHSAERAGGHWILARLGKKVLRPGGRETTQFLLENLSLTGATVVEFAPGL
GVTARDILGKGPARYIGVDSDADACANVRAILPAGPHEVRNTNATDTGLESDSFDVVIGE
AMLTMQTDKHKLELMREAARILKPGGLYGIHELSLVPDNVSTAVKEDIAKALARSIKVNA
RPITVPEWAALAREAGFDVINIRQADMALLSLKRNLKDEGLKGVFTIVRNVISQPDLRKR
VLGMRKTFTEHKDHLGAVGIILQKRAQ

>RXN01923 TRANSLATE of: rxn01923.seq check: 3715 from: 1 to: 750
MSALIKGSGPHHVVVLNGWFGHAAGWGAFADYLDLGNYTWHFWDYRGYGNRKDDAGEFTL
EEISADIVAYIDSIEAEKVSILGHSMGGVFMQKVLADSATPIASLVGISAVAAAGTPFDE
DSRKLFTSAGHNPDSRRAIIDFTSGSRQPAAWLDDLTDSAVQNSTPEAVEKYFFAWADCN
FAADLGTQDLPVDILTGDLDPAVTKTAVESAFGPIYQNLTVEELHDVGHYAIFEHPLGLA
ARVLRFLDAV

>RXN01963 TRANSLATE of: rxn01963.seq check: 1780 from: 1 to: 684
MKNRKKIMSTLTTVCAVLGIVAAHPFHASAVIGGSVPSTDSVANAVAKIGPGALNCSGVM
ISPSWALTARHCVDDINILGDIDTITPITPGIHRNEGNYMGEVYRAPSGDLALININGVH
KGTIAQLPTQEYPLGTAAQSVGFGGGGVNIRTAESVNMILTDIYSVRSGKFHHGVGRSHY
LLFDYDSAETGRIHKGDSGGPIFIGDEVVGIMSHGTINKNDGSFDDES

>RXN01974 TRANSLATE of: rxn01974.seq check: 7604 from: 1 to: 1785
MTQVVAGTLVGESINREIDEDKYPYLSSYAAPVAVPVREIIGREEEVNKIMAALMRPEIS
NVMLVGPAGSGKTTLVQQALVKDPERNYIEVDVAKMVADLSTPAQMAARIKGVFEDAIAY
RKHEGHELVLFVDEFHQIVQLSNAAVEAIKPILAMSGVLGVRVIAATTLEEFHEHIRPNQ
ALTERLQEIRLTPTDQKTTVAILRGMADRYGVSDQFYDDHVFEQIYSTTERFMPSSVQPR
KSIRVLDAMVGWHRLSGKPMDMDLLGDVLHDAIGVDIAFKVDGTSIKDKLDEKVMAQSLA
TTVVARRLQLVVADLHDKSRPLSNFLFTGPTGVGKTELVKQLARVLFGDDTGRLIRFDMS
EFALESSLDLFRSELTRRVADQGNAIVLLDEVEKADRAIARLLLQVLDDGRLSDDYNREV
SFLNTYIVMTTNAGSEIFETISNYATDDTGDGRAIKDFVKNIHTSIKNKGFPPELLGRVD
EIVPFQPLSETTQDRIISKKLQDVATEVYERHGVKLHCSQKVMEFLLVDQVEESAESGGA
RGAVRSLQREVVTEVATFINTYPEVRDIYVDVDGQMRNKTNRVSTARVVIKRVEG

>RXN01993 TRANSLATE of: rxn01993.seq check: 8105 from: 1 to: 1128
MTLSERKLTTTAKILPHPLNAWYVAAWDYEVTSKKPMARTIANKPLALYRTKDGRAVALA
DACWHRLAPLSKGKLVGTDGIQCPYHGLEYNSAGRCMKMPAQETLNPSAAVNSYPVVEAH
RFVWVWLGDPTLADPTQVPDMHQMSHPEWAGDGRTISADCNYQLVLDNLMDLTHEEFVHS
SSIGQDELSESEFVVTHTEDSVTVTRWMHDIDAPPFWQKNMNDKFPGFEGKVDRWQIIHY
YYPSTICIDVGVAKAGTGAQEGDRSQGVNGYVMNTITPDSDRSSHYFWAFMRNYRLESQT
ITTQLRDGVSGVFKEDEDMLTAQQDAIDANTDYEFYSLNIDAGGMWVRRILEEALSKEGR
LDIPTTFPRATPKPEA

>RXN01997 TRANSLATE of: rxn01997.seq check: 5274 from: 1 to: 486
MTINEKIASAFNNQVTAELEASMVYLQLSYVLDDLGLTGMRDWMKAQSKEELEHAQKFAQ
HLLDRDYTPQIGDIAPPKLDVTSAIEAFEASLAHEQKISGLIRELAAIQDAEKDYDSRAL
IDWFLNEQIEEEATVGEIIDRLRIAGDSGSGILRIDGELGSR

>RXN02001 TRANSLATE of: rxn02001.seq check: 4280 from: 1 to: 1158
MPVINSIASFSDEMTRWRRHLHQNPEISFDCVETAAFVAEQLRSFGVDEIHTGIAKTGII
ALIHGREAGPVVGLRADMDALPLTEITGVDYASTTPGKMHACGHDGHTTMLLGAAKYLAE
TRNFAGTVALIFQPAEENGGGAGVMVDEGVLDRFAIAEVYALHNQPGLPLGHFMTTAGPI
MAAVDTFDINITGRGGHGAKPHQTRDPIVAAVGIVQAFQTIVSRNHNPVEDLVVSVTQIH
TGSADNIIPETAYINGTVRTFNKDVQAMVITRMEEIVAGQAAAYGVEATLTYNRNYPATI
NDAAKAAIAAEVAGEVGLGVNPNGSRGMGAEDFSYFLEKRPGAYLFVGNGDSAGLHNPAY
NFNDEAAPYGASFLARMAERPLPLKG

>RXN02053 TRANSLATE of: rxn02053.seq check: 1600 from: 1 to: 579
MSLSVVEAITNRRATRKYTDEAPTPELIDKIVDLALEAPSAFNAQQREIVVITDPAQKQK
LYEASHQKQFLTAPVTFIAVARVENEPEDLEEILGTERAERVAGFINGRSIQQAREATLR
DASLAAAFLILAAQAEGLSTSPTTGWDEEKVKEAIGLGGREDRAIALVIATGFPNEQPEH
PGRLQNRRIDNSY

>RXN02146 TRANSLATE of: rxn02146.seq check: 3577 from: 1 to: 627
VGKHRRNNSNATRKAVAASAVALGATAAIASPAQAAEVVVPGTGISVDIAGIETTPGLNN
VPGIDQWIPSLSSQAAPTAYAAVIDAPAAQAAPAASTGQAIVDAARTKIGSPYGWGATGP
NAFDCSGLTSWAYSQVGKSIPRTSQAQAAQGTPVAYSDLQAGDIVAFYSGATHVGIYSGH
GTVIHALNSSTPLSEHSLDYMPFHSAVRF

>RXN02274 TRANSLATE of: rxn02274.seq check: 3347 from: 1 to: 1710
MSFEISRKQYTDLYGPTVGDSVRLADTELFLCVEKDYAAIGEEVAFGGGKVIRDGMGQNG
TLVRDVDIPDTVITNVIVLDYTGVYKADVALRDGKIFRIGKAGNPNVMENVDIVIGVATD
IIAGEGKILTAGGIDTHVHFLGTDQVNTALASGITTMIGGGTGPSQASMATTVTPGQWNT
YNMLSAFEGMPMNFGILGKGHGSSKSPLAEQVRAGAIGLKIHEDWGATPSSINTALEVAD
DMDIQVALHSDTLNEAGFVEDTIEAIAGRVIHTFHTEGAGGGHAPDLIRVAALPNVLPAS
TNPTLPYTRNTVEEHLDMVMVAHHLNPDIPEDVAFADSRIRAETIAAEDVLHDMGIFSIT

SSDSQAMGRVGETITRTWQVADHMKRTRGSLTGDAPYNDNNRLRRFIAKYTINPAIAHGV
DYVVRSVEEGKFADLVLWDPKFFGVKPDLVIKGGLMVNSLMGDSNGSIPTPQPRTLRNTW
GAFGQAVSRSSITFLSQDAIDANVPDLLNLRKQIRGVRGVRNLTKRDMKLNAEMPDIRVD
PETYQVFVNGELITSKPAETVPMARRYFLF

>RXN02334 TRANSLATE of: rxn02334.seq check: 4801 from: 1 to: 723
VKDLNDPLTRDFIDGEAFAELMNRKGIARDDTVVVYGDKSNWWAAFTLWVFELFGHSDVR
LLNGGRDAWMAEERDTSYVVPEYPSANYPVVERVDENQRAFVAEVLGSLTQSGGMTLVDV
RTPSEFSGLDEHGNPTSNTGVLRGGHIPGAINLDWSDAVLPNGNFRTRAELDKLYADLNP
ADDTVVYCQVGDRAAHTWFVLKYLLGFNNVRNYDGSWAEWGNMVRMPIETGENTKNNVSV
S

>RXN02478 TRANSLATE of: rxn02478.seq check: 2398 from: 1 to: 1215
MRTSLIARGLYRIPALVWDQGLLTLFDARLSVDDLPAPIDVVSARSSDGITWTTPEPAIV
ETEHRGVGDVCLVTGDLCFHGLSNLAGFFEDPTDLEPRLARRDVSGWTSISMAHYFADVD
AAFASSGTGLVLADGRWIQSFVVRRGREISLRILRSDGHITDIAGGNESAMTQLPSGRIV
LHSRGVGHRLSSVSDDFGETFTPLEPVPELIDPGCNGHVFYWKAAGMLAATHLADPDLRR
HLVVDLSSDEGATWAHRITIEREEAAYSTAAEMPNGDVAVVWEAEGTRAIKCTVISVNDI
SLRIDEPISDAISLRHVVINDDHDGIEVALPDASQWGEGVFKIVSNPDASTQKIRTRGKP
ARQTLEIGDELVFDIRKGGEVAYGVTVPYDGRSLGEVKQDFGVGL

>RXN02508 TRANSLATE of: rxn02508.seq check: 3436 from: 1 to: 1854
MRTSIATVCLSGTLAEKLRAAADAGFDGVEIFEQDLVVSPHSAEQIRQRAQDLGLTLDLF
QPFRDFEGVEEEQFLKNLHRLEEKFKLMNRLGIEMILLCSNVGTATINDDDLFVEQLHRA
ADLAEKYNVKIAYEALAWGKFVNDFEHAHALVEKVNHKALGTCLDTFHILSRGWETDEVE
NIPAEKIFFVQLADAPKLSMDILSWSRHHRVFPGEGDFDLVKFMVHLAKTGYDGPISLEI
FNDSFRKAEVGRTAIDGLRSLRWLEDQTWHALNAEDRPSALELRALPEVAEPEGVDFIEI
ATGRLGETIRVLHQLGFRLGGHHCSKQDYQVWTQGDVRIVVCDRGVTGAPTTISAMGFDT
PDPEAAHARAELLRAQTIDRPHIEGEVDLKGVYAPDGVELFFAGPSPDGMPEWLPEFGVE
KQEAGLIEAIDHVNFAQPWQHFDEAVLFYTALMALETVREDEFPSPIGLVRNQVMRSPND
AVRLLLSVAPEDGEQGDFLNAAYPEHIALATADIVAVAERARKRGLDFLPVPENYYDDVQ
ARFDLPQEFLDTLKENHLLYDRDENGEFLHFYTRTLGTLFFEVVERRGGFAGWGETNAPV
RLAAQYREVRDLERGIPN

>RXN02513 TRANSLATE of: rxn02513.seq check: 7035 from: 1 to: 732
MLPIWMGLPFKKAGALSRRKAVFSALGAAALMGAALPTIPTAQAQTPTGYGFDATASISE
EPEFSTQQLADGGTLGFDCYRIPSLGVAPNGNVLASWDGRPNNCSDAPQPNSIVGKVSTD
NGATWGEQHDISAGITAEPKTGYSDPSIVVDWERGDVFNFHVKSFDAGYFTSQPGTDPDD
RNVAHVAYAKSSDNGSTWVADTVITDQVVAHDTWDSRFATSGNGIQLQYGAYKGRLVQPS
VTRM

>RXN02530 TRANSLATE of: rxn02530.seq check: 7593 from: 1 to: 657
MSTNYEAIIIGAGQAGLAAAHELSRRGFTPGKDFLVLDSNDGPGGAWRHRWDSLTLGKAH
GIADLPGLPMNRPDPKTPASTLVAGYYGAYENEFSFAVVRPVKVSRVEPTSEDPSSPLRV
SSDDGREWITRMVLNATGTWTNPYVPYIPGIDKFQGKQLHTVNYRKAEDFKGKKVLVVGG
GLSAVQFLLELEGLAETTWATRRPRTYAARVRRRLGHCG

>RXN02565 TRANSLATE of: rxn02565.seq check: 9394 from: 1 to: 1266
VNDLTPDSGQEIRNAESLERFFEGTPNVKITKLEPHPGRTSIIVTVPGSDPDAEPLTLLG
HTDVVPVDLPKWTKDPFGAEISDGQIWGRGSVDMLFITATQAAVTRQVAREGGLRGTLTF
VGVADEEARGGLGAKWLSEEHQNLFSWKNCLSESGGSHLPVHDGSDAVVINVGEKGAAQR
RIHVNGDAGHGSIPFDRDSAIVKIGEVARRIAAADLKVAKDDIWQGFVQAHRFDPETEQA
LLSGTSPEAYAEFGGLSRFAHAVSHLTIAQTVVRAGQAINVLPSHAYLELDIRTLPGQTN
DYVDDTLRAALGDLADEVEIEHLISEEATVSPTDSRLYNTLEKVLGDFFPDAPVVPIISS
GGSDLRFGRRLGGVGYGFAVHARERTLAEAMGQLHSHDEALYLEDLELTVRGYDSVVREF

LG

>RXN02589 TRANSLATE of: rxn02589.seq check: 3006 from: 1 to: 765
MSISDNSRDQLGELPAGRPLQSDFDNDLDYPRLGSVTFRRGTLTENQQTMWDEKWPELGR
VLEDELIDVDAWFGREGAKTIVEIGSGTGTSTAAMAPLEADTNIVAVELYKPGLAKLMGS
VVRGEIDNVRMVRGDGIEVLNRMFADGSLDGIRVYFPDPWPKARHNKRRIIQSGPLNLFA
KKLKPGGVLHVATDHADYAEWINELVEVEPLLEYKGWPWEECPQLTDRQVITKFEGKGLE
KDHVINEYLWQKVQN

>RXN02704 TRANSLATE of: rxn02704.seq check: 1921 from: 1 to: 1689
MTTGASKKPARPNTGAKTRTGLGIRERISGAWNDLLARPLTDYIMILCIVVILSCLGVVM
VYSSSMTWSLREGGSVWGTAVRQGIMIVLGFFAMWVALMTRPQTIRNLSNLILIVSIVLL
LAVQIPGIGTGKEEVGSQSWIALGPIQFQPSEIAKVAIAVWGAHYLAGKGPVQHWFNNHL
MRFGGVGAFMAFLIFMEGDAGMAMSFVLVVLFMLFFAGIAMGWIAIAGVLIIAALAVLAL
GGGFRSSRFEVYFDALFGNFHDVRGIAFQSYQGFLSLADGSGLGVGLGQSRAKWFYLPEA
KNDFIFAIIGEELGLWGGALVIALFAGLLYFGLRTAKKSHDPFLGLMAATLTASVVSQAF
INIGYVVGLLPVTGIQLPMISAGGTSAIITLASMGLLISCARHEPETVSAMASYGRPAID
RLLGLREPSSTLTTSNASLRSNKTKAAKQKPSPQKESRDRFGEPVTARRAQAPRSGRAGV
QSEAPRRSTGSVKGRSSGQDNGRSNEGTARSQSTTGGRAADRSVDRSRQSRPTERRSESR
AMIGVTTATADKCEIRRTTNKDG

>RXN02707 TRANSLATE of: rxn02707.seq check: 464 from: 1 to: 1530
MTLGEIADIVGGRLTGGAQEDTLVSSSVEFDSRSLTPGGLFLALPGARVDGHDFAATAIE
KGAVAVLAAREVDVPAIVVPPVKIQESNADIYAHDPDGHGAAVVEALSRLARHVVDICVA
GHQLNVVAITGSAGKTSTKDFIATVLDQDGPTVAPPGSFNNELGLPHTALRCTTDTKYLV
AEMSARGIGHIKHLTEIAPPRIAAVLNVGHAHLGEFGSRENIAQAKGEIIEALPSKKTSS
VPVLNTDPFVARMAPRTKARVVWFTTDAGQAKKSDYWATSISLDAVARASFTLNTKDGSW
PVTLQVFGEHQVANALAAAAIAMEAGVAPELVVAGLEAHSAASAHRMDVKTRADGVTIIN
DSYNANPDSMRAGIAALAYTASGRSEATSWAVLGQMGELGDDASEAHAELGAELAKYNVQ
ELVAVGENPNCAALAESAASLGVSTHVVSDVDAALELLAGHIKRDDVVLVKASNADRLWR
VAEALHGMVPGLKNTGGSVNDDSRRNVEGQ

>RXN02723 TRANSLATE of: rxn02723.seq check: 9251 from: 1 to: 666
VNKKVIAIVVGVVVVLVAILGVVAWFVPILKVGNIEVTGATRTYPDQVLEVSGIVEGKNL
FRVDATAAGQNIVELPWVKSVTVNRALPSTITVELTEREPAVFIKRADGDHVIDTEGKEI
IIGTPPVGTVEVSGADEGNSEVLPAVIAVINAIKAQDAQMTESIQVVEAPDQFDILLKMN
DGREIYWGSSENNHDKAVAMSTVLKREGQRWNISSPSMVTVR

>RXN02813 TRANSLATE of: rxn02813.seq check: 4724 from: 1 to: 999
VEAALAVAAAPEHAAMAKATIDSYQLDVEELSRRAAEGGNPLIPLVTDLKAINPAGIHIG
ATSQDIIDSALMLCMKEGVGEVVDKLKKLARDLAELTAEHKATPIMGRTLGQIATPTTFG
ALTGGWLVAVDNAARALEALEFPVSYGGASGNMTAVHPRGFEIQAKLAEELGLFDPQWVW
HSDRTPITAIASALATAAGVVRKIAGDVVFYSQTEVGELREKSPGGSSAMPHKANPAAAI
ACDGYARRAPGLLATLFDALDCRLQRGTGSWHAEWATLRELAAVTHSAVSRAATSIDGIT
VNVDVMASRVNGPTGHAEDLAERALEIYGKGRS

>RXN02820 TRANSLATE of: rxn02820.seq check: 6804 from: 1 to: 1311
MKVTQSTFLKSVAAFTVAALTLTISSCSSGEDTSASSTDTENSSTQAAASPPLAPCELPA
DASAEEEVEGTHTGEDISVAPEIGTGYREGMTPVQTQGYAVATANPIASEAACAVLREGG
TAADALVTAQFVLGLTEPQSSGLGGGGYILYYDAEANAVTAIDGRETAPVAADENYLIHV
SAEDQTAPVPDARRSGRSIGVPGIVAALGQLHDSFGKTSWQDVLTTPQQLATDGFSISPR
MSASIANSAEDLSHDPEAAAYFLDENGDAKAPGTLLQNPDYAETIRLISEGGPDAFYTGE
IAADIVERATREVDGFTPSLMSTADLAAYTPETREALCAPYRDKIVCGMPPSSSGGVTVM
ETLGILNNFDLAQYPPTEVGLDGGLPNAEAVHLISEAERLAYADRDAYIGDPAFVEVPAG
GVQQWINHVHTGEHSKL

>RXN02839 TRANSLATE of: rxn02839.seq check: 5996 from: 1 to: 447
CVVNDYADRKFDGHVKRTANRPLPSGAVTEKEARALFVVLVLISFLLVLTLNTMTILLSI
AALALAWVYPFMKRYTHLPQVVLGAAFGWSIPMAFAAVSESVPLSCWLMFLANILWAVAY
DTQYAMVDRDDDVKIGIKSTAILLANTIN

>RXN02908 TRANSLATE of: rxn02908.seq check: 6002 from: 1 to: 261
LKLHPEVLERAIADIKGVTAACVVGIPDPRLGQAIVAAYSGSISPSEVIEGLDDLPRWQL
PKRLKHLESLPSIGPGKADRRAIAKLF

>RXN02913 TRANSLATE of: rxn02913.seq check: 5023 from: 1 to: 486
MIPGEYILSSESLTGNVGREAKTIEIINTGDRPVQIGSHFHFAEVNPSISFDRSEGYGFR
LDIPSGTAVRLEPGDARTVNLVAIGGDRIVAGFRDLVDGPLEDLKVNVWEGREDGWRRSS
AAGDAPQELPQVEAAERGRKLDDATDVDTNVGTEEGFEEGRN

>RXN02937 TRANSLATE of: rxn02937.seq check: 1915 from: 1 to: 402
VISNGEGPVVALRGDIDALPMAERSGKEYAATGVTQVDNTTGQETPVAHTCGHDVHISSL
LGAVQAFNSHRELWNGTLMAVFQPAEETAAGARMMADQDNAPGNHSPAFAPDMQPTLDRG
VEALVVAASAWLVK

>RXN02944 TRANSLATE of: rxn02944.seq check: 4495 from: 1 to: 678
VNAQNLIDPEHSMGQATAGVSQNPVMAALPESGTSHISIIDSYGNAASLTTSVEAAFGSF
HFTRGFILNNQLTDFSAEPLDEDGEPVANRVESAKRPRSSMSPMLVFNASGDGEIADLNM
VLGSPGGSLIIQYVVKTLVNIIDWDMDPQQAVSAPNFGAMNQPKTGLGSEHPLIANDSAE
LVSELESKGHEVNVGEQSSGLSALVKNGDTIVGGADPRREGVVLGG

>RXN02952 TRANSLATE of: rxn02952.seq check: 9893 from: 1 to: 516
MSSPALDAAKQRLAESDGLIAVTPVFTASYSGIFKMFFDVLDPKTIVGLPTIIAASAGTA
RHSLVLDHAIRPLFTYLRAVVVPTGVFAATEDFGTEAGADIERRVNRAAGELATLMLQDY
SSVQGLGGATANQDADLSFRRTTGVTPGENFSSFADLSQRTRRKRLNSRISV

>RXN02972 TRANSLATE of: rxn02972.seq check: 3943 from: 1 to: 411
VEIARDYVAERIQEVKAIVPISKAKTFVGCAGTFTTISAWVQGLESYDRDAIHLSALNFD
ALRVVTDEIISESSSQRASNPVVDPGRADVIGGGSVVVQAAIDLASKEAGVDYIIISEKD
ILDGLILGLVEADSLKK

>RXN02973 TRANSLATE of: rxn02973.seq check: 9389 from: 1 to: 654
VSDAGKKDSSKVEIGLTGRPLRELPEPSPLEKHGPATIIAMANQKGGVGKTTSTINLGAC
LAEAGRKVLLVDLDPQGALTAGLGIHYDDVDITVYDLMVDNNSTIDQAIHHTGLPDLDVV
PANIDLSAAEIQLVNEVGREQTLARALRPVMKDYDFIILDCQPSLGLLTVNALACAHGVI
IPMECENLSLRGLALLTDTVEKVADRLNFDLEILGILV

>RXN02974 TRANSLATE of: rxn02974.seq check: 3965 from: 1 to: 195
MQDLYSDPGELKPGAQGGFSALIDGDTLVISGGDAGATPVAALRTALDVAWAATEQSPRY
ALIQR

>RXN03000 TRANSLATE of: rxn03000.seq check: 5213 from: 1 to: 567
MSLPHSDELRGQKIIISGGGIGGAAGALALALRGADVTLYERAAEFKEVGAGLQIGPHGW
RMLESWGLLDQIVVAGYLPEDMQFRDAVNRETILTMRFDEEFQQHYGGRYLVIHRSDLLN
ILVTNAEAAGAKLHNGVLVTDSRTVDGGIEVDIESSINKGEDNKTLLVDAFLAFDGIHSV
MRKKLVDDA

>RXN03026 TRANSLATE of: rxn03026.seq check: 3330 from: 1 to: 267
MPGKILLLNGPNLNMLGKREPDIYGHDTLEDVVALATAEAAKHGLEVEALQSNHQGELID

ALHNARGTHIGCVINPGGLTTLRWRFWML

>RXN03028 TRANSLATE of: rxn03028.seq check: 9204 from: 1 to: 2775
MFERFTDRARRVIVLAQEEARMLNHNYIGTEHILLGLIHEGEGVAAKALESMGISLDAVR
QEVEEIIGQGSQPTTGHIPFTPRAKKVLELSLREGLQMGHKYIGTEFLLLGLIREGEGVA
AQVLVKLGADLPRVRQQVIQLLSGYEGGQGGSPEGGQGAPTGGDAVGAGAAPGGRPSSGS
PGERSTSLVLDQFGRNLTQAAKDGKLDPVVGRDKEIERIMQVLSRRTKNNPVLIGEPGVG
KTAVVEGLALDIVNGKVPETLKDKQVYSLDLGSLVAGSRYRGDFEERLKKVLKEINQRGD
IILFIDEIHTLVGAGAAEGAIDAASLLKPKLARGELQTIGATTLDEYRKHIEKDAALERR
FQPVQVPEPSVDLTVEILKGLRDRYEAHHRVSITDGALTAAAQLADRYINDRFLPDKAVD
LIDEAGARMRIKRMTAPSSLREVDERIADVRREKEAAIDAQDFEKAAGLRDKERKLGEER
SEKEKQWRSGDLEDIAEVGEEQIAEVLANWTGIPVFKLTEAESSRLLNMEEELHKRIIGQ
DEAVKAVSRAIRRTRAGLKDPKRPSGSFIFAGPSGVGKTELSKALAGFLFGDDDSLIQID
MGEFHDRFTASRLFGAPPGYVGYEEGGQLTEKVRRKPFSVVLFDEIEKAHKEIYNTLLQV
LEDGRLTDGQGRIVDFKNTVLIFTSNLGTADISKAVGLGFSGSSETDSDAQYDRMKNKVH
DELKKHFRPEFLNRIDEIVVFHQLTKDQIVQMVDLLIGRVSNALAEKDMSIELTEKAKDL
LANRGFDPVLGARPLRRTIQREIEDQMSEKILFGEIGAGEIVTVDVEGWDGESKDTDRAK
FTFTPRPKPMPEGKFSEISVEAAEAIQDVDSAADGDVPETDSLSDIDLETLEKFEEDVEN
GTDIDQVSGDYYGTDDQGGTAPSKE

>RXN03036 TRANSLATE of: rxn03036.seq check: 4467 from: 1 to: 666
MAEQLRQFEGRVLPNQSEDLEDQGLGFDLGTVFSRRKVLGFIGVGGAGVALAACSPSGSS
AASSTSSASSSAAATTSAAAETLTEMKSETAGPYPGDGSNGPDVLEVSGVERQDITKSID
SDTVAEGVPLTLTMTILDMNNNNQPMEGAAVYVWHCDAPGRYSMYDSELEDETYLRGVQI
TDKYGQVTFDTIFPGCYAGRWVHIHFEVFPDRDSITDSTNNI

>RXN03077 TRANSLATE of: rxn03077.seq check: 553 from: 1 to: 1185
VMEIGVQVASWMDRHHDEVIKWRRHLHSHPELSHMEYRTTEYLASVLKDHGMEPHLFPGT
GLMVDIGPEGDSRLAFRADIDALPLLESTGLEFSSTATGVAHACGHDVHTVIALALACAL
NTIELPIGIRVIFQPAEEVMTGGATDVIAHGGLDGVDAIYAIHVEPKLKVGRVGVRAGAI
TSASDVIEIRVKGEGGHSARPHLSADVVYALSKLVVDLPGLLSRRVDPRTGTVLVFGTIN
AGYAPNAIPDSGIVSGTLRTADISTWRDMRPLISELVEQVLAPTGVTHELIYNPGVPPVL
NDDVATALLASAARDMDTQSVVQAPQSSGGEDFSWYLEHVPGSMARLGCWPGHGPKQDLH
QSDLVVDERAIGVGVRLFGSLVQQYSSRSEAFLNS

>RXN03088 TRANSLATE of: rxn03088.seq check: 1646 from: 1 to: 387
MGQTRIISGDARGRKIEVPPAGTRPTSDRAREGLFSSLQVRFGFEGQRVLDIFAGSGALG
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DPPYELATT

>RXN03091 TRANSLATE of: rxn03091.seq check: 9170 from: 1 to: 546
MLAKDSYTIKLTLDPDVQDAAHNAVSSHVDPTTPGVAEVVNVIEPGENSRDILAITSSRN
YGLDLDAGETMLPQATSRVGNGAGSIFKIFTAAAAIQQGAGLDTMLDVPSRYEVKGMGSG
GAANCPANTYCVENAGSYAPRMTLQDALAQSPNTAFVEMIEQVGVDTRCGSFSKAGPAKL
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>RXN03092 TRANSLATE of: rxn03092.seq check: 7622 from: 1 to: 885
VSTTNSLTKLVASTVAAGVLGALALVPFASLSGVAVARTNDTMQTNLSDLTDGRGPGVTT
ITDSTDQPIAYIYAQRRFEVGGDQISTSMKDAIVSIEDRRFYEHDGVDLQGFGRAILTNL
AAGGVEQGASTINQQYVKNFLLLVEADDEAEQAAAVETSIPRKLREMKMASDLEKTLSKD
EILTRYLNIVPFGNGAYGVEAAARTYFGTSAAELTIPQSAMLAGIVQSSSYLNPYTNHDA
VFERRNTVLGAMADAGAISPDEASAFQQEPLGVLETPQGLSNGCIGAGDRWFFLQ

>RXN03094 TRANSLATE of: rxn03094.seq check: 3583 from: 1 to: 1752

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LAEAKKLVASYPKASGANMANPNFNRDALNAFTAAQELAGELGDEYVSTEVLLAGIARGK
SDAADLLTNKGATYDAIKEAFPSVRGSQRVTTQDPEGQFQALEKYSTDLTKLAREGKIDP
VIGRDQEIRRVVQVLSRRTKNNPVLIGEPGVGKTAIVEGLARRIVAGDVPESLKGKTLIS
LDLGSMVAGAKYRGEFEERLKAVLDEIKGANGEVVTFIDELHTIVGAGASGESAMDAGNM
IKPLLARGELRLVGATTLNEYRKYIEKDAALERRFQQVYVGEPTVEDAIGILRGLKERYE
VHHGVRIQDSALVAAAELSNRYITSRFLPDKAIDLVDEAASRLRMEIDSSPQEIDELERI
VRRLEIEEMALSKESDAASKERLEKLRSELADEREKLSELKARWQNEKTAIDDVREMKEE
LEALRSESDIAKRDGNYCRVAKLRYGRIPELEKQIEDAESKVEVNENAMLTEEVTPDTIA
DVVSAWTGIPAGKMMQGETEKLLNMERVLGNRVVGQLESGNCSV

>RXN03128 TRANSLATE of: rxn03128.seq check: 7599 from: 1 to: 855
NGLAIPDIGFGVFQTPPDETRNSVNAALEAGYRHIDTAAAYGNEREVGEAIAASGIGRDE
ITIETKIWVTDYGFEETLHAFDKATGKLGVDTLDILILHQAVPSSFDRTIAAYKALEKLL
FDGAVRAIGVSNFMPEHLDKLLLETSIVPALNQIECHPYFQQRDVLARNEQLGILTQAWS
PIGGITFYRDGQLPSTLENEVIAGIAAEVGKTPAQVMLRWHLQRRRHAIPKSVTPSRIVE
NFEIFDFELSDEQLQQIDALNTDLRGGPEPENITMENYYREIPEA

>RXN03131 TRANSLATE of: rxn03131.seq check: 2811 from: 1 to: 273
MTTSVPASTKALSVAGENPGLRIGTAPDSWGVWFPEDPKQIPWERFLYEVVKAGYTWIEL
GPYGYLPTDANQLEDELGKRGLKLSAGTEFT

>RXN03133 TRANSLATE of: rxn03133.seq check: 1541 from: 1 to: 684
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LAKIGAVATWEKTLVDAASWAELPHPPVIVGDTPPSTVTPDNAWYQFRVGKHLGRDAFAE
IVMCLGHVFCHHVPQVWSTTCASQDADSTTMLIEAETAGALAIARVGGPTRRGGSFFGDA
LLKEGTPLPAGFRLDVVLHAASEIEDLLRGDTTAVVSGAWSVEDRRGY

>RXN03145 TRANSLATE of: rxn03145.seq check: 4840 from: 1 to: 447
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ENHIWVQATIRSGRTEKQKEELLLRLTQEIALILGIPNEEVWVYIPEIPGSNMTEYGRLL
MEPGEEEKWFNSLPEGLRERLTELEGSSE

>RXN03178 TRANSLATE of: rxn03178.seq check: 6627 from: 1 to: 801
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WGDNEGFQVWNDNALFMNDPDGIGGKTGYTDDANHTFVGGLDRGGRRLAAVLLDSTVSDI
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>RXN02021 TRANSLATE of: rxn02021.seq check: 9962 from: 1 to: 948
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PLSIGQNCNFGVSSGIIGVSLGDNCDIGNNIVLDGDTPIWFAADEELRTIDSIEGQANWS
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>RXC00110 TRANSLATE of: RXC00110.seq check: 7663 from: 1 to: 549
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AAIGGGAFSVAGVIALYSSFFFFFFVAALLSEWIKPWAAFLIVFLFMLVIAAALALFGWRKVKKMGAPK
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NVFAACAIHPTKADQLDGAARARLTQMAADPNCVAIGETGLDSYWIKHDPEDTAALDVQEEALRWHIDL
AISADKPLMIHNREADADLMRVLADAPPPKDTILHCFSSPLDVAKEALDRGYVLSFAGNVTFKRNEELR

EAARIAPISQILIETDAPYMTPEPFRGSRNEPSLIGHTALCIAEVRGMAVEDVAAALNENFDRVYGVTN
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>RXS00004 TRANSLATE of: RXS00004.seq check: 8907 from: 1 to: 471
VLTQLIESSIFDNVASRESSEFLGHAAIDLLAGLVYEKATPYAPDEALRVAVYGYIRENLGSSQLTVAA
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AKYGVPPAEFRRGYINSAA

>RXS00156 TRANSLATE of: RXS00156.seq check: 311 from: 1 to: 1110
MNERTSDAFDALLVLSFGGPEGHEEVRPFLENVTHGRGIPPERLDEVAVHYHHFGGISPINALNREIIA
NVEKELASRDHKLPVYFGNRNWKPFDNEAAEQMADDGVKNALVLATSAWGGYSGCRQYQEDIQGMIKHL
ESQGQSITFTKLRQFYDHPRFVSTMAQLVQDSYAKLPDELRDEARLVFTAHSIPLTADNAAGTPEDGSL
YSTQVKEASALIAEAVGVSDFDVVWQSRSGSPHTPWLEPDIVDHAVELNEKGQKALVVCPVGFISDHME
VIWDLDSELMEEAEKRNMVVERVATVGPTDEFAALVVDLIEEAELKRVIERLGKLPARGSSVNGAPCGD
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VELARGFGRVLDVGAGTGKLTSELTADQVLALDPSMDMLRVFRSALPAVPCWQATAEHTGIRDNAVDLI
TCAQTWHWVDVTAASAEFDRVIAPEGAVLLVWNNLDTSIAWVHRLSRIMHAGDVLKPGFTPETAAPWII
DREIRTTWNQHLTPEEIIQLAHTRSYWLNASEKIKERVDQNLQWYLYEHLGFSPDNPVELPYRCDAFLL
SRSGTLAGRSSNL

>RXS00197 TRANSLATE of: RXS00197.seq check: 7429 from: 1 to: 1212
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DIAGMTAQDELDPEDLPRAMYLKPWWQRIIVLSGGVIMNLIVGFLVLYGVAVSSGIPNPDVDTTATVDT
VQCVPETQISATELSSCVGSGPAGDAGIEHGDKILAVNGQEMASFTAIRDAILELPGETATLTIEREGT
LFDVDLQVASVTRLASDGSEITVGAVGMSSLPPTDVYKKYGPIEGVGATARFTGDMISATWDGLKAFPA
KIPGVVASIFGAERDVESPMSVVGAVRIGGEFVERSMWDMFMMMLASLNFFLALFNLVPLPPLDGGHIA
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PKILGFDAAGEVVAVGSQVTLFNVGDKVFYAGSNQRPGSNAEYQVVDERLVGHAPQSLGAHDAAALPLV
ALTAWESLFDRLGVTQSTTGTLLVLGGSGGVPSALIQLARALTGLKVVATASRPESQEWVTKLGAHEVI
DHSKDLSEQISDVDFVFSSWTTGREVELATLMKPQSHLVLIDDPVDPNLGAFKQKAIALHWEFMFTRAM
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>RXS00624 TRANSLATE of: RXS00624.seq check: 6054 from: 1 to: 687
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LNGFDQAVQGRRSEFANLERHEARLRLTGAIRQMQKIGFEFQIFAPPRWRMSEGTFAVLPEFDFNVAAS
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>RXS00949 TRANSLATE of: RXS00949.seq check: 7131 from: 1 to: 648
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AEAVERLIK

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VVAPSN

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TVTVGPHQINTLKGKALRDARGQIGMIFQGFNLSERSSVFQNVLVGRFAHTAWWRNLLGFPTEHDKQIA
FHALESVGILHKVWTRAGALSGGQKQRVAIARALSQDPSVMLADEPVASLDPPTAHSVMRDLENINNVE
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LPRTWLPMLETLQMALVGAVLSAAVSVPLTLWAAQATNTSAIGRGIVRTIINVVRSVPDLVYATILVAM
VGVGALPGILTLFLFNLGIVVKLVSEAIDSTEHPYMEAGRAAGGSQFQINRVSALPEVMPLFANQWLYT
LELNVRISAILGIVGAGGIGRLLDERRAFYAYADVSVIILEILIVVIVIEVISNALRKRLV

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DMQLRDRLAEARETAGGRNHPIPGGMIETAENLRREYGISREEQDKISAASQQRWGKAADAGLFDDEIV
PVTVPAKKRGQEPTIVSRDEHGRPGTTVEKLAALRPIMGRQDAEATVTAGNASGQNDGAAAVIVTTRAK
AEEKGLRPVMRLAGWSVAAVPPETMGIGPVPATKKVLDRLGLTLEDIGAIELNEAFAAQALSVLKEWNI
SWEDERVNPLGSGISMGHPVGATGARMAVTLAHRMQRENTQYGLATMCIGGGQGLAAVFEKEN

>RXS01205 TRANSLATE of: RXS01205.seq check: 7949 from: 1 to: 531
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SPIIVVLAAVAIPLLDLVMAVVRRVGRGASPFSPDKMHLHHRLLSIGHTHRRVVLVLYTWASAVAFGAV
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>RXS01223 TRANSLATE of: RXS01223.seq check: 5210 from: 1 to: 612
MTSVSFLSKIQALFAPKPELPAAKWLVVGLGNPGAKYESTRHNVGYMCQDMLIDAHQQQPLTPATGYKA
LTTQLAPGVLAVRSTTFMNHSGQGVAPIAAALGIPAERIIVIHDELDLPAGKVRLKKGGNENGHNGLKS
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>RXS01269 TRANSLATE of: RXS01269.seq check: 7324 from: 1 to: 441
VVFEMIKFRTMLEPDEKHVTDEQRLTKVGKLLRETSLDELPTLWNVFKGDMSLVGPRPLLVSYLEHYSS
EQARRHEVRPGITGLAQVNGRNQTTWDERLKLDVEYVDRCSLKLDFKILIATVKTVLSKKGISNEGHVT
MPSFIEERK

>RXS01421 TRANSLATE of: RXS01421.seq check: 1863 from: 1 to: 387
MTSKSISGKRPNLPSLTGARWLAALAVYFLHALVFLSVYPFQQSELFATIHKFVPMQLGSAGVTFFFIL
SGFLIYWSNSQLKGMKNVLYYCKRRITKIYPMHLIALPMFIEASAKFTTTGITWVLILRE

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MLDESLFPNSAKFSFIKTGDAVNLDHFHQLHPLEKALVAHSVDIRKAEFGDARWCAHQALQALGRDSGD
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PDSGIISIKQTSSYVRTREDSNVGTLSTLAESIHRALDSGAHVINISVVSCLPQSPDEAASFQPLTDAL
NRAELQGVIVVAAAGNLGQDCPVGSTVYPAHSDTVLSVSARFDSHTLAEYSMPGNQQILSAPSHIQAGL
SPRGDGFASHMITTAGESPFEGTSFAAPVVSATAALLRQHFPFATPYEIRARIFNSIDPARGAIDPYLA
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HMDDARIKYQRERLTPVISELNVDLVLGGHDHIYTRSHLMNGFTPVDAGREAVVGETLNPKAGEVVYLA
TNSSSGSKFYDFYDFQLGQRYDTGLDFQETVDQKKIRTYTAVWNQDQVQDYTNVELTPEGLTVTTKDAV
SGELVDQFTLSKQDRDEESEVPVEDDKDGDNATGSSNLGLAAILAPVLAIFGFVGGLFVGGGSLAEFFA
NLGVKMPF

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MKSIFISGAANGIGKAVALKFLHEGWLVGAYDLAEITYSHPNLRWGYLNVRQSESWDKALEDFATHTGG
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IAVYSASKFYVAGLTEALNLEWRKDDIRVVDVWPLWAKTDLVNGVKAKSLKRLGVRITPEQVAQAVWDA
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SAIDEAAEKLGGFDVLVNNAGIAQIKPLLEVTEEDLKQIYSVNVFSVFFGIQAASRKFDELGVKGKIIN
AASIAAIQGFPILSAYSTTKFAVRGLTQAAAQELAPKGHTVNAYAPGIVGTGMWEQIDAELSKINGKPI
GENFKEYSSSIALGRPSVPEDVAGLVSFLASENSNYITGQVMLVDGGMLYN

>RXS02485 TRANSLATE of: RXS02485.seq check: 7602 from: 1 to: 1101
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LVVADGDLDVIAVIIETDDVSINLTDGLLTADAGAVWDDVVHLSVDAGLGGIECLSGIPGSAGATPVQN
VGAYGTEVSDVLTRVQLLDRTTHQVSWVDASELDLSYRYSNLKFTNRAVVLAIELQLLTDGLSAPLRFG
ELGRRLAISEAEPHPRRPVRMVRDAVLELRRAKGMVVEHTDHDTWSAGSFFTNPIVDPALADAVFEKVG
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>RXS02539 TRANSLATE of: RXS02539.seq check: 6480 from: 1 to: 1518
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RSSQIDHNTVAYHFNEPIGVVGQIIPWNFPILMATWKLAPALAAGNAIVMKPAEQTPASILYLINIIGD
LIPEGVLNIVNGLGGEAGAALSGSNRIGKIAFTGSTEVGKLINRAASDKIIPVTLELGGKSPSIFFSDV
LSQDDAFAEKAVEGFAMFALNQGEVCTCPSRALVHESIADEFLELGVKRVQNIKLGNPLDTETMMGAQA
SQEQMDKISSYLKIGPEEGAQTLTGGKVNKVDGMENGYYIEPTVFRGTNDMRIFREEIFGPVLSVATFS
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IEQDAGTGRAIAYATDDVDAGAQVAQLIKSFGFVPLNIGALENGRILEPGQEAFGAHLNKDSRLELVNQ
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>RXS02560 TRANSLATE of: RXS02560.seq check: 4626 from: 1 to: 867
MQGNSLNLADNSERKKPMPSPGELLAARYGQPATWTPPQWNETLDVIHQHRSVRRWLDKPVDDDTIRTI
ISAAQSAGTSSNKQVISVIVVKDPELRKGLAGITRQMFPHLEQVPAVLIWLIDYSRISAVAAREDLPTG
ALDYLDEAAWGFLDAGIAAQNAAIAAESLGLGTLYLGSVRNDAEAVHKLLGLPPEIVPVVGLEMGHADP
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FYLVMPLLAWVLDRFGRPVRILLIVGGAVLSLAWPWIPLVEHALDEGWANMQIWPPAYACWFAVGMIAA
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DPQGLIAAGTKVAWCDAMGSYAQQVCVPRDRLVAVPEGVSSEVAASMLMQGITAHYLTNGVYELEEGDS
CLITAGAGGVGLLATQMAAAKGVRVYSVVSTDEKAELALDAGAYEVFRYSDNLAEQVRRHNGGRGVDVV
YDGVGQSTFNESLEAVRPRGTVCLFGAASGPVEPFDPQLLNTHGSIFLTRPSIGAWTSEEGEFAKRAQA
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SKLKGSRSLLDVGSGDHSFADLAGRQVAHVDVVDPLINTTFEEFQPTQSYDAITFIASLHHMNAEEGLN
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>RXS03061 TRANSLATE of: RXS03061.seq check: 2307 from: 1 to: 330V
SLTFPVINPSDGSTITELENHDSTQWMSALSDAVAAGPSWAAKTPRERSVVLTAIFEALTERAQELAEI
IHLEAGKSDAEALGEVAYGAEYFRWFAEEAVRLPGRYGQS

>RXS03119 TRANSLATE of: RXS03119.seq check: 3185 from: 1 to: 132
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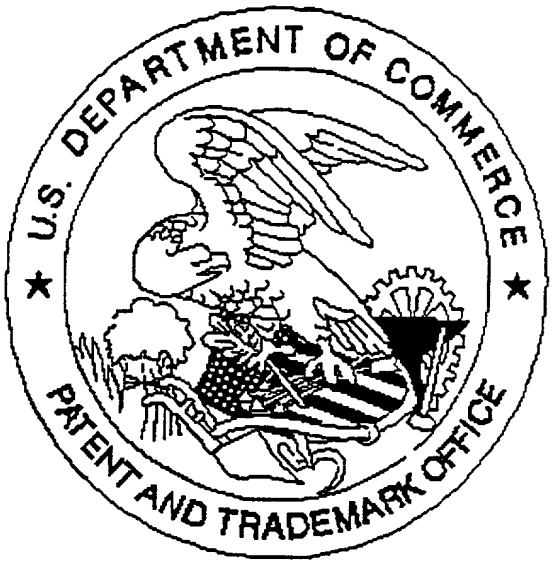
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YISQGKNAGARITVGGSRPRDLDAGFFVEPTVFADVDNRAAIAQDEIFGPVPSVVSYQDDEHAIQLAND
SEFGLGGTVWTSDPERGAALARRVHTGTIGINRYIPDPAAPFGGVKNSGLGRELGPEGLASYQETQTIY
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